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**METHODS FOR THE DIAGNOSIS AND TREATMENT
OF PREECLAMPSIA**

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METHODS FOR THE DIAGNOSIS AND TREATMENT OF PREECLAMPSIA

1. TECHNICAL FIELD

The present invention provides novel methods for the diagnosis of preeclampsia by determination of both lower and higher levels of proteins and/or polynucleotides or combinations thereof in patient tissue samples. Furthermore, it presents methods of treatment of preeclampsia through either inhibition of function of proteins or polynucleotides that are expressed higher in preeclampsia, or through replacement therapy of proteins or polynucleotides that are expressed lower in preeclampsia.

1.2 SEQUENCE LISTING

The sequences of the polynucleotides and polypeptides of the invention are listed in the Sequence Listing and are submitted on a compact disc containing the file labeled "821A.txt" – 4.69 MB (4,921,344 bytes) which was created on an IBM PC, Windows 2000 operating system on Thursday, April 1, 2004 at 12:22:06 PM. The Sequence Listing entitled "821A.txt" is herein incorporated by reference in its entirety. A computer readable format ("CRF") and two duplicate copies ("Copy 1" and "Copy 2") of the Sequence Listing "821A.txt" are submitted herein. Applicants hereby state that the content of the CRF and Copies 1 and 2 of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e), respectively, are the same.

2. BACKGROUND

Preeclampsia is a disorder complicating 5% of pregnancies in U. S. Moreover, it is the second major cause of maternal death in both U. S. and Japan, and is the leading cause of neonatal morbidity and mortality. It is a maternal disease, presenting with wide spectrum of symptoms, including hypertension, edema, proteinuria, fatigue, rapid weight gain, cardiac, pulmonary and renal failure. Pregnancy can further be complicated with hemolytic and liver manifestations, i. e. disease can progress into HELLP syndrome (Hemolysis, which is the breaking down of red blood cells, Elevated Liver enzymes, and Low Platelet count), or can progress into eclampsia, manifested by seizures and eventual death.

The fact that there is no effective predelivery treatment and that ultimately, the treatment of choice is delivery of the placenta, leads to two observations: First, there is a substantial lack of understanding of both etiology and pathophysiology of the disorder. Suggested treatments are

symptomatic and include seizure prophylaxis with use of magnesium sulfate, aspirin (generally unsuccessful), and prevention by increasing the dietary intake of calcium. Attempts of mapping the genes or loci involved have yielded no obvious success, leaving the root cause of the disorder unknown. Secondly, research on the subject of preeclampsia has revolved around placental growth and angiogenesis, as both are central to the etiology of the disease. Available evidence implicates the placenta in the maternal systemic effects seen in preeclampsia. Therefore, extracellular placental factor(s) secreted by the placenta are likely to be synthesized by the placenta and may be useful in the diagnosis and therapy of preeclampsia.

Several differentially-expressed genes have been previously examined for roles in both diagnosis and treatment of preeclampsia. Despite this fact, there remains no reliable diagnostic nor treatment for this disease. Thus, there exists a need in the art to identify and develop agents, such as peptides, nucleic acids, or antibodies that provide therapeutic compositions and diagnostic methods for treating and identifying preeclampsia.

3. SUMMARY OF THE INVENTION

This invention is based on the discovery that SEQ ID NO: 1-852 encode nucleotides that are either up-regulated or down-regulated in preeclamptic placenta as compared to control placenta. SEQ ID NO: 853-1704 comprise the protein or protein fragments encoded by the nucleotide sequences of SEQ ID NO: 1-852.

The invention provides therapeutic and diagnostic methods for targeting tissue or tissue samples expressing SEQ ID NO: 853-1704 by using diagnostic, therapeutic, or targeting elements such as SEQ ID NO: 853-1704 polypeptides, and nucleic acids encoding said SEQ ID NO: 853-1704 polypeptides. SEQ ID NO: 1-852 exhibit differential expression profiles in preeclamptic placental tissue samples as compared to healthy placental tissues (see Examples, specifically 3 and 11). Thus, detection of expression levels of these genes individually or in combination will provide a means through which to detect preeclampsia during pregnancy. Additionally, genes that exhibit lower expression in preeclamptic tissues as compared to healthy tissues provide a means through which a patient experiencing preeclampsia may be treated therapeutically, as replacement therapy with these gene products individually or in combination may ameliorate signs or symptoms of the disease. Furthermore, genes that exhibit higher expression in preeclamptic tissues as compared to healthy tissues provide a means through which a patient experiencing preeclampsia may be treated

therapeutically, as targeting of these genes in order to decrease the effect of their overexpression may ameliorate signs or symptoms of the disease.

The present invention provides a variety of diagnostic elements and compositions. One such embodiment is a diagnostic kit comprising antibody preparation that is specific for SEQ ID NO: 853-1704. The kit would be utilized to detect levels of any of the polypeptides of SEQ ID NO: 853 through 1704 that are differentially expressed in tissues derived from preeclamptic patients as compared to a normal range of expression derived from healthy patients. Exemplary diagnostic antibodies include a single antibody selective for a polypeptide of the invention, a combination of 2 or more such antibodies of the invention, and a combination of at least one such antibody of the invention with an antibody that does not recognize a polypeptide of the invention. Such a kit includes a standard for any of SEQ ID NO: 853-1704 indicative of a higher risk of diagnosis of preeclampsia. Exemplary tissues subject to this diagnostic kit include serum, plasma, urine, vaginal mucous, amniotic fluid, and fetal and/or maternal cells.

Another diagnostic embodiment of the invention is a kit comprising a protein chip for quantification of levels of SEQ ID NO: 853-1704 in biological samples. Such a chip is a solid surface array with specific chemical (e.g. anion, cation, hydrophobic, hydrophilic, metal) or biochemical (e.g. antibody, receptor, DNA, enzyme) moiety precoated on the surface. The chemical moieties are designed to capture and recognize whole classes of polypeptides from a tissue sample, while the biochemical moieties are designed to capture and recognize specific polypeptide sequences.

Another diagnostic embodiment of the invention is a kit comprising one or more polynucleotide sequences of SEQ ID NO: 1-852 coupled to a surface. Polynucleotides derived from the messenger RNA (mRNA) from fetal cells or maternal tissues will be hybridized to the surface-coupled polynucleotides of any of SEQ ID NO: 1-852. The kit will be utilized to detect differentially-expressed levels of one or more of the polynucleotides of SEQ ID NO: 1-852 in fetal cells or placental tissues derived from preeclamptic patients, as compared to a normal range of expression derived from healthy patients. Such a kit includes a standard for any of SEQ ID NO: 1-852 indicative of a higher risk of diagnosis of preeclampsia. An exemplary source of fetal cells or placental tissues is from cells or tissues shed into the maternal blood, and maternal cells as well.

The present invention provides for compositions that can be utilized for replacement therapeutics in order to ameliorate the signs and symptoms of preeclampsia wherein one or more of the genes set forth in SEQ ID NO: 1-852 are down-regulated in preeclampsia. One such

embodiment is a composition comprising one or more isolated polypeptides that include, but are not limited to, a polypeptide comprising the polypeptide sequence set forth in SEQ ID NO: 853-1704; or a fragment of SEQ ID NO: 853-1704. This embodiment further includes amelioration of the signs or symptoms of preeclampsia via administration of one or more of the polypeptides of SEQ ID NO: 853-1704 and a pharmaceutically acceptable carrier.

Another embodiment of the invention is a composition comprising one or more isolated polynucleotides that include, but are not limited to, a polynucleotide comprising the polynucleotide sequence set forth in SEQ ID NO: 1-852; or a fragment of SEQ ID NO: 1-852; or a full length coding sequence SEQ ID NO: 1-852. This embodiment further includes amelioration of the signs or symptoms of preeclampsia via administration of one or more of the polynucleotides of SEQ ID NO: 1-852 and a pharmaceutically acceptable vector for delivery of a functional gene corresponding to polynucleotides of SEQ ID NO: 1-852, wherein the loss of normal function of the corresponding gene has been observed through diagnostics.

The present invention provides for targeting elements and compositions for genes expressed at higher levels in preeclamptic tissues than healthy. One such embodiment is a composition comprising an antibody preparation selective for a polypeptide of SEQ ID NO: 853-1704. Exemplary therapeutic antibodies include a single such antibody of the invention, a combination of two or more such antibodies of the invention, a combination of at least one antibody of the invention with an antibody that does not recognize a polypeptide of the invention, humanized antibodies that retain all or a portion of antigen-binding sites of said antibody or complementarity-determining regions (CDR) that recognize SEQ ID NO: 853-1704, Fab antibodies or fragments thereof, including a fragment of an antibody that retains one or more CDRs that recognize SEQ ID NO: 853-1704, and antibody fusion proteins that recognize a polypeptide of the invention.

Another targeting embodiment of the invention is a vaccine comprising a polypeptide of the invention, or a fragment or variant thereof and optionally comprising a suitable adjuvant.

4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the expression ratios of SEQ ID NO: 357 to SEQ ID NO: 551 relative to each other, using a real-time PCR protocol (TaqMan assay). The raw cycle count scores for each gene in the measured tissues were selected, with each score representing the number of doublings required to detect the message. The inverse expression ratios were computed for each gene in each measured tissue using the following formula:

(2 raised to the power of the SEQ ID NO: 347 raw cycle count score)
divided by (2 raised to the power of the SEQ ID NO: 551 raw cycle
count score).

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5. DETAILED DESCRIPTION OF THE INVENTION

The development of the human fetus depends on the ability of trophoblast cells to invade the maternal tissues in order to anchor the placenta and fetus to the maternal endometrium and to gain access to, and control of, the maternal circulation. Human haemochorial placentation involves proliferation, migration and invasion of the endometrium and its vasculature by trophoblast cells (extravillous trophoblast, EVT). A completion of remodeling of uteroplacental arteries, which is dependent on trophoblast invasion, appears to provide a means of unhindered placental perfusion with maternal blood. Poor placental perfusion in a hypoinvasive placenta of preeclampsia is believed to impede fetal growth and thus affect fetal well being in some cases.

The pathophysiology of preeclampsia is poorly understood. Two stages of vascular dysfunction seem to be involved. In the early stage suboptimal development of the placenta and a hemodynamic maladaptation to pregnancy exist. At this stage maternal constitutional factors such as genetic and immunological factors and preexisting vascular diseases could play a role. However, no causal relationship has yet been proven. Extracellular placental factor(s), supposedly under the influence of ischemia due to defective placentation, may be responsible for the development of the preeclampsia condition rather than preeclampsia being a simple consequence of improper placentation. Thus, these factors may cause late vascular dysfunction characterized mainly by a generalized endothelial dysfunction, thus leading to the clinical presentation of preeclampsia.

There are three distinct regions of the maternal-fetal interface, any or all of which may be involved in the clinical manifestation of preeclampsia pregnancy disorder. It has been demonstrated that there is differential gene expression of some growth factors and their receptors between these regions in normal and preeclamptic pregnancy, and thus their spatial and temporal regulation is suggested in pregnancy disorders. The compositions of the present invention are based on an analysis of tissues from the maternal-fetal interface including 2 different areas of the placental bed: the basal plate (deciduas basalis) and marginal zone (deciduas marginalis) as well as trophoblastic villi (see Examples 1-2).

The deciduas basalis is the portion of the maternal endometrium that participates with the chorion in the formation of the placenta at the site of implantation. The invasive function of the

trophoblast cells is achieved by two distinctive pathways: 1) the villous pathway, in which cytotrophoblast cells proliferate and fuse, giving rise to the syncytiotrophoblast layer of the floating villi, which is engaged primarily in exchange and endocrine functions; and 2) the extravillous pathway, in which certain cytotrophoblast cells break out of the villi as discrete cell columns, migrate and invade the decidua and its vasculature. These “extravillous trophoblast cells” (EVT) are highly proliferative and invasive. In the placental bed, these cells segregate into several subsets. Of high importance are endovascular EVTs, which replace the endothelium (maternal blood vessel lining) of the uteroplacental arteries during the process of remodeling (endovascular invasion). Poor EVT cell invasion and remodeling of uteroplacental arteries are key features of preeclampsia, whereas uncontrolled invasion is a feature of trophoblastic neoplasias including choriocarcinomas.

The decidua marginalis represents the lateral part of the placenta, responsible for the lateral placental growth.

The trophoblast villi is from the middle area of placental body represent fetal placental pathology and could provide valuable information about placental development. Moreover, the analysis of molecular pathophysiology of this region could indicate abrogated functions in pregnancy disorders.

This invention is based on the discovery that SEQ ID NO: 1-852 encode nucleotides that are either up-regulated or down-regulated in preeclamptic placenta as compared to control placenta. SEQ ID NO: 853-1704 comprise the protein or protein fragments encoded by the nucleotide sequences of SEQ ID NO: 1-852

5.1 Definitions

It must be noted that as used herein and in the appended claims, the singular forms “a”, “an” and “the” include plural references unless the context clearly dictates otherwise.

The term “active” refers to those forms of the polypeptide that retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms “biologically active” or “biological activity” refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise “biologically active” or “biological activity” refers to the capability of the natural, recombinant or synthetic polypeptide of the invention, or any peptide thereof, to induce a specific biological response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

5 The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the
10 hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers
15 to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult
20 specialized organs, but are able to regenerate themselves. The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism. The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

25 The term "expression modulating fragment," EMF, means a series of nucleotides that modulates the expression of an operably linked ORF or another EMF. As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs is nucleic acid
30 fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences, A is adenine, C is cytosine, G is guanine, and T is thymine, while N is A, T, G, or C. It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequence herein may be replaced with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to a portion of SEQ ID NO: 1-852.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh *et al.* (Walsh, P.S. *et al.*, *PCR Methods Appl.* 1:241-250 (1992)). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. *et al.*, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY; or

Ausubel, F.M. *et al.*, 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from any of the nucleic acid sequences of SEQ ID NO: 1-852. The sequence information can be a segment of SEQ ID NO: 1-852 that uniquely identifies or represents the sequence information of SEQ ID NO: 1-852. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1 \div 4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms “polypeptide” or “peptide” or “amino acid sequence” refer to an oligopeptide, peptide, polypeptide, or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide “fragment,” “portion,” or “segment” is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term “naturally occurring polypeptide” refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term “translated protein coding portion” means a sequence which encodes for the full length protein which may include any leader sequence or a processing sequence.

The term “mature protein coding sequence” refers to a sequence which encodes a peptide or protein without any leader/signal sequence. The “mature protein portion” refers to that portion of the protein without the leader/signal sequence. The peptide may have the leader sequences removed during processing in the cell or the protein may have been produced synthetically or using a polynucleotide only encoding for the mature protein coding sequence. It is contemplated that the mature protein portion may or may not include an initial methionine residue. The initial methionine is often removed during processing of the peptide.

The term “derivative” refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term “variant” (or “analog”) refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid

sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other components normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. *Cytokine* 4:134-143 (1992)) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. *et. al. Annu. Rev. Immunol.* 16:27-55 (1998)).

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1× SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2× SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6× SSC/0.05% sodium pyrophosphate at 37°C (for 14-

base oligonucleotides), 48°C (for 17-base oligonucleotides), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequence of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J. *Methods Enzymol.* 183:626-645 (1990)). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term

"transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

5.2 Nucleic Acids of the Invention

The invention is based on the discovery of differentially-expressed polynucleotides in pre-eclamptic versus normal placental tissues, the polynucleotides encoding corresponding polypeptides and the use of these compositions for the diagnosis, treatment or prevention of preeclampsia.

The isolated polynucleotides of the invention include, but are not limited to a polynucleotide comprising any of the nucleotide sequences of SEQ ID NO: 1-852; a fragment of SEQ ID NO: 1-852; a polynucleotide comprising the full length protein coding sequence of SEQ ID NO: 1-852 (for example coding for SEQ ID NO: 853 through 1704); and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO: 853-1704. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-852; (b) a polynucleotide encoding any one of the polypeptides of SEQ ID NO: 853-1704; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 853-1704. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains;

domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-852 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-852 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-852 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more typically at least about 90%, 91%, 92%, 93%, or 94% and even more typically at least about 95%, 96%, 97%, 98% or 99% sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-852, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e.

specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

5 The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1-852, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-852 with a sequence from another isolate of the same species.
10 Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor result for the nucleic acids or polypeptides of the present invention,
15 including SEQ ID NO: 1-852, and SEQ ID NO: 853-1704 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)).

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also
20 provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally occurring alternative forms of the isolated polynucleotide that also encode proteins
25 which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the
30 location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ

in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, *e.g.*, by substituting first with conservative choices (*e.g.*, hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (*e.g.*, hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, NY (1989), and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which

encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those that are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

5 Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or
10 synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences, coding for any one of SEQ ID NO: 853-1704, or functional equivalents thereof,
15 may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al.
20 (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication
25 functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

30 The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-852 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present

invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-852 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably
5 linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44,
10 PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia/Pfizer).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also
15 known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and
25 promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-
30 phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of

translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), hereby incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that can hybridize to, or are complementary to, the nucleic acid molecules comprising SEQ ID NO: 1-852, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to

the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand of SEQ ID NO: 1-852, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of SEQ ID NO: 1-852 or antisense nucleic acids complementary to SEQ ID NO: 1-852 nucleic acid sequences of are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding like protein of any of SEQ ID NO: 1-852. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "conceding region" of the coding strand of a nucleotide sequence encoding the proteins of SEQ ID NO: 853-1704. The term "conceding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the polypeptides of SEQ ID NO: 853-1704 disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SEQ ID NO: 1-852-like mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of said mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SEQ ID NO: 1-852-like mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-

isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polynucleotide or polypeptide of the invention to thereby inhibit expression of the protein (e.g., by inhibiting transcription and/or translation). The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an alpha-anomeric nucleic acid molecule. An alpha-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual alpha-units, the strands run parallel to each other. See, e.g., Gaultier, et al., 1987. Nucl. Acids Res. 15: 6625-6641. The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (see, e.g., Inoue, et al.

1987. Nucl. Acids Res. 15: 6131-6148) or a chimeric RNA-DNA analogue (see, e.g., Inoue, et al., 1987. FEBS Lett. 215: 327-330.

Nucleic acid modifications include, by way of non-limiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they can be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach 1988. Nature 334: 585-591) can be used to catalytically cleave mRNA transcripts corresponding to SEQ ID NO: 1-852 to thereby inhibit translation of said mRNA. A ribozyme having specificity for SEQ ID NO: 1-852-like-encoding nucleic acid can be designed based upon the nucleotide sequence of a corresponding cDNA disclosed herein. For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in SEQ ID NO: 1-852-like encoding mRNA. See, e.g., U.S. Patent 4,987,071 to Cech, et al. and U.S. Patent 5,116,742 to Cech, et al. mRNA corresponding to SEQ ID NO: 1-852 can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, SEQ ID NO: 1-852 gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the said nucleic acids (e.g., the promoter and/or enhancers of each gene corresponding to the polynucleotide of the invention) to form triple helical structures that prevent transcription of the genes in target cells. See, e.g., Helene, 1991. Anticancer Drug Des. 6: 569-84; Helene, et al. 1992. Ann. N.Y. Acad. Sci. 660: 27-36; Maher, 1992. Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids. See, e.g., Hyrup, et al., 1996. Bioorg Med Chem 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (e.g., DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide

backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, et al., 1996. *supra*; Perry-O'Keefe, et al., 1996. *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

PNAs of the nucleic acids of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the nucleic acids of the invention can also be used, for example, in the analysis of single base pair mutations in a gene (e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (see, Hyrup, et al., 1996.*supra*); or as probes or primers for DNA sequence and hybridization (see, Hyrup, et al., 1996, *supra*; Perry-O'Keefe, et al., 1996. *supra*).

In another embodiment, PNAs of nucleic acids of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of the nucleic acids of the invention can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (e.g., RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (see, Hyrup, et al., 1996. *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, et al., 1996. *Supra*, et al., 1996. *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. See, e.g., Mag, et al., 1989. *Nucl Acid Res* 17: 5973-5988. PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. See, e.g., Finn, et al., 1996. *supra*. Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, e.g., Petersen, et al., 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger, et al., 1989. Proc. Natl. Acad. Sci. U.S.A. 86: 6553-6556; Lemaitre, et al., 1987. Proc. Natl. Acad. Sci. 84: 648-652; PCT Publication No. WO88/09810) or the blood-
5 brain barrier (see, e.g., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, e.g., Krol, et al., 1988. BioTechniques 6:958-976) or intercalating agents (see, e.g., Zon, 1988. Pharm. Res. 5: 539-549). To this end, the oligonucleotide can be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

10

5.3 Use of nucleic acids as probes

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO: 1-852. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-852 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, *in situ* hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include *in situ* hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent *in situ* hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic

disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

5.4 Preparation of Support Bound Oligonucleotides

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, 1990 J. Clin Microbiol 28(6) 1462-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, Mol. Cell Probes 1989 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci USA 91(8) 3072-6 describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Alternatively, DNA may be covalently bound to the microwell surface using CovaLink NH technology (Nunc Laboratories, Naperville, IL). CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal Biochem 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen *et al.*, 1991, Ann Biol Clin (Paris). 1990;48(9):647-50). In this technology, a phosphoramidate bond is employed (Chu *et al.*, 1983 Nucleic Acids 11(18) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have

a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A single stranded DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), hereby incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, hereby incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal Biochem 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) Proc. Natl. Acad. Sci USA 91(11) 5022-6. These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes

(DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

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5.5 Preparation of Nucleic Acid Fragments

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

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DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

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The nucleic acids are then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6. In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

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One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, *Cvi*JI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

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The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76

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clones showed that *CviJI*** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

5.6 Preparation of DNA Arrays

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

5.7 Polypeptides of the Invention

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequence set forth as any one of SEQ ID NO: 853-1704 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-852 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-852 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO: 853-1704 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO: 853-1704 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, or 89%, more typically at least about 90%, 91%, 92%, 93%, or 94% and even more typically at least about 95%, 96%, 97%, 98% or 99%, most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 853-1704.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer. Chem. Soc.* 114, 9245-9253 (1992), both of which are hereby incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part

or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which it is expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

5 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid
10 fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or
15 conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in
20 immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells that have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or
25 which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell that produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a
30 culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector

that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells that naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, High Performance Liquid Chromatography (HPLC), size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays that are well known in the art to identify molecules that bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO: 853-1704.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or

deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program or the Pfam program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), hereby incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or

Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

5.8 Determining Polypeptide and Polynucleotide Identity and Similarity

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, hereby incorporated herein by reference), the eMatrix software (Wu et al., J. Comp. Biol., vol. 6, pp. 219-235 (1999), hereby incorporated herein by reference), eMotif software (Nevill-Manning et al, ISMB-97, vol 4, pp. 202-209, hereby incorporated herein by reference), the GeneAtlas software (Accelrys, Inc. San Diego, CA) (Sanchez and Sali (1998) Proc. Natl. Acad. Sci., 95, 13597-13602; Kitson DH et al, (2000) "Remote homology detection using structural modeling – an evaluation" Submitted; Fischer and Eisenberg (1996) Protein Sci. 5, 947-955), and the Kyte-Doolittle hydrophobicity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), hereby incorporated herein by reference). The BLAST programs are publicly available from the National Center for

Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

5.9 Chimeric and Fusion Proteins

The invention also provides chimeric or fusion proteins of the polypeptides of the invention.

5 As used herein "chimeric protein" of the polypeptides of the invention or "fusion protein" of the polypeptides of the invention comprises a polypeptide of the invention operatively linked to a polypeptide not of the invention. A "polypeptide not of the invention" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the polypeptides of the invention, e.g., a protein that is different from the polypeptide or polypeptides of
10 the invention in question and that is derived from the same or a different organism. Within a fusion protein of the polypeptides of the invention the polypeptide of the invention can correspond to all or a portion of a polypeptide of the invention. In one embodiment, a fusion protein of the polypeptide of the invention comprises at least one biologically active portion of a polypeptide of the invention. In another embodiment, a fusion protein of the polypeptide of the invention comprises at least two
15 biologically active portions of a polypeptide of the invention. In yet another embodiment, a fusion protein of the polypeptide of the invention comprises at least three biologically active portions of a polypeptide of the invention. Within the fusion protein, the term "operatively-linked" is intended to indicate that the polypeptide of the invention and the polypeptide not of the invention are fused in-frame with one another. The polypeptide not of the invention can be fused to the N-terminus or C-
20 terminus of polypeptide of the invention.

In one embodiment, the fusion protein is a GST-fusion protein of the polypeptides of the invention in which the polypeptide of the invention sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant polypeptides of the invention. In another embodiment, the fusion protein is a
25 polypeptide of the invention containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of the polypeptides of the invention can be increased through use of a heterologous signal sequence.

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein of the polypeptide of the invention in which the sequences corresponding to the polypeptides of the
30 invention are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the polypeptides of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between ligand

that is a polypeptide of the invention and a polypeptide of the invention on the surface of a cell, to thereby suppress signal transduction in vivo mediated by polypeptides of the invention. The immunoglobulin fusion proteins of the polypeptides of the invention can be used to affect the bioavailability of a polypeptide of the invention cognate ligand. Inhibition of the polypeptide of the invention ligand/polypeptide of the invention interaction can be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g. promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the polypeptides of the invention can be used as immunogens to produce anti-polypeptides of the invention-like antibodies in a subject, to purify ligands to the polypeptides of the invention, and in screening assays to identify molecules that inhibit the interaction of polypeptides of the invention with ligands for the polypeptide of the invention.

Chimeric or fusion protein of the polypeptides of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, e.g., Ausubel, et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polynucleotide or polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

5.10 Hosts

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a

regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by methods well-known to those of skill in the art, for example calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., Basic Methods in Molecular Biology (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated herein by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion

chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical
5 disruption, or use of cell lysing agents.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro
10 culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of
15 expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known
20 chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to
25 replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or
30 protein produced may be replaced, removed, added, or otherwise modified by targeting, including polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or

modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

5.11 Gene Therapy

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g.,

liposomes or chemical treatments). See, for example, Anderson, *Nature*, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, *Science*, 244: 1275-1281 (1989); Verma, *Scientific American*: 68-84 (1990); and Miller, *Nature*, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron

DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose

include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

5.12 Antibodies

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen-binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 853-1704, or designated in Tables from Examples 2, 4, and 5 and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred

epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a surface region of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828 (1981); Kyte and Doolittle, *J. Mol. Biol.* 157: 105-142 (1982), each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

The terms “specific for” and “selective for” indicate that the variable regions of the antibodies of the invention recognize and bind polypeptides of the invention exclusively (*i.e.*, able to distinguish the polypeptide of the invention from other similar polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow *et al.* (Eds), *Antibodies A Laboratory Manual*; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, full-length polypeptides of the invention. As with antibodies that are specific for full length polypeptides of the invention, antibodies of the invention that recognize fragments are those which can distinguish polypeptides from the same family of polypeptides despite inherent sequence identity, homology, or similarity found in the family of proteins.

Antibodies of the invention are useful for, for example, therapeutic purposes (by modulating activity of a polypeptide of the invention, or immunotargeting cells expressing said polypeptide of the invention to induce cell death or targeting by the immune system), diagnostic purposes to detect or quantitate a polypeptide of the invention, as well as purification of a polypeptide of the invention.

5 Kits comprising an antibody of the invention for any of the purposes described herein are also comprehended. In general, a kit of the invention also includes a control antigen for which the antibody is immunospecific. The invention further provides a hybridoma that produces an antibody according to the invention. Antibodies of the invention are useful for detection and/or purification of the polypeptides of the invention.

10 Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be
15 useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the polypeptide of interest is expressed. The antibodies may also be used directly in therapies or other diagnostics. The present invention
20 further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and Sepharose®, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10
25 (1986); Jacoby, W.D. *et al.*, Meth. Enzym. 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immuno-affinity purification of the proteins of the present invention.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments,
30 analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.12.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface-active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, *etc.*), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants that can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.12.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen-binding site

capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized *in vitro*.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent

assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

5 After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown *in vivo* as ascites in a mammal.

10 The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention
15 can be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host
20 cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, *Nature* 368:812-13 (1994)) or by covalently
25 joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.12.3 Humanized Antibodies

30 The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered

immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones *et al.*, *Nature*, 321:522-525 (1986); Riechmann, *et al.*, *Nature*, 332:323-327 (1988); Verhoeyen, *et al.*, *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539). In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, 1986; Riechmann *et al.*, 1988; and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)).

5.12.4 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies" or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, *Immunol Today* 4: 72 (1983)) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, *Proc Natl Acad Sci USA* 80: 2026-2030 (1983)) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks *et al.*, *J.*

Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks *et al.* (*Bio/Technology* 10,:779-783 (1992)); Lonberg *et al.* (*Nature* 368:856-859 (1994)); Morrison (*Nature* 368:812-13 (1994)); Fishwild *et al.*, (*Nature Biotechnology*, 14:845-51 (1996)); Neuberger (*Nature Biotechnology*, 14:826 (1996)); and Lonberg and Huszar (*Intern. Rev. Immunol.* 13:65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being

effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.12.5 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, *Science* 246:1275-1281 (1989)) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.12.6 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full-length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in

the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, *J. Immunol.* 148:1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, *J. Immunol.* 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an

immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.12.7 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.12.8 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff *et al. Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.12.9 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), *momordica charantia* inhibitor, curcin, crotin, *sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

5.13 Assays for Detection of Polypeptides and Polynucleotides of the Invention

5.13.1 Sample Collection and Processing

The polypeptides of the invention individually or in combination are preferably quantified in a biological sample obtained from a patient. In the same manner, polynucleotides of the invention individually or in combination are preferably quantified in a biological sample obtained from a patient. As used herein, a biological sample is a sample of biological tissue or fluid that contains a concentration of any of the polypeptides or polynucleotides of the invention that may be correlated with blood or tissue levels of any of the polypeptides or polynucleotides of the invention. Particularly preferred biological samples include blood serum (blood lacking a cellular component and clotting factors), blood plasma (blood lacking a cellular component), urine, cervicovaginal mucous, amniotic fluid, or fetal cells.

In one preferred embodiment, the polypeptides of the invention individually or in combination are quantified in whole blood or blood derivatives such as blood plasma or blood serum. Said samples are isolated from a patient according to standard methods well known to those of skill in the art, including venipuncture. After blood isolation from the patient, the blood sample may either be pretreated by dilution in an appropriate buffer solution, or be concentrated. Any of a number of standard aqueous buffer solutions at physiological pH may be employed, including phosphate, Tris, or others. Means of preparing blood serum or blood plasma are well known to those skilled in the art and typically involve centrifugation or filtration to produce blood plasma, or clotting followed by centrifugation or filtration to produce blood serum. Blood plasma or serum may be diluted by the addition of buffers or other reagents well known to those of skill in the art, and may be stored for up to 24 hours at 2-8 °C, or at -20 °C or lower for longer periods, prior to measurement of any of the polypeptides of the invention individually or in combination.

In another preferred embodiment, any of the polynucleotides of the invention individually or in combination are quantified from cells present in the amniotic fluid. Said samples are isolated from the pregnant patient according to standard methods well known to those of skill in the art, including amniocentesis. Preferably within the second trimester of pregnancy, a thin, hollow needle is inserted from the abdomen through the uterus into the amniotic sac. A small amount (approximately 1 or 2 tablespoons) of amniotic fluid is withdrawn, with the needle then being removed. Subsequently, living cells from the withdrawn amniotic fluid are cultured for approximately two weeks before quantification of expression of any of the polynucleotides of the invention individually or in combination.

In another preferred embodiment, any of the polypeptides of the invention individually or in combination are quantified from vaginal mucous. Cervicovaginal mucous is removed from an area within the vaginal cavity such as the posterior fornix, cervical canal, or uterine cavity. The sample is removed with a swab having a fibrous tip, aspirator, suction device, lavage device or the like and transferred to a suitable container for storage and transport to the testing laboratory. It is important that the sample be dispersed in a liquid that preserves the sensitive protein analytes such as any of the polypeptides of the invention which may be unstable in the sampled composition. The storage and transfer medium should prevent decline in the protein analyte level during storage and transfer. One example of a suitable preserving solution for storage and transfer consists of 0.05M Tris-HCL, pH 7.4; 0.15M NaCl, 0.02% NaN₃, 1% BSA, 500 Kallikrein Units/mL aprotinin, 1 mM phenylmethylsulfonyl fluoride (PMSF) and 5 mM EDTA.

In another preferred embodiment, any of the polypeptides of the invention individually or in combination are quantified from a sample of urine from a patient during pregnancy. The sample can be taken from any time of day, but preferably from the first morning void. One example of urine specimen collection and storage includes having the patient void into a plastic urine specimen container, and then immediately storing the container with the urine sample at 2 to 30 °C until testing. If the sample is to be stored for longer than 30 days, then it should be frozen between -20 and -70 °C until testing.

In another preferred embodiment, any of the polynucleotides of the invention individually or in combination are quantified from a sample of fetal cells and/or maternal cells derived from maternal blood. Fetal cell isolation from samples of maternal blood is achieved using any number of well- recognized detection and isolation techniques. (See for example *Clin Chem Lab Med.* 2002 Feb;40(2):126-31, *Int J Mol Med.* 2002 Sep;10(3):257-61, *Cytometry.* 2001 Dec 1;45(4):267-76, and *Expert Rev Mol Diagn.* 2002 Jul;2(4):303-11 which are hereby incorporated by reference). Isolation of maternal blood cells is well-known to those of skill in the art.

5.13.2 Quantification of the Polypeptides of the Invention

Any of the polypeptides of the invention individually or in combination may be detected and quantified by any of a number of means well known to those of skill in the art. These may include analytic biochemical methods such as electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, by surface-enhanced laser desorption/ionization (SELDI), and the like, or various immunological methods such as fluid or gel precipitation reactions, immunodiffusion (single or double),

immuno-electrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, western blotting, and the like.

As used herein, an immunoassay is an assay that utilizes an antibody to specifically bind to the analyte. The immunoassay is characterized by the use of specific binding to a particular antibody as opposed to other physical or chemical properties to isolate, target, and quantify the analyte.

5.13.3 Immunological Binding Assays

In a preferred embodiment, any of the polypeptides of the invention individually or in combination may be detected and quantified using any of a number of well-recognized immunological binding assays. (See for example, U.S. Patent No 5,712,103 hereby incorporated herein by reference.) For a review of the general immunoassays, see also *Methods in Cell Biology Volume 37: Antibodies in Cell Biology*, Asai, ed. Academic Press, Inc. N.Y. (1993); *Basic and Clinical Immunology* 7th Edition, Stites & Terr, eds. (1991), which are hereby incorporated herein by reference.

Immunological binding assays (or immunoassays) typically utilize a “capture agent” to specifically bind to and often immobilize the analyte (in this case any of the polypeptides of the invention). The capture agent is a moiety that specifically binds to the analyte. In a preferred embodiment, the capture agent is an antibody that specifically binds one of the polypeptides of the invention.

The antibody may be provided by any of a number of means well known to those of skill in the art (see, for example *Methods in Cell Biology* Vol. 37: *Antibodies in Cell Biology*, Asai, ed. Academic Press, Inc. N.Y. (1993); and *Basic and Clinical Immunology* 7th Edition, Stites & Terr, eds. (1991), which are hereby incorporated herein by reference). The antibody may be a whole antibody or an antibody fragment. It may be polyclonal or monoclonal, and it may be produced by challenging an organism (e.g. mouse, rat, rabbit, etc.) with any of the polypeptides of the invention or an epitope derived therefrom. Alternatively, the antibody may be produced *de novo* using recombinant DNA methodology (e.g. DNA vaccination) and any of the polynucleotides of the invention in full-length gene form or a fragment derived therefrom. Additionally, antibodies that specifically bind any of the polypeptides of the invention may be produced using standard methods well-known to those of skill in the art, or may be obtained commercially.

Immunoassays also often utilize a labeling agent to specifically bind to and label the binding complex formed by the capture agent and the analyte. The labeling agent may itself be one of the moieties comprising the antibody/analyte complex. Thus, the labeling agent may be a labeled version of any of the polypeptides of the invention or a labeled antibody selectively recognizing any of the polypeptides of the invention. Alternatively, the labeling agent may be a third moiety, such as another antibody, that specifically binds to an antibody complexed with a polypeptide of the invention.

In a preferred embodiment, the labeling agent is an antibody that specifically binds to the capture agent (the antibody specifically recognizing any of the polypeptides of the invention). Such agents are well known to those of skill in the art, and most typically comprise labeled antibodies that specifically bind antibodies of the particular animal species from which the capture agent is derived. Thus, for example, where the capture agent is rabbit derived anti-human antibody to any of the polypeptides of the invention, the label agent may be a goat anti-rabbit IgG; an antibody that is specific to the constant region of the rabbit antibody.

Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins are normal constituents of the cell walls of streptococcal bacteria. They exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to 24 hours. However, the incubation time will depend upon the assay format, analyte, volume of solution, concentration, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10 °C to 40 °C.

5.13.4 Non-Competitive Assay Formats

Immunoassays for detecting any of the polypeptides of the invention may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of captured analyte (in this case any of the polypeptides of the invention) is directly measured. In one preferred "sandwich" assay, for example, the capture agent (antibodies selective for any of the polypeptides of the invention) can be bound directly to a solid substrate where they are immobilized. These immobilized antibodies then capture the protein encoded from any of the polypeptides of the

invention present in the test sample. The protein thus immobilized is then bound by a labeling agent, such as a second human antibody selective for any of the polypeptides of the invention bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived.

5 Sandwich assays are particularly preferred as diagnostics for the present invention. Such an assay provides immobilized antibodies selective for any of the polypeptides of the invention, the polypeptides of the invention concentration standards, ^{125}I labeled antibodies selective for any of the polypeptides of the invention, and positive and negative controls for the polypeptides of the invention. As described above, the immobilized antibodies specifically bind to the the polypeptides
10 of the invention present in the sample. Then the ^{125}I labeled antibodies selective for any of the polypeptides of the invention bind to the already bound polypeptides of the invention. Free ^{125}I labeled antibodies selective for any of the polypeptides of the invention are washed away and the remaining bound ^{125}I labeled antibodies selective for any of the polypeptides of the invention are detected using a gamma detector.

15 5.13.5 Competitive Assays

In competitive assays, the amount of analyte (any of the polypeptides of the invention) present in the sample is measured indirectly by measuring the amount of an added (exogenous) analyte (the polypeptides of the invention) displaced (or competed away) from a capture agent
20 (antibody selective for the polypeptides of the invention) by the analyte present in the sample. In one competitive assay, a known amount of any of the polypeptides of the invention is added to the sample and the sample is then contacted with a capture agent, in this case an antibody that specifically binds to one of the polypeptides of the invention. The amount of the polypeptides of the invention bound to the antibody is inversely proportional to the concentration of protein present in
25 the sample.

In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of any of the polypeptides of the invention bound to the antibody may be determined either by measuring the amount of the polypeptides of the invention present in an complex consisting of an antibody specific for the polypeptides of the invention and the corresponding polypeptide of the
30 invention, or alternatively by measuring the amount of remaining uncomplexed polypeptides of the invention. The amount of polypeptides of the invention may be detected by providing a labeled version of nay of the polypeptides of the invention.

A hapten inhibition assay is another preferred competitive assay. In this assay a known analyte, in this case any of the polypeptides of the invention is immobilized on a solid substrate. A known amount of antibody selective for any of the polypeptides of the invention is added to the sample, and the sample is then contacted with the immobilized quantity of the polypeptides of the invention. In this case, the amount of antibody selective for any of the polypeptides of the invention that is bound to the immobilized quantity of any of the polypeptides of the invention is proportional to the amount of actual polypeptides of the invention present in the sample. Again the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct wherein the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

5.13.6 Reduction of Non-Specific Binding

One of skill in the art will appreciate that it is often desirable to reduce non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

5.13.7 Other Assay Formats

Western blot (immunoblot) analysis can also be used to detect and quantify the presence of any of the polypeptides of the invention in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with an antibody that specifically binds one of the polypeptides of the invention. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (e.g. labeled sheep anti-mouse antibodies) that specifically bind to the antibodies specific for the polypeptides of the invention.

5.13.8 Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, so long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g. Dynabeads.TM), fluorescent dyes (e.g., fluorescein isothiocyanate, texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic (e.g. polystyrene, polypropylene, latex, etc.) beads.

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (e.g., streptavidin) molecule which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labeling or signal producing systems which may be used, see, U.S. Pat. No. 4,391,904, which is hereby incorporated herein by reference.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

5.13.9 Substrates

As mentioned above, depending upon the assay, various components, including the antigen, target antibody, or anti-human antibody, may be bound to a solid surface. Many methods for immobilizing biomolecules to a variety of solid surfaces are known in the art. For instance, the solid surface may be a membrane (e.g., nitrocellulose), a microtiter dish (e.g., PVC, polypropylene, or polystyrene), a test tube (glass or plastic), a dipstick (e.g. glass, PVC, polypropylene, polystyrene, latex, and the like), a microcentrifuge tube, or a glass or plastic bead. The desired component may be covalently bound or noncovalently attached through nonspecific bonding.

A wide variety of organic and inorganic polymers, both natural and synthetic may be employed as the material for the solid surface. Illustrative polymers include polyethylene, polypropylene, poly(4-methylbutene), polystyrene, polymethacrylate, poly(ethylene terephthalate), rayon, nylon, poly(vinyl butyrate), polyvinylidene difluoride (PVDF), silicones, polyformaldehyde, cellulose, cellulose acetate, nitrocellulose, and the like. Other materials which may be employed, include paper, glasses, ceramics, metals, metalloids, semiconductive materials, cements or the like. In addition, are included substances that form gels, such as proteins (e.g., gelatins), lipopolysaccharides, silicates, agarose and polyacrylamides can be used. Polymers which form

several aqueous phases, such as dextrans, polyalkylene glycols or surfactants, such as phospholipids, long chain (12-24 carbon atoms) alkyl ammonium salts and the like are also suitable. Where the solid surface is porous, various pore sizes may be employed depending upon the nature of the system.

5 In preparing the surface, a plurality of different materials may be employed, particularly as laminates, to obtain various properties. For example, protein coatings, such as gelatin can be used to avoid non-specific binding, simplify covalent conjugation, enhance signal detection or the like.

10 If covalent bonding between a compound and the surface is desired, the surface will usually be polyfunctional or be capable of being polyfunctionalized. Functional groups which may be present on the surface and used for linking can include carboxylic acids, aldehydes, amino groups, cyano groups, ethylenic groups, hydroxyl groups, mercapto groups and the like. The manner of linking a wide variety of compounds to various surfaces is well known and is amply illustrated in the literature. See, for example, Cuatrecasas, J. Biol. Chem. 245 3059 (1970) which is hereby incorporated herein by reference.

15 In addition to covalent bonding, various methods for noncovalently binding an assay component can be used. Noncovalent binding is typically nonspecific absorption of a compound to the surface. Typically, the surface is blocked with a second compound to prevent nonspecific binding of labeled assay components. Alternatively, the surface is designed such that it nonspecifically binds one component but does not significantly bind another. For example, a surface bearing a lectin such as
20 Concanavalin A will bind a carbohydrate containing compound but not a labeled protein that lacks glycosylation. Various solid surfaces for use in noncovalent attachment of assay components are reviewed in U.S. Pat. Nos. 4,447,576 and 4,254,082, which are hereby incorporated herein by reference.

5.13.10 Mass Spectrometry

25 Levels of polypeptides can be detected also by mass spectrometry. Detection of disease biomarkers using mass spectrometry with protein biochip analysis is well known to those of skill in the art, and is detailed in: Rosty et al. Cancer Research 62: 1868 (2002), and Qu et al. Expert Rev Mol Diagn 2: 549 (2002), and are hereby incorporated herein by reference.

5.13.11 Determination of Levels of the Polypeptides of the Invention for Prediction of Preeclampsia

The preeclamptic condition is predicted by a statistically significant change in the concentration of any of the polypeptides of the invention individually or in combination in maternal blood, urine, or cervicovaginal mucous during pregnancy. Thus, the levels of any of the polypeptides of the invention individually or in combination provide an advantageous diagnostic of preeclampsia.

Baseline healthy levels of any of the polypeptides of the invention individually or in combination and levels indicative of preeclampsia may be determined by means well known to those of skill in the art. Generally this simply involves routine screening of healthy patients and patients that ultimately develop preeclampsia. Any variation between the two patient populations in the polypeptides of the invention individually or in combination that is determined by time of gestation, may be controlled by sampling uniformly at approximately the same gestational period, or alternatively, by determining blood, urine, or cervicovaginal mucous levels of the polypeptides of the invention (individually or in combination) as a function of period of gestation.

5.13.12 Quantification of the Polynucleotides of the Invention

Levels of any of the polynucleotides of the invention individually or in combination may be detected and quantified from tissue samples by any of a number of means well known to those of skill in the art. These may include analytic methods or techniques such as microarrays, PCR (polymerase chain reaction), RT-PCR (reverse transcriptase PCR), real-time PCR, TaqMan (Applied Biosystems), or Northern analysis.

5.14 Diagnostic Kits

5.14.1 Diagnostic Kits for Detection or Prediction of Preeclampsia Using any of the polypeptides of the invention Individually or in Combination

The present invention provides for kits for the diagnosis of women at risk for preeclampsia. The kits preferably include one or more antibodies that specifically bind to the polypeptides of the invention. The antibodies may be free or immobilized on a solid support such as a test tube, a microtiter plate, a dipstick and the like. The kit may also contain instructional materials teaching the use of the antibody in an assay for the detection of a predilection to preeclampsia.

Additionally, the kit may contain one or more second antibodies that specifically bind to one of the polypeptides of the invention or alternatively, the first antibody. The second antibody may be labeled, or alternatively, the kit may contain a labeled third antibody that specifically binds the second antibody. The kit may also contain appropriate control series of any of the polypeptides of the invention, buffer solutions, positive and negative controls, washing solutions, dilution buffers and the like for the preparation and analysis of any of the polypeptides of the invention in samples derived from tissues, including blood plasma, blood serum, urine, or cervicovaginal mucous.

5.14.2 Diagnostic Kits for Detection or Prediction of Preeclampsia Using any of the Polynucleotides of the Invention Individually or in Combination

The present invention also provides for kits for the diagnosis of women at risk for preeclampsia. The kits preferably include one or more pairs of primers that specifically hybridize to the polynucleotides of the invention plus reagents well known to those of skill in the art for polymerase chain reaction (PCR) amplification of the polynucleotides of the invention, for example Medhurst et al. Methods Mol Med. 2003;79:229 and Dotsch et al. Expert Rev Mol Diagn. 2001 Jul;1(2):233.

Another preferred embodiment of the diagnostic kit for detection of preeclampsia using polynucleotides of the invention individually or in combination, is a microarray detection kit. Said microarray is comprised of a solid surface onto which single or double stranded polynucleotides of the invention are chemically or physically bonded or attached. Detection of levels of the polynucleotides of the invention are quantified by hybridization of the polynucleotides of the invention derived from tissue samples with like polynucleotides of the invention attached onto said solid surface. Either the polynucleotides of the invention derived from tissues or attached onto the solid surface may be attached to a detection label, for example Cy3 or Cy5 dyes (Amersham, Piscataway, NJ). Microarray techniques are well known to those of skill in the art, and are detailed in Iyer VR, et al. (1999) Science 283(5398):83-7 and Whitney AR, et al. (2003). Proc Natl Acad Sci U S A 100(4):1896-901, hereby incorporated herein by reference.

5.15 Therapeutic Methods

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have applications in the treatment of preeclampsia.

5.15.1 Example

One embodiment of the invention is the administration of an effective amount of the one or more of the polypeptides or other composition of the invention to individuals affected by preeclampsia that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of polypeptides of the invention or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention or other composition of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

5.16 Pharmaceutical Formulations and Routes of Administration

A polypeptide or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN,

TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects.

Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

5.16.1 Routes of Administration

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into the amniotic cavity or placental tissue, often in a depot or sustained release formulation. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, placental tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar

studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

5.16.2 Compositions and Formulations

5 Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, 10 granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical 15 composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or 20 synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active 25 ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active 30 ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an

isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such

administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are hereby incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg to about 100 mg (preferably about 0.1 μg to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically

acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention.

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredient of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type protein used in co-administration. For example, the addition of other known protein factors, cytokines or the like to the final composition, may also affect the dosage. Progress can be monitored by periodic assessment of symptoms (for example high blood pressure).

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

5.16.3 Effective Dosage

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated (for example, high blood pressure). Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a

circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, *e.g.*, Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen that maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight daily, with the preferred dose being

about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

5.16.4 Packaging

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

5.17 Examples

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

EXAMPLES

EXAMPLE 1

Isolation of SEQ ID NO: 1 through 852 from a cDNA Libraries of Human Cells

The novel nucleic acids of SEQ ID NO: 1 through 852 were obtained from several human normal and pre-eclamptic placental cDNA libraries using standard PCR, sequencing by hybridization sequence signature analysis, and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for vector sequences flanking the inserts. These samples were spotted onto nylon membranes and interrogated with oligonucleotide probes to give sequence signatures. The clones were clustered into groups of similar or identical sequences, and single representative clones were selected from each group for gel sequencing. The 5' sequence of the amplified inserts were then deduced using the reverse M13 sequencing primer in a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single-pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer. These inserts was identified as a novel sequence not previously obtained from this library and not previously reported in public databases. These sequences are designated as SEQ ID NO: 1 through 852 in the attached sequence listing.

EXAMPLE 2

ASSEMBLAGE OF SEQ ID NO: 1 through 852

The nucleic acids (SEQ ID NO: 1 through 852) of the invention were assembled from sequences that were obtained from various cDNA libraries by methods described in Example 1 above, and in some cases obtained from one or more public databases. The final sequence was assembled using the EST sequence as seed. Then a recursive algorithm was used to extend the seed into an extended assemblage, by pulling additional sequences from different databases (i.e. Nuvelo's database containing EST sequences, dbEST, gb pri, and UniGene) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor results for the assembled contigs (SEQ ID NO: 1-852) were obtained by using the BLASTN algorithm against the nucleotide (nt) database from Genbank (National Center for Biotechnology Information <http://www.ncbi.nlm.nih.gov>). The nucleotide database used was the

version as of December 30, 2002. The nearest neighbor results for the polypeptides (SEQ ID NO: 853-1704) corresponding to the assembled contigs were obtained by a FASTA search against Genpept, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment that allows in-codon frame shifts. The version of the Genpept database was the version as of January 10, 2003. The nearest neighbor results showed the closest homologue for each assemblage from Genpept (and contain the translated amino acid sequences for which the assemblages encodes SEQ ID NO 853 through 1704). The predicted amino acid sequences corresponding to SEQ ID NO: 1 through 852 were obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), incorporated herein by reference). For ease of creating SEQ ID Numbers, the following formula was used: nucleotide SEQ ID NO added to 852. (For example, the polypeptide corresponding to nucleotide SEQ ID NO 1 is SEQ ID NO 853).

The nearest neighbor results for both the nucleotide contigs (SEQ ID NO 1 through 852) and corresponding polypeptides (SEQ ID NO 853 through 1704) are set forth below. In some cases, no nearest neighbor result could be determined, and therefore are excluded from the following table.

TABLE 1

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1	AF090949	1710	97	HBV-X associated protein 2	Cercopithecus aethiops
1	U31913	1736	99	HBV-X associated protein	Homo sapiens
1	U78521	1740	100	immunophilin homolog ARA9	Homo sapiens
2	AAH12333	1168	100	BC012333 Unknown (protein for MGC:2084)	Homo sapiens
2	AF187981_1	1168	100	AF187981 delta7-sterol-C5-desaturase	Homo sapiens
2	D85181	1273	100	fungus sterol-C5-desaturase homolog	Homo sapiens
4	A84511	1017	99	unnamed protein product	unidentified
4	AF498970_1	1016	100	AF498970 small GTP binding protein RhoA	Homo sapiens
4	AX427410	1017	99	unnamed protein product	unidentified
5	AAH04312	485	98	BC004312 insulin-like growth factor binding protein 2 (36kD)	Homo sapiens
5	AAH09902	485	98	BC009902 Unknown (protein for MGC:2339)	Homo sapiens
5	AAH12769	485	98	BC012769 Unknown (protein for MGC:16256)	Homo sapiens
6	AAH02434	430	100	BC002434 p8 protein (candidate of metastasis 1)	Homo sapiens
6	AF069074	430	100	P8 protein	Homo sapiens
6	AF135266_1	430	100	AF135266 p8 protein homolog	Homo sapiens
7	AB047892	258	82	hypothetical protein	Macaca fascicularis
8	AAH01199	833	99	BC001199 Similar to glucose regulated protein, 58 kDa	Homo sapiens
8	AJ440721	833	99	thioredoxin related protein	Homo sapiens
8	AL834423	833	99	hypothetical protein	Homo sapiens
9	AAH00866	1124	100	BC000866 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity,	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				collagenase inhibitor)	
9	M59906	1124	100	collagenase inhibitor	Homo sapiens
9	X03124	1124	100	precursor	Homo sapiens
10	AAH00518	834	83	BC000518 Similar to brain acid-soluble protein 1	Homo sapiens
10	AF039656	822	81	neuronal tissue-enriched acidic protein	Homo sapiens
10	AF521668_1	516	59	AF521668 CAP23	Gallus gallus
11	AAH05931	733	100	BC005931 hemoglobin, alpha 2	Homo sapiens
11	AAH08572	733	100	BC008572 hemoglobin, alpha 2	Homo sapiens
11	BC032122	733	100	hemoglobin, alpha 2	Homo sapiens
12	AF347006	1171	90	cytochrome c oxidase subunit I	Homo sapiens
12	AF382012	1159	91	cytochrome c oxidase subunit I	Homo sapiens
12	AF382013	1159	91	cytochrome c oxidase subunit I	Homo sapiens
13	AF242729_1	1242	100	AF242729 HT022	Homo sapiens
13	AJ245874	1242	100	putative ATG/GTP binding protein	Homo sapiens
13	AJ250344	1242	100	hypothetical protein	Homo sapiens
14	AAH17050	1367	100	BC017050 2,3-bisphosphoglycerate mutase	Homo sapiens
14	M23068	1367	100	2,3-bisphosphoglycerate	Homo sapiens
14	X04327	1367	100	2,3 biphosphoglycerated mutase (AA 1 - 259)	Homo sapiens
15	AAH02334	921	100	BC002334 DAZ associated protein 2	Homo sapiens
15	AAH07900	921	100	BC007900 DAZ associated protein 2	Homo sapiens
15	D31767	921	100	KIAA0058	Homo sapiens
16	AAH09571	308	98	BC009571 Similar to stimulated by retinoic acid 13	Homo sapiens
16	U95006	309	98	D9 splice variant A	Homo sapiens
16	U95007	273	98	D9 splice variant B	Homo sapiens
17	AAH11674	493	66	BC011674 Similar to procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Homo sapiens
17	AC004876_4	493	66	AC004876 lysyl hydroxylase 3	Homo sapiens
17	AF207069	493	66	lysyl hydroxylase 3	Homo sapiens
18	AAH16765	1778	99	BC016765 Unknown (protein for MGC:22663)	Homo sapiens
18	AF153882_1	1785	100	AF153882 reversion-induced LIM protein	Homo sapiens
18	AF154335_1	1785	100	AF154335 reversion-induced LIM protein	Homo sapiens
19	AF023268	1150	74	metaxin	Homo sapiens
19	BC023071	1050	68	metaxin	Mus musculus
19	U46920	1150	74	metaxin	Homo sapiens
20	AF033815	363	34	Pr180	Mason-Pfizer monkey virus
20	AF193053_1	575	100	AF193053 unknown	Homo sapiens
20	Y10392	500	43	protease	Human endogenous retrovirus K
21	AF318351_1	3211	100	AF318351 unknown	Homo sapiens
21	AF318377_1	3211	100	AF318377 unknown	Homo sapiens
21	AX106709	3211	100	unnamed protein product	Homo sapiens
22	AL357374	2678	100	bA353C18.3.2 (splicing factor CC1.3, isoform 2 (CC1.4))	Homo sapiens
22	AY061882	2663	99	transcription coactivator CAPER	Mus musculus
22	L10911	2678	100	splicing factor	Homo sapiens
23	AAH08807	2069	90	BC008807 keratin 6A	Homo sapiens
23	AAH14152	2069	90	BC014152 Similar to keratin 6A	Homo sapiens
23	L42583	2069	90	keratin type II	Homo sapiens
24	AK000496	301	72	unnamed protein product	Homo sapiens
24	AK025116	271	67	unnamed protein product	Homo sapiens
24	AK090511	282	60	unnamed protein product	Homo sapiens
25	AAH16842	2431	99	BC016842 Unknown (protein for MGC:10135)	Homo sapiens
25	AK027643	2435	100	unnamed protein product	Homo sapiens
25	AL834398	2529	99	hypothetical protein	Homo sapiens
26	AAH02563	1176	100	BC002563 Similar to zinc/iron	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				regulated transporter-like	
26	AAH07886	1176	100	BC007886 Unknown (protein for MGC:14180)	Homo sapiens
26	AAH14303	1176	100	BC014303 Unknown (protein for MGC:16418)	Homo sapiens
27	AF056732	3342	100	prostaglandin transporter	Homo sapiens
27	BC041140	3453	99	solute carrier family 21 (prostaglandin transporter), member 2	Homo sapiens
27	U70867	3342	100	prostaglandin transporter hPGT	Homo sapiens
28	AAH15206	335	100	BC015206 guanine nucleotide binding protein 10	Homo sapiens
28	AAH16319	335	100	BC016319 guanine nucleotide binding protein 10	Homo sapiens
28	AF493877_1	335	100	AF493877 guanine nucleotide binding protein gamma 10	Homo sapiens
29	D26307	1148	66	Jun-D	Rattus norvegicus
29	X51346	1419	97	jun-D gene product (AA 1-303)	Homo sapiens
29	X56681	1388	96	junD protein	Homo sapiens
30	AY081680	693	100	chlorophyll a/b-binding protein CP29	Arabidopsis thaliana
30	AY133566	693	100	At5g01530/F7A7_50	Arabidopsis thaliana
30	BT000363	693	100	chlorophyll a/b-binding protein CP29	Arabidopsis thaliana
31	AY086905	622	100	photosystem II type I chlorophyll a /b binding protein, putative	Arabidopsis thaliana
31	AY128345	622	100	photosystem II type I chlorophyll a/b binding protein, putative	Arabidopsis thaliana
31	BT000726	622	100	putative photosystem II type I chlorophyll a /b binding protein	Arabidopsis thaliana
32	AF177203_1	847	98	AF177203 cerebral cell adhesion molecule	Homo sapiens
32	AK074519	872	100	unnamed protein product	Homo sapiens
32	AK074523	872	100	unnamed protein product	Homo sapiens
33	AY050935	497	100	putative photosystem II type I chlorophyll a/b binding protein	Arabidopsis thaliana
33	AY058180	497	100	At1g29930/F1N18_23	Arabidopsis thaliana
33	AY091169	497	100	putative chlorophyll a/b-binding protein	Arabidopsis thaliana
34	AF178954	2149	88	monocarboxylate transporter 4	Mus musculus
34	U81800	2399	100	monocarboxylate transporter	Homo sapiens
34	U87627	2164	88	putative monocarboxylate transporter	Rattus norvegicus
35	AAH18345	173	100	BC018345 Unknown (protein for MGC:8802)	Homo sapiens
35	AF237776_1	173	100	AF237776 MAP kinase-interacting kinase 2b	Homo sapiens
35	AL137565	173	100	hypothetical protein	Homo sapiens
36	AF006013	3773	99	dishevelled 3	Homo sapiens
36	BC032459	3784	99	dishevelled, dsh homolog 3 (Drosophila)	Homo sapiens
36	U75651	3806	100	dishevelled 3	Homo sapiens
37	AK000268	2659	100	unnamed protein product	Homo sapiens
37	AK053678	1598	71	unnamed protein product	Mus musculus
37	L00193	1342	58	epidermal keratin subunit I	Mus musculus
38	AX354357	840	100	unnamed protein product	Homo sapiens
38	BC002198	243	42	Similar to hypothetical protein FLJ20093	Mus musculus
38	BC039642	658	75	Unknown (protein for IMAGE:5352548)	Mus musculus
39	AF012348	857	84	smooth muscle gamma actin	Gallus gallus
39	S63494	857	84	gamma-actin	Gallus gallus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
39	U20365	857	84	smooth muscle gamma-actin	Mus musculus
40	AB023209	2102	61	KIAA0992 protein	Homo sapiens
40	AF077041_1	2057	100	AF077041 SIH002	Homo sapiens
40	AF151909_1	2161	100	AF151909 CGI-151 protein	Homo sapiens
41	AF287271_1	714	100	AF287271 ribosomal protein L23	Mus musculus
41	AF401577_1	714	100	AF401577 ribosomal protein L23	Ictalurus punctatus
41	BC025918	714	100	ribosomal protein L23	Mus musculus
42	U43916	817	100	TMP	Homo sapiens
42	Y07909	817	100	progression associated protein	Homo sapiens
42	Z50751	817	100	B4B	Homo sapiens
43	AAH09647	2778	99	BC009647 Unknown (protein for MGC:5096)	Homo sapiens
43	M13078	2773	99	alkaline phosphatase precursor	Homo sapiens
43	M19159	2780	100	placental alkaline phosphatase-1	Homo sapiens
44	AF326591	2240	100	fenestrated-endothelial linked structure protein	Homo sapiens
44	AF348827	2232	99	PV1 protein	Homo sapiens
44	AL834363	2304	99	hypothetical protein	Homo sapiens
45	AAH11686	5877	100	BC011686 damage-specific DNA binding protein 1 (127kD)	Homo sapiens
45	L40326	5877	100	X-associated protein 1	Homo sapiens
45	U18299	5877	100	DDBa p127	Homo sapiens
46	U66661	1330	100	GABA-A receptor epsilon subunit	Homo sapiens
46	Y07637	1330	100	putative GABA-gated chloride channel	Homo sapiens
46	Y09765	1330	100	GABA receptor epsilon subunit	Homo sapiens
47	AF380181_1	11506	99	AF380181 SON DNA binding protein isoform C	Homo sapiens
47	AF380184_1	12117	99	AF380184 SON DNA binding protein isoform F	Homo sapiens
47	AY026895	11842	97	NREBP	Homo sapiens
48	A20470	2142	99	preA-PAI-2	synthetic construct
48	AAH12609	2148	100	BC012609 Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	Homo sapiens
48	Y00630	2139	99	PAI-2 precursor (AA -22 to 393)	Homo sapiens
49	AB037819	7936	100	KIAA1398 protein	Homo sapiens
49	AL132765	5785	95	bA462D18.3.2 (ribosome binding protein 1 (dog 180 kDa homolog) (KIAA1398) (isoform 2))	Homo sapiens
49	X87224	6518	84	ribosome receptor	Canis familiaris
50	AAH00716	1700	99	BC000716 seryl-tRNA synthetase	Homo sapiens
50	D49914	1700	99	Seryl tRNA Synthetase	Homo sapiens
50	X91257	1700	99	seryl-tRNA synthetase	Homo sapiens
51	D29640	4698	57	KIAA0051	Homo sapiens
51	L33075	4698	57	ras GTPase-activating-like protein	Homo sapiens
51	U51903	8003	100	RasGAP-related protein	Homo sapiens
52	AAH17338	2576	99	BC017338 fucosidase, alpha-L- 1, tissue	Homo sapiens
52	M29877	2581	100	alpha-L-fucosidase precursor (EC 3.2.1.5)	Homo sapiens
52	M80815	2576	99	alpha-L-fucosidase	Homo sapiens
53	AAH03067	3601	100	BC003067 growth arrest and DNA-damage-inducible 34	Homo sapiens
53	AK001361	3568	99	unnamed protein product	Homo sapiens
53	U83981	3601	100	apoptosis associated protein	Homo sapiens
54	AAH02717	379	77	BC002717 Similar to chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
54	AAH05921	379	77	BC005921 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
54	AAH20756	379	77	BC020756 chorionic somatomammotropin hormone 1	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				(placental lactogen)	
55	M57939	2349	100	ribonucleoprotein antigen	Homo sapiens
55	X04654	2385	97	70 K protein (AA 1-614)	Homo sapiens
55	X84841	2349	100	68 kDa (U1) ribonucleoprotein	Homo sapiens
56	AAH09945	3737	99	BC009945 Unknown (protein for IMAGE:4123572)	Homo sapiens
56	AB018289	5502	100	KIAA0746 protein	Homo sapiens
56	AK030487	4620	87	unnamed protein product	Mus musculus
57	AJ422147	664	100	C15 protein	Homo sapiens
57	AX352692	664	100	unnamed protein product	Homo sapiens
57	AX357061	664	100	unnamed protein product	Homo sapiens
59	AAH01501	1520	100	BC001501 Unknown (protein for MGC:2233)	Homo sapiens
59	AAH14078	1520	100	BC014078 cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Homo sapiens
59	BC025302	1520	100	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Homo sapiens
60	BC036285	1936	100	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	Homo sapiens
60	M18468	1936	100	cAMP-dependent protein kinase regulatory subunit type 1	Homo sapiens
60	M33336	1936	100	cAMP-dependent protein kinase type I-alpha subunit	Homo sapiens
61	BC024165	600	100	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Homo sapiens
61	X82385	600	100	RNA polymerase II subunit	Homo sapiens
61	X98433	600	100	RNA polymerase II subunit	Homo sapiens
62	AL138761	8033	99	bA16H23.2 (collagen, type XVII, alpha 1 (BP180))	Homo sapiens
62	M91669	8228	100	autoantigen	Homo sapiens
62	U76604	8037	99	180 kDa bullous pemphigoid antigen 2/type XVII collagen	Homo sapiens
63	AAH03575	2373	100	BC003575 mannosyl (alpha-1,3-) - glycoprotein beta-1,2-N-acetylglucosaminyltransferase	Homo sapiens
63	M55621	2363	99	N-acetylglucosaminyltransferase I	Homo sapiens
63	M61829	2373	100	alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase	Homo sapiens
64	L13923	16639	99	fibrillin	Homo sapiens
64	L28748	16362	97	putative	Bos taurus
64	X63556	17359	100	fibrillin	Homo sapiens
65	AAH02576	3661	100	BC002576 matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)	Homo sapiens
65	J03210	3584	100	collagenase type IV precursor	Homo sapiens
65	M55593	3661	100	type IV collagenase	Homo sapiens
66	AAH22087	2466	99	BC022087 Similar to CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	Homo sapiens
66	AF467889_1	2380	86	AF467889 high density lipoprotein receptor SR-BI	Sus scrofa
66	Z22555	2684	100	CLA-1	Homo sapiens
67	AF106202_1	1249	100	AF106202 endothelial cell protein C receptor precursor	Homo sapiens
67	AF375468_1	1249	100	AF375468 endothelial protein C receptor	Homo sapiens
67	X89079	1249	100	centrocyclin	Homo sapiens
68	AF153603_1	666	100	AF153603 TSC-22 related protein	Homo sapiens
68	AF183393_1	666	100	AF183393 TSC-22-like Protein	Homo sapiens
68	AF228339	666	100	glucocorticoid-induced GILZ	Homo sapiens
69	AF111168	3586	99	unknown	Homo sapiens
69	AK075445	2876	99	unnamed protein product	Homo sapiens
69	AX136231	2876	99	unnamed protein product	Homo sapiens
70	AAH11234	1220	100	BC011234 Similar to splicing factor 30, survival of motor neuron-related	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
70	AF083385	1220	100	30kDa splicing factor; SPF 30	Homo sapiens
70	AF107463	1220	100	splicing factor	Homo sapiens
71	AAH10240	1921	100	BC010240 cathepsin B	Homo sapiens
71	L16510	1912	99	cathepsin B	Homo sapiens
71	M14221	1915	99	preprocathepsin B	Homo sapiens
72	AK056033	398	83	unnamed protein product	Homo sapiens
73	AE014836_21	182	23	AE014836 hypothetical protein	Plasmodium falciparum 3D7
73	AK033354	174	24	unnamed protein product	Mus musculus
74	AF222743_1	2415	100	AF222743 Sec61 alpha-1	Mus musculus
74	BC003707	2415	100	sec61 homolog	Mus musculus
74	M96630	2415	100	sec61-like protein	Rattus sp.
75	AF332086_1	3193	96	AF332086 Rad21	Mus musculus
75	D38551	3284	100	The hal237 gene product is related to S.pombe rad21 gene product.	Homo sapiens
75	X98294	3275	99	HR21spA	Homo sapiens
76	AAH16325	925	100	BC016325 ADP-ribosylation factor 4	Homo sapiens
76	AF493883_1	925	100	AF493883 ADP-ribosylation factor protein 4	Homo sapiens
76	BC022866	925	100	ADP-ribosylation factor 4	Homo sapiens
77	AAH18201	763	100	BC018201 Unknown (protein for MGC:21505)	Homo sapiens
77	AF217965_1	763	100	AF217965 unknown	Homo sapiens
77	AF217972_1	763	100	AF217972 unknown	Homo sapiens
78	AAH00211	1127	97	BC000211 eukaryotic translation elongation factor 1 beta 2	Homo sapiens
78	AAH04931	1127	97	BC004931 eukaryotic translation elongation factor 1 beta 2	Homo sapiens
78	X60489	1127	97	elongation factor-1-beta	Homo sapiens
79	D82984	1758	93	C/EBP alpha protein	Bos taurus
79	U34070	1857	96	CCAAT/enhancer binding protein alpha	Homo sapiens
79	Y11525	1927	100	CCAAT/enhancer binding protein alpha	Homo sapiens
80	AK025116	341	71	unnamed protein product	Homo sapiens
80	AK090511	358	72	unnamed protein product	Homo sapiens
80	AK096373	341	70	unnamed protein product	Homo sapiens
81	AAH13963	2458	100	BC013963 Similar to adenylyl cyclase-associated protein	Homo sapiens
81	AAH17196	2458	100	BC017196 adenylyl cyclase-associated protein	Homo sapiens
81	M98474	2458	100	CAP protein	Homo sapiens
82	AAH02464	2175	99	BC002464 coagulation factor II (thrombin) receptor	Homo sapiens
82	AF391809_1	2179	99	AF391809 coagulation factor II (thrombin) receptor	Homo sapiens
82	M62424	2187	100	thrombin receptor	Homo sapiens
83	AF085250	759	100	calmodulin	Perca flavescens
83	D83350	759	100	calmodulin	Anas platyrhynchos
83	K01945	759	100	calmodulin (cDNA clone 71)	Xenopus laevis
84	AL050265	2193	100	hypothetical protein	Homo sapiens
84	BC033475	2128	96	similar to TAR DNA-binding protein-43 (TDP-43)	Mus musculus
84	U23731	2193	100	TAR DNA-binding protein-43	Homo sapiens
85	AAH01495	1673	99	BC001495 chromosome 1 open reading frame 8	Homo sapiens
85	AAH16374	1697	100	BC016374 chromosome 1 open reading frame 8	Homo sapiens
85	AF290615_1	1673	99	AF290615 liver membrane-bound protein	Homo sapiens
86	AK025047	319	69	unnamed protein product	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
86	AK090511	327	70	unnamed protein product	Homo sapiens
86	AK092450	358	69	unnamed protein product	Homo sapiens
87	AAH00642	683	99	BC000642 MY047 protein	Homo sapiens
87	AF063605	688	100	brain my047 protein	Homo sapiens
87	AX136119	683	99	unnamed protein product	Homo sapiens
88	AF035947_1	1394	100	AF035947 cytokine-inducible inhibitor of signalling type 1b	Homo sapiens
88	AF132297_1	1332	99	AF132297 cytokine-inducible SH2-containing protein	Homo sapiens
88	BC031590	1321	100	cytokine inducible SH2-containing protein	Homo sapiens
89	AF151018_1	863	100	AF151018 HSPC184	Homo sapiens
89	AK012047	863	100	unnamed protein product	Mus musculus
89	AK075227	863	100	unnamed protein product	Homo sapiens
90	AK025116	323	68	unnamed protein product	Homo sapiens
90	AK090929	316	70	unnamed protein product	Homo sapiens
90	U22376	203	61	alternatively spliced product using exon 13A	Homo sapiens
91	AAH09357	782	98	BC009357 transgelin 2	Homo sapiens
91	AY007127	887	98	similar to Homo sapiens mRNA for KIAA0120 gene with GenBank Accession Number D21261.1	
91	D21261	782	98	similar to human 22kDa, SM22 mRNA (HUM22SM) .	Homo sapiens
92	AE005963	413	91	TonB-dependent receptor	Caulobacter crescentus CB15
92	AE005978	307	67	TonB-dependent receptor	Caulobacter crescentus CB15
92	AE005979	307	67	TonB-dependent receptor	Caulobacter crescentus CB15
93	AAH14006	367	81	BC014006 Similar to 6-phosphogluconolactonase	Homo sapiens
93	AJ243972	367	81	6-phosphogluconolactonase	Homo sapiens
93	BC006594	325	71	RIKEN cDNA 1110030K05 gene	Mus musculus
94	AAH03125	2055	99	BC003125 Unknown (protein for MGC:3222)	Homo sapiens
94	AK027877	2055	99	unnamed protein product	Homo sapiens
94	AL136916	2055	99	hypothetical protein	Homo sapiens
95	AAH03681	2956	100	BC003681 Unknown (protein for IMAGE:3453235)	Homo sapiens
95	AL096828	3008	100	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	Homo sapiens
95	AX400070	2878	96	unnamed protein product	Homo sapiens
96	AF161372_1	872	100	AF161372 HSPC254	Homo sapiens
96	BC021602	519	98	Unknown (protein for IMAGE:5102170)	Mus musculus
96	BC021603	519	98	Unknown (protein for IMAGE:5102465)	Mus musculus
97	AAH11714	476	100	BC011714 Similar to heterogeneous nuclear ribonucleoprotein D-like	Homo sapiens
97	AB017020	476	100	JKTBP	Mus musculus
97	BC021374	476	100	heterogeneous nuclear ribonucleoprotein D-like	Mus musculus
98	AAH02673	1063	100	BC002673 protein kinase H11; small stress protein-like protein HSP22	Homo sapiens
98	AF191017_1	1063	100	AF191017 E2IG1	Homo sapiens
98	AF250138_1	1063	100	AF250138 small stress protein-like protein HSP22	Homo sapiens
99	AAH05033	2990	99	BC005033 Unknown (protein for MGC:12692)	Homo sapiens
99	AAH15620	2990	99	BC015620 Unknown (protein for IMAGE:4843317)	Homo sapiens
99	D89980	2990	99	alpha actinin 4	Homo sapiens
100	AAH11908	1787	100	BC011908 Unknown (protein for	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				MGC:20321)	
100	AAH14564	1787	100	BC014564 Unknown (protein for MGC:2063)	Homo sapiens
100	AAH18695	1787	100	BC018695 Unknown (protein for MGC:3838)	Homo sapiens
101	AAH12977	1363	100	BC012977 nuclear LIM interactor-interacting factor	Homo sapiens
101	AF229162_1	1363	100	AF229162 nuclear LIM interactor-interacting factor	Homo sapiens
101	AF229163	1363	100	nuclear LIM interactor-interacting factor	Homo sapiens
102	AAH09718	355	76	BC009718 epithelial membrane protein 3	Homo sapiens
102	U52101	355	76	YMP	Homo sapiens
102	U87947	355	76	hematopoietic neural membrane protein	Homo sapiens
103	AF162781_1	4987	88	AF162781 SH2-containing inositol 5-phosphatase 2	Mus musculus
103	L36818	6041	99	51C protein	Homo sapiens
103	Y14385	5272	92	inositol polyphosphate 5-phosphatase	Homo sapiens
104	AAH17369	1011	92	BC017369 splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
104	AAH17908	1011	92	BC017908 splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
104	BC022328	1011	92	splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
105	AAH14323	1209	99	BC014323 Similar to accessory proteins BAP31/BAP29	Homo sapiens
105	X81109	1213	100	tumor-associated antigen	Homo sapiens
105	Z31696	1213	100	CDM	Homo sapiens
106	AAH15763	3102	100	BC015763 hypothetical protein FLJ20258	Homo sapiens
106	AK000265	3093	99	unnamed protein product	Homo sapiens
106	AK075098	2998	99	unnamed protein product	Homo sapiens
107	AAH07858	2250	100	BC007858 inhibin, beta A (activin A, activin AB alpha polypeptide)	Homo sapiens
107	M13436	2250	100	beta-A inhibin	Homo sapiens
107	X57578	2250	100	activin beta-A subunit	Homo sapiens
108	AK027598	3474	100	unnamed protein product	Homo sapiens
108	AX481758	3498	99	unnamed protein product	Homo sapiens
108	AX481760	3498	99	unnamed protein product	Homo sapiens
109	AAH15958	1926	86	BC015958 Unknown (protein for MGC:15290)	Homo sapiens
109	AJ401269	1926	86	polyadenylate-binding protein 1	Bos taurus
109	AK044829	1922	85	unnamed protein product	Mus musculus
110	AAH10623	3729	96	BC010623 Similar to nuclear factor (erythroid-derived 2)-like 1	Homo sapiens
110	AK090459	4032	100	FLJ00380 protein	Homo sapiens
110	X77366	3926	100	hbZ17	Homo sapiens
111	AAH03177	3500	100	BC003177 KIAA1536 protein	Homo sapiens
111	AK027881	3480	99	unnamed protein product	Homo sapiens
111	AL136895	3500	100	hypothetical protein	Homo sapiens
112	AY054301	4981	94	type III procollagen alpha 1 chain	Homo sapiens
112	BC028178	6603	100	Similar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	Homo sapiens
112	X14420	4981	94	prepro-alpha-1 type 3 collagen	Homo sapiens
113	AAH11819	3473	99	BC011819 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	Homo sapiens
113	AF000982	3476	100	dead box, X isoform	Homo sapiens
113	AF000983	3476	100	dead box, X isoform	Homo sapiens
114	AAH14959	1160	100	BC014959 RING1 and YY1 binding protein	Homo sapiens
114	AF179286_1	1160	100	AF179286 death effector domain-associated factor	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
114	BC036459	1156	99	RING1 and YY1 binding protein	Homo sapiens
115	AK002791	282	81	unnamed protein product	Mus musculus
115	AK003292	282	81	unnamed protein product	Mus musculus
115	BC016191	282	81	RIKEN cDNA 0610038D11 gene	Mus musculus
116	AAH08442	1106	100	BC008442 Similar to transmembrane 4 superfamily member 1	Homo sapiens
116	AAH10166	1106	100	BC010166 Similar to transmembrane 4 superfamily member 1	Homo sapiens
116	M90657	1106	100	L6	Homo sapiens
117	AAH10354	1764	100	BC010354 PTD010 protein	Homo sapiens
117	AB009685	1764	100	DERP2	Homo sapiens
117	AF131820	1764	100	Unknown	Homo sapiens
118	AF217787	1172	99	extracellular glutathione peroxidase	Homo sapiens
118	D00632	1192	99	glutathione peroxidase	Homo sapiens
118	X58295	1192	99	glutathione peroxidase	Homo sapiens
119	AAH00531	939	97	BC000531 insulin-like growth factor 2 (somatomedin A)	Homo sapiens
119	AF517226_1	939	97	AF517226 insulin-like growth factor 2 (somatomedin A)	Homo sapiens
119	M17863	942	97	preproinsulin-like growth factor II, domains A-E	Homo sapiens
120	AJ310544	2183	100	EGLN2 protein	Homo sapiens
120	AX553864	2183	100	unnamed protein product	Homo sapiens
120	BC036051	2183	100	Similar to egl nine homolog 2 (C. elegans)	Homo sapiens
121	AAH00867	915	98	BC000867 PRO0659 protein	Homo sapiens
121	AL834135	1118	99	hypothetical protein	Homo sapiens
121	AX405861	1118	99	unnamed protein product	Homo sapiens
122	AB051480	1087	60	KIAA1693 protein	Homo sapiens
122	AL136890	1741	83	hypothetical protein	Homo sapiens
122	AX402334	1084	60	unnamed protein product	Homo sapiens
123	AB037755	4896	99	KIAA1334 protein	Homo sapiens
123	AF155135_1	4845	99	AF155135 novel retinal pigment epithelial cell protein	Homo sapiens
123	AF202315_1	4141	85	AF202315 ankyrin	Mus musculus
124	AK090929	329	76	unnamed protein product	Homo sapiens
124	AK097965	338	77	unnamed protein product	Homo sapiens
124	BC033959	336	70	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
125	AAH12444	1319	100	BC012444 Similar to chloride intracellular channel 4	Homo sapiens
125	AF097330_1	1305	99	AF097330 H1 chloride channel; p64H1; CLIC4	Homo sapiens
125	AL117424	1319	100	hypothetical protein	Homo sapiens
126	AB034747	904	100	small integral membrane protein of lysosome/late endosome	Homo sapiens
126	AF171100	812	85	TBX1 protein	Mus musculus
126	BC018559	812	85	LPS-induced TNF-alpha factor	Mus musculus
127	AAH10645	1737	100	BC010645 Similar to sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)	Homo sapiens
127	AY040826	1715	97	alpha 2,3-sialyltransferase IV type B+18	Homo sapiens
127	L23767	1710	100	a2,3 sialyltransferase	Homo sapiens
128	AAH09329	639	64	BC009329 triosephosphate isomerase 1	Homo sapiens
128	AAH11611	639	64	BC011611 Similar to triosephosphate isomerase 1	Homo sapiens
128	AAH15100	639	64	BC015100 triosephosphate isomerase 1	Homo sapiens
129	AAH18986	1064	91	BC018986 Unknown (protein for MGC:20092)	Homo sapiens
129	AB059653	1060	90	prostaglandin dehydrogenase I	Macaca fascicularis
129	L76465	1057	90	NAD+-dependent 15-	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				hydroxyprostaglandin dehydrogenase	
130	AAH00690	794	100	BC000690 ribosomal protein L24	Homo sapiens
130	BC002110	794	100	ribosomal protein L24	Mus musculus
130	X78443	794	100	ribosomal protein L24	Rattus norvegicus
131	AAH11402	1122	100	BC011402 Similar to decidual protein induced by progesterone	Homo sapiens
131	AB022718	1122	100	DEPP	Homo sapiens
131	AL136653	1116	99	hypothetical protein	Homo sapiens
132	AF108841	402	81	pol protein	Homo sapiens
132	AF108843	415	75	pol protein	Homo sapiens
132	U88902	317	73	integrase	Homo sapiens
133	A07358	1408	99	VAC beta	Mus musculus
133	AAH04376	1417	100	BC004376 annexin A8	Homo sapiens
133	X16662	1408	99	vascular anticoagulant-beta (AA 1 - 327)	Homo sapiens
134	AF068227	2236	100	putative transmembrane protein	Homo sapiens
134	AK032293	1426	76	unnamed protein product	Mus musculus
134	BC025487	1447	77	Similar to ceroid-lipofuscinosis, neuronal 5	Mus musculus
135	AAH10652	1355	100	BC010652 Unknown (protein for MGC:9753)	Homo sapiens
135	AF217980_1	1338	98	AF217980 unknown	Homo sapiens
135	AX119063	965	96	unnamed protein product	Homo sapiens
136	AK000496	374	71	unnamed protein product	Homo sapiens
136	AK025116	400	72	unnamed protein product	Homo sapiens
136	AK057830	369	72	unnamed protein product	Homo sapiens
137	AF001900	1702	100	secreted frizzled-related protein	Homo sapiens
137	AF056087	1702	100	secreted frizzled related protein	Homo sapiens
137	BC036503	1690	99	Unknown (protein for MGC:43294)	Homo sapiens
138	AAH14052	2127	100	BC014052 transcriptional co-activator with PDZ-binding motif (TAZ)	Homo sapiens
138	AJ299431	2127	100	transcriptional coactivator	Homo sapiens
138	AK022036	2127	100	unnamed protein product	Homo sapiens
139	AAH07493	254	80	BC007493 galactosidase, beta 1	Homo sapiens
139	M22590	254	80	beta-galactosidase precursor (EC 3.2.1.23)	Homo sapiens
139	M34423	254	80	beta-galactosidase precursor (EC 3.2.1.23)	Homo sapiens
140	AAH15928	2186	100	BC015928 Unknown (protein for MGC:8773)	Homo sapiens
140	AB037797	2313	100	KIAA1376 protein	Homo sapiens
140	AK088288	2153	98	unnamed protein product	Mus musculus
141	AF087873_1	383	100	AF087873 protein kinase inhibitor	Homo sapiens
141	AF225513_1	383	100	AF225513 cAMP-dependent protein kinase inhibitor beta	Homo sapiens
141	BC036011	383	100	protein kinase (cAMP-dependent, catalytic) inhibitor beta	Homo sapiens
142	X53305	736	100	stathmin	Homo sapiens
142	X94912	736	100	Pr22	Homo sapiens
142	Z11566	736	100	Pr22 protein	Homo sapiens
143	AF148856_2	150	79	AF148856 unknown	Homo sapiens
143	AL096744	153	82	hypothetical protein	Homo sapiens
143	M80341	150	79	ORF2	Homo sapiens
144	AF421375	619	44	unknown	Homo sapiens
144	AK002154	798	94	unnamed protein product	Homo sapiens
144	AK023417	819	100	unnamed protein product	Homo sapiens
145	AF151807_1	2197	99	AF151807 CGI-49 protein	Homo sapiens
145	AK075178	2150	97	unnamed protein product	Homo sapiens
145	BC026185	2137	97	Similar to CGI-49 protein	Homo sapiens
146	AAH10123	2134	100	BC010123 SH3-domain binding protein 5 (BTK-associated)	Homo sapiens
146	AB005047	2134	100	SH3 binding protein	Homo sapiens
146	AB027562	2008	94	vascular endothelial cell specific protein 18	Rattus norvegicus
147	AJ131023	5309	99	oxytocinase/insulin-responsive	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				aminopeptidase, variant 1	
147	U62768	5318	99	oxytocinase splice variant 1	Homo sapiens
147	U62769	5242	99	oxytocinase splice variant 2	Homo sapiens
148	AF234263	2521	99	cathepsin C	Homo sapiens
148	U79415	2527	100	prepro dipeptidyl peptidase I	Homo sapiens
148	X87212	2527	100	cathepsin C	Homo sapiens
149	BC003426	1438	94	Similar to eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD)	Mus musculus
149	U05821	1419	92	translation initiation factor eIF-2B alpha-subunit	Rattus norvegicus
149	X95648	1526	100	alfa subunit	Homo sapiens
150	AAH14093	2678	97	BC014093 Similar to amiloride binding protein 1 (amine oxidase (copper-containing))	Homo sapiens
150	M55602	2431	89	amiloride-binding protein	Homo sapiens
150	X78212	2678	97	amiloride binding protein	Homo sapiens
151	AK003633	925	98	unnamed protein product	Mus musculus
151	AK007989	925	98	unnamed protein product	Mus musculus
151	AK076212	925	98	unnamed protein product	Mus musculus
152	AAH18340	1692	99	BC018340 Unknown (protein for MGC:9372)	Homo sapiens
152	X79066	1692	99	ERF-1	Homo sapiens
152	X99404	1684	99	Berg36	Homo sapiens
153	AB055977	492	93	I3 protein	Homo sapiens
153	AF041430	492	93	PRGR2	Homo sapiens
153	AF106966	492	93	I3 protein	Homo sapiens
154	AAH14438	1018	100	BC014438 Unknown (protein for MGC:22947)	Homo sapiens
154	AE006639_3	1018	100	AE006639 HN1 like	Homo sapiens
154	AK023154	1018	100	unnamed protein product	Homo sapiens
155	J03779	3944	100	common acute lymphoblastic leukemia antigen precursor	Homo sapiens
155	M26628	3919	99	enkephalinase	Homo sapiens
155	Y00811	3919	99	CALLA protein (AA 1 - 750)	Homo sapiens
156	AB035304	4092	100	cadherin-5	Homo sapiens
156	U84722	4086	99	vascular endothelial cadherin	Homo sapiens
156	X79981	4092	100	VE-cadherin	Homo sapiens
157	AX019983	739	100	unnamed protein product	Homo sapiens
157	BC026254	739	100	insulin-like 4 (placenta)	Homo sapiens
157	L34838	739	100	EPIL	Homo sapiens
158	AF139894_1	1813	100	AF139894 RNA-binding protein alpha-CP1	Mus musculus
158	AF139895_1	1813	100	AF139895 RNA-binding protein alpha-CP1	Mus musculus
158	BC004793	1813	100	poly(rC)-binding protein 1	Mus musculus
159	U12390	369	67	beta-galactosidase alpha peptide	Cloning vector pSport1
159	U12391	355	88	beta-galactosidase alpha peptide	Cloning vector pSport2
159	Y14836	294	68	beta-galactosidase	Phagemid cloning vector pTZ19U
160	AF218012_1	1751	100	AF218012 unknown	Homo sapiens
160	AF218030_1	1751	100	AF218030 unknown	Homo sapiens
160	AL121586	1778	100	dJ47704.1.1 (novel protein similar to otoferlin and dysferlin, isoform 1)	Homo sapiens
161	AAH00352	1286	100	BC000352 proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	Homo sapiens
161	AAH07503	1286	100	BC007503 proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	Homo sapiens
161	AF078829_1	1286	100	AF078829 proteasome activator	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				PA28 alpha	
162	AAH16155	382	100	BC016155 Ras homolog enriched in brain 2	Homo sapiens
162	AF493921_1	382	100	AF493921 Ras family small GTP binding protein RHEB2	Homo sapiens
162	Z29677	382	100	Ras-related GTP-binding protein	Homo sapiens
163	AAH10423	2657	100	BC010423 Ig superfamily receptor LNIR	Homo sapiens
163	AF160477_1	2655	99	AF160477 Ig superfamily receptor LNIR precursor	Homo sapiens
163	AF426163_1	2657	100	AF426163 nectin 4	Homo sapiens
164	AJ295142	3578	99	Clq receptor protein	Homo sapiens
164	BC028075	3577	99	complement component 1, q subcomponent, receptor 1	Homo sapiens
164	U94333	3587	100	ClqR(p)	Homo sapiens
165	AAH14271	3392	100	BC014271 endoglin (Osler-Rendu-Weber syndrome 1)	Homo sapiens
165	J05481	3319	99	endoglin precursor	Homo sapiens
165	U37439	3385	99	endoglin	Homo sapiens
166	AAH07411	323	98	BC007411 Unknown (protein for MGC:2554)	Homo sapiens
166	AF051782	319	97	diaphanous 1	Homo sapiens
166	U96963	322	98	p140mDia	Mus musculus
167	AF151966_1	1875	66	AF151966 GTPase activating protein Rap1-GAP	Gallus gallus
167	BC030891	2109	95	Unknown (protein for IMAGE:4485689)	Mus musculus
167	M64788	3477	100	GTPase activating protein	Homo sapiens
168	AX206708	1968	100	unnamed protein product	Homo sapiens
168	M92934	1968	100	connective tissue growth factor	Homo sapiens
168	X78947	1968	100	connective tissue growth factor	Homo sapiens
169	AAH18823	849	100	BC018823 Unknown (protein for MGC:1236)	Homo sapiens
169	AK007729	809	97	unnamed protein product	Mus musculus
169	U30826	849	100	SRp40-1	Homo sapiens
170	AAH07333	2823	100	BC007333 ets variant gene 5 (ets-related molecule)	Homo sapiens
170	X76184	2823	100	ets-related protein	Homo sapiens
170	X96381	2823	100	erm	Homo sapiens
171	AAH02599	996	99	BC002599 corticotropin releasing hormone	Homo sapiens
171	AAH11031	996	99	BC011031 Similar to corticotropin releasing hormone	Homo sapiens
171	V00571	996	99	corticotropin releasing factor	Homo sapiens
172	AF151872_1	1069	100	AF151872 CGI-114 protein	Homo sapiens
172	AL110239	1066	99	hypothetical protein	Homo sapiens
172	AX399865	1069	100	unnamed protein product	Homo sapiens
173	AAH00732	1553	100	BC000732 glioblastoma amplified sequence	Homo sapiens
173	AAH01837	1553	100	BC001837 glioblastoma amplified sequence	Homo sapiens
173	BC030821	1553	100	glioblastoma amplified sequence	Homo sapiens
174	AAH01483	2103	100	BC001483 Unknown (protein for MGC:1364)	Homo sapiens
174	AAH09241	2103	100	BC009241 Unknown (protein for MGC:3556)	Homo sapiens
174	BC023599	2103	100	TRK-fused gene	Homo sapiens
175	AAH12806	3278	100	BC012806 solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Homo sapiens
175	AAH15631	3278	100	BC015631 solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Homo sapiens
175	AF116241	3272	99	sodium-dependent multivitamin transporter	Homo sapiens
177	AAH04324	744	100	BC004324 ribosomal protein S16	Homo sapiens
177	AAH07977	744	100	BC007977 ribosomal protein S16	Homo sapiens
177	X17665	744	100	ribosomal protein S16 (AA 1-146)	Rattus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
					rattus
178	AB047555	624	90	IZP6	Mus musculus musculus
178	AK007948	624	90	unnamed protein product	Mus musculus
178	BC004729	624	90	RIKEN cDNA 1810063P04 gene	Mus musculus
179	BC003337	1957	100	actin, gamma 1	Mus musculus
179	BC021796	1957	100	actin, gamma 1	Mus musculus
179	BC023248	1957	100	actin, gamma, cytoplasmic	Mus musculus
180	AAH11700	2048	100	BC011700 glutamate-ammonia ligase (glutamine synthase)	Homo sapiens
180	AAH11852	2048	100	BC011852 glutamate-ammonia ligase (glutamine synthase)	Homo sapiens
180	AAH18992	2048	100	BC018992 Unknown (protein for MGC:20095)	Homo sapiens
181	AF234654_1	1155	100	AF234654 PLAC1	Homo sapiens
181	AK075086	1155	100	unnamed protein product	Homo sapiens
181	BC022335	1155	100	placenta-specific 1	Homo sapiens
182	AAB67977	4108	99	AF019413 complement factor B	Homo sapiens
182	AAH04143	4121	100	BC004143 B-factor, properdin	Homo sapiens
182	AAH07990	4121	100	BC007990 B-factor, properdin	Homo sapiens
183	AAH17399	355	98	BC017399 Similar to RIKEN cDNA 1810037I17 gene	Homo sapiens
183	AK007721	236	68	unnamed protein product	Mus musculus
183	BC002135	236	68	Unknown (protein for MGC:7243)	Mus musculus
184	AAH13383	1701	100	BC013383 calumenin	Homo sapiens
184	AF013759	1701	100	calumein	Homo sapiens
184	U67280	1695	99	calumenin	Homo sapiens
185	AF069065	596	97	inducible cAMP early repressor type 1	Homo sapiens
185	AJ311667	588	95	induced cAMP early repressor, ICER 1	Mus musculus
185	D14826	608	100	hCREM 2alpha-a protein	Homo sapiens
186	AAH00452	1043	100	BC000452 Similar to thioredoxin peroxidase 1	Homo sapiens
186	AAH03022	1043	100	BC003022 Similar to thioredoxin peroxidase 1	Homo sapiens
186	BC039428	1043	100	Similar to peroxiredoxin 2	Homo sapiens
187	AB056107	2995	100	zinc finger protein homologous to mouse Zfp91	Homo sapiens
187	AB057443	2775	100	testis specific ZFP91	Homo sapiens
187	AF310246_1	2586	99	AF310246 FKSG11	Homo sapiens
188	AF023476	4954	100	meltrin-L precursor	Homo sapiens
188	AF023477	3855	99	meltrin-S	Homo sapiens
188	D50411	3939	80	meltrin alpha	Mus musculus
189	AF154121_1	2195	94	AF154121 sodium-dependent high-affinity dicarboxylate transporter	Homo sapiens
189	AL034424.	2126	91	dJ257E24.2.1 (sodium-dependent high-affinity dicarboxylate transporter (NADC3, SDCT2) (isoform 1))	Homo sapiens
189	AY072810	2126	91	energy metabolism-related sodium-dependent high-affinity dicarboxylate transporter	Homo sapiens
190	AF400594	352	54	endothelial nitric oxide synthase	Homo sapiens
190	AF519768_1	352	54	AF519768 nitric oxide synthase 3 (endothelial cell)	Homo sapiens
190	D26607	350	53	endothelial nitric oxide synthase	Homo sapiens
191	AAH01462	1835	100	BC001462 protease, serine, 8 (prostasin)	Homo sapiens
191	L41351	1835	100	prostasin	Homo sapiens
191	U33446	1835	100	prostasin	Homo sapiens
192	AK025116	272	73	unnamed protein product	Homo sapiens
192	AK090913	310	71	unnamed protein product	Homo sapiens
192	BC033959	200	70	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
193	AF346465	7291	91	latent transforming growth factor	Mus musculus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				beta binding protein 1S	
193	AF489528_1	7887	99	AF489528 transforming growth factor-beta binding protein-1S	Homo sapiens
193	M34057	7903	100	transforming growth factor-beta 1 binding protein precursor	Homo sapiens
194	AY004254	1199	90	endoplasmic reticulum protein 29 precursor	Rattus norvegicus
194	X94910	1334	100	ERp28	Homo sapiens
194	Y10264	1199	90	ERp29 precursor	Rattus norvegicus
195	AF119917_58	250	100	AF119896 PRO2751	Homo sapiens
196	AB020692	4158	100	KIAA0885 protein	Homo sapiens
196	BC016898	4107	98	Unknown (protein for MGC:19174)	Mus musculus
196	X52311	4102	98	unr protein (AA 1-798)	Rattus norvegicus
198	AL049698	7034	98	dJ470B24.1.3 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 3))	Homo sapiens
198	AL049698	7050	98	dJ470B24.1.5 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 5))	Homo sapiens
198	AL161973	7363	100	hypothetical protein	Homo sapiens
199	AAH21288	2134	100	BC021288 Unknown (protein for MGC:29494)	Homo sapiens
199	J03263	1934	98	membrane glycoprotein	Homo sapiens
199	J04182	2041	96	lysosomal membrane glycoprotein-1	Homo sapiens
200	AC002400	817	100	Acyl carrier protein, Mitochondrial (ACP) (5'partial)	Homo sapiens
200	AF087660_1	788	100	AF087660 NADH:ubiquinone oxidoreductase SDAP subunit	Homo sapiens
200	AK018717	672	85	unnamed protein product	Mus musculus
201	AB031550	1298	87	pctp-L	Mus musculus
201	AF151810_1	1470	90	AF151810 CGI-52 protein	Homo sapiens
201	Z81134	419	39	Hypothetical protein T28D6.7	Caenorhabditis elegans
203	AAH09392	5306	99	BC009392 Unknown (protein for MGC:15329)	Homo sapiens
203	AB011149	5318	100	KIAA0577 protein	Homo sapiens
203	AP000512	5318	100	RNA helicase	Homo sapiens
204	AAH08751	3757	99	BC008751 calpain 1, (mu/I) large subunit	Homo sapiens
204	AAH17200	3762	100	BC017200 calpain 1, (mu/I) large subunit	Homo sapiens
204	X04366	3762	100	CANP, large subunit (aa 1-714)	Homo sapiens
205	AB093679	740	100	ribosomal protein L26	Macaca fascicularis
205	X69392	740	100	ribosomal protein L26	Homo sapiens
205	X80699	740	100	L26	Mus musculus
206	AAH06391	1974	100	BC006391 inhibin, alpha	Homo sapiens
206	M13981	1974	100	inhibin A-subunit precursor	Homo sapiens
206	X04445	1974	100	preproinhibin	Homo sapiens
207	AK025116	190	66	unnamed protein product	Homo sapiens
207	AK092450	300	63	unnamed protein product	Homo sapiens
207	AK097214	305	68	unnamed protein product	Homo sapiens
208	AF130117_48	337	73	AF130089 PRO2550	Homo sapiens
208	AK000385	333	70	unnamed protein product	Homo sapiens
208	AK092450	336	70	unnamed protein product	Homo sapiens
209	AB062485	161	77	OK/SW-CL.18	Homo sapiens
209	AF090930_1	172	51	AF090930 PRO0478	Homo sapiens
209	AX399919	158	68	unnamed protein product	Homo sapiens
210	AF063591_1	1401	99	AF063591 brain my033 protein	Homo sapiens
210	BC022522	1411	100	antigen identified by monoclonal antibody MRC OX-2	Homo sapiens
210	BC031103	1411	100	antigen identified by monoclonal	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				antibody MRC OX-2	
211	AAH00692	2582	100	BC000692 Similar to hyaluronoglucosaminidase 2	Homo sapiens
211	AC002455	2579	99	human PH-20 homolog (LUCA-2)	Homo sapiens
211	U09577	2579	99	lysosomal hyaluronidase	Homo sapiens
212	AAH02700	2294	100	BC002700 Similar to keratin 7	Homo sapiens
212	AF509887	2294	100	keratin 7	Homo sapiens
212	AF509892	2294	100	keratin 7	Homo sapiens
213	AF523361_1	1951	99	AF523361 CD34 antigen	Homo sapiens
213	M81945	1955	100	hematopoietic stem cell antigen	Homo sapiens
213	S53910	1951	99	CD34	Homo sapiens
214	AB037891	493	100	Bcl10	Mus musculus
214	AF303656_1	493	100	AF303656 bladder cancer-related protein	Mus musculus
214	BC026935	493	100	bladder cancer associated protein	Mus musculus
215	AF322909	3026	100	transmembrane glycoprotein HGFIN	Homo sapiens
215	BC032783	3003	97	Similar to glycoprotein (transmembrane) nmb	Homo sapiens
215	X76534	3026	100	NMB	Homo sapiens
216	AAH17352	3091	100	BC017352 Unknown (protein for MGC:29525)	Homo sapiens
216	AF230388_1	3085	99	AF230388 tripartite motif protein TRIM29 alpha	Homo sapiens
216	L24203	3085	99	ataxia-telangiectasia group D-associated protein	Homo sapiens
217	AK003609	523	100	unnamed protein product	Mus musculus
217	AL136635	523	100	hypothetical protein	Homo sapiens
217	BC016408	523	100	RIKEN cDNA 1110011F09 gene	Mus musculus
218	AF073310	7103	100	insulin receptor substrate-2	Homo sapiens
218	AF385932_1	7014	99	AF385932 insulin receptor substrate 2 insertion mutant	Homo sapiens
218	AF385933_1	7026	99	AF385933 insulin receptor substrate 2 insertion mutant	Homo sapiens
219	AAH09586	1584	70	BC009586 Unknown (protein for MGC:14649)	Homo sapiens
219	D26485	1584	70	core I protein	Homo sapiens
219	L16842	1584	70	ubiquinol-cytochrome c reductase core I protein	Homo sapiens
220	AF062534	1919	100	genethonin 1	Homo sapiens
220	AK050416	1083	62	unnamed protein product	Mus musculus
220	BC022301	1919	100	genethonin 1	Homo sapiens
221	AAH08950	956	100	BC008950 Unknown (protein for MGC:3593)	Homo sapiens
221	AF112202_1	956	100	AF112202 prenylated rab acceptor 1	Homo sapiens
221	AJ133534	951	99	prenyated Rab acceptor 1 (PRA1)	Homo sapiens
222	AAH14257	888	100	BC014257 Similar to DKFZp564J157 protein	Homo sapiens
222	AAH16064	888	100	BC016064 DKFZp564J157 protein	Homo sapiens
222	AX405840	888	100	unnamed protein product	Homo sapiens
223	AAH02394	2275	100	BC002394 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Homo sapiens
223	AAH04433	2275	100	BC004433 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Homo sapiens
223	U32680	2275	100	CLN3 protein	Homo sapiens
224	AF443072_1	17656	99	AF443072 laminin alpha5 chain precursor	Homo sapiens
224	AL354836	17668	99	ba157P1.1.1 (laminin alpha 5)	Homo sapiens
224	AX463738	17656	99	laminin 5	Homo sapiens
225	BC024366	703	100	ribosomal protein L27	Mus musculus
225	X07424	703	100	ribosomal protein L27 (AA 1 - 136)	Rattus norvegicus
225	X56852	703	100	ribosomal protein L27	Gallus gallus
226	AAH13131	969	100	BC013131 Similar to hypothetical protein FLJ10702	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
226	AK001564	969	100	unnamed protein product	Homo sapiens
226	BC013719	969	100	hypothetical protein FLJ10702	Mus musculus
227	AF214737_1	5676	100	AF214737 C9orf10a	Homo sapiens
227	BC010304	3765	93	Unknown (protein for IMAGE:3597827)	Mus musculus
227	D80005	5676	100	KIAA0183	Homo sapiens
228	AF113127_1	1186	99	AF113127 S1R protein	Homo sapiens
228	AF151877_1	1203	94	AF151877 CGI-119 protein	Homo sapiens
228	AF182041_1	1186	99	AF182041 z-protein	Homo sapiens
229	AAH11616	1514	100	BC011616 Similar to cyclin D3	Homo sapiens
229	AF517525_1	1511	99	AF517525 cyclin D3	Homo sapiens
229	M92287	1514	100	cyclin D3	Homo sapiens
230	AAH11581	4280	100	BC011581 Similar to oxysterol binding protein	Homo sapiens
230	AF185696_1	4280	100	AF185696 oxysterol-binding protein 1	Homo sapiens
230	AF185705	4280	100	oxysterol binding protein 1	Homo sapiens
231	AF053745	462	32	pol polyprotein	Mus dunni endogenous virus
231	AF151794	473	35	pol protein	Phascolarctos cinereus
231	D10032	506	36	gag-pol precursor polyprotein	Baboon endogenous virus strain M7
232	AF012920	625	100	GEC-1	Cavia porcellus
232	AF312680	625	100	GEC-1	Cavia porcellus
232	BC004602	625	100	RIKEN cDNA 9130422N19 gene	Mus musculus
233	AAH14241	1733	100	BC014241 Similar to hypothetical protein, MGC:7035	Homo sapiens
233	AB093636	1687	96	hypothetical protein	Macaca fascicularis
233	AK046512	1274	74	unnamed protein product	Mus musculus
234	AF140240_1	749	100	AF140240 transcription factor TBX3	Homo sapiens
234	AK075457	749	100	unnamed protein product	Homo sapiens
234	BC025258	749	100	T-box 3 (ulnar mammary syndrome)	Homo sapiens
235	AB062477	166	64	OK/SW-CL.41	Homo sapiens
235	AK054840	167	65	unnamed protein product	Homo sapiens
235	AK092888	224	74	unnamed protein product	Homo sapiens
236	AAH01863	320	100	BC001863 hypoxia-inducible protein 2	Homo sapiens
236	AF144755_1	320	100	AF144755 hypoxia-inducible protein 2	Homo sapiens
236	AX105363	320	100	unnamed protein product	Homo sapiens
237	AAH00718	1025	97	BC000718 Similar to dynactin (dynactin complex 50 kD subunit)	Homo sapiens
237	AAH09468	1025	97	BC009468 dynactin 2 (p50)	Homo sapiens
237	AAH14083	1025	97	BC014083 dynactin 2 (p50)	Homo sapiens
238	AB037669	2790	100	L-type amino acid transporter 2	Homo sapiens
238	AF171669_1	2790	100	AF171669 glycoprotein-associated amino acid transporter LAT2	Homo sapiens
238	Y18483	2778	99	SLC7A8 protein	Homo sapiens
239	AF118094_21	187	48	AF118082 PRO1902	Homo sapiens
239	AF119917_13	158	61	AF119851 PRO1722	Homo sapiens
239	AK097266	185	60	unnamed protein product	Homo sapiens
240	AK075392	1353	90	unnamed protein product	Homo sapiens
240	AX136157	1353	90	unnamed protein product	Homo sapiens
240	AX179293	1356	90	21676 ADH	Homo sapiens
241	AF328769_1	2426	91	AF328769 PC2-glutamine-rich-associated protein	Homo sapiens
241	AK090465	2677	99	FLJ00386 protein	Homo sapiens
241	BC017110	2677	99	Unknown (protein for MGC:16010)	Homo sapiens
242	AAH10514	2363	100	BC010514 clusterin (complement lysis inhibitor, SP-40,40,	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	
242	AAH19588	2363	100	BC019588 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	Homo sapiens
242	X14723	2363	100	SP-40,40 preproptide (AA -22 to 427)	Homo sapiens
243	AAH06786	1161	100	BC006786 cellular repressor of E1A-stimulated genes	Homo sapiens
243	AAH08628	1161	100	BC008628 cellular repressor of E1A-stimulated genes	Homo sapiens
243	AF084523	1161	100	cellular repressor of E1A-stimulated genes CREG	Homo sapiens
244	AX167114	8220	99	unnamed protein product	Homo sapiens
244	BC036531	8206	99	Unknown (protein for MGC:33668)	Homo sapiens
244	Z74615	8220	99	prepro-alpha1(I) collagen	Homo sapiens
245	AB025412	5671	98	Ten-m3	Mus musculus
245	AF195418_1	5676	99	AF195418 ODZ3	Mus musculus
245	AK001336	5447	100	unnamed protein product	Homo sapiens
246	AAH03550	1419	100	BC003550 Similar to CGI-20 protein	Homo sapiens
246	AF132954_1	1577	99	AF132954 CGI-20 protein	Homo sapiens
246	AK003551	1613	95	unnamed protein product	Mus musculus
247	BC022512	242	96	platelet/endothelial cell adhesion molecule (CD31 antigen)	Homo sapiens
247	L34657	242	96	platelet endothelial cell adhesion molecule-1	Homo sapiens
247	M28526	242	96	PECAM-1 precursor	Homo sapiens
248	AAH12138	1849	100	BC012138 Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Homo sapiens
248	AF493906_1	1849	100	AF493906 guanine nucleotide binding protein alpha i2	Homo sapiens
248	X04828	1849	100	G protein alpha-subunit (AA 1-355)	Homo sapiens
249	AF081258_1	3091	100	AF081258 testis-specific chromodomain Y-like protein	Homo sapiens
249	AF081259_1	3091	100	AF081259 testis-specific chromodomain Y-like protein	Homo sapiens
249	AF081261_1	2614	88	AF081261 testis-specific chromodomain Y-like protein	Mus musculus
250	AF162856_1	5147	65	AF162856 receptor-like protein tyrosine phosphatase rho-1	Mus musculus
250	X58287	7569	97	protein-tyrosine phosphatase	Mus musculus
250	X58288	7731	99	protein-tyrosine phosphatase	Homo sapiens
251	AK096998	303	65	unnamed protein product	Homo sapiens
251	AK097965	304	73	unnamed protein product	Homo sapiens
251	BC033959	333	77	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
252	AAH18991	1272	100	BC018991 hepatoma-derived growth factor (high-mobility group protein 1-like)	Homo sapiens
252	AJ237996	1205	95	hepatoma derived growth factor	Bos taurus
252	D16431	1272	100	hepatoma-derived GF	Homo sapiens
253	AAH17197	1785	99	BC017197 myeloid cell leukemia sequence 1 (BCL2-related)	Homo sapiens
253	AF147742_1	1785	99	AF147742 myeloid cell differentiation protein	Homo sapiens
253	AF162677	1785	99	myeloid cell leukemia protein 1	Homo sapiens
254	AF274892	2520	100	glucose transporter 3	Homo sapiens
254	BC039196	2520	100	solute carrier family 2 (facilitated glucose transporter), member 3	Homo sapiens
254	M20681	2520	100	glucose transporter-like protein	Homo sapiens

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255	AAH00730	3448	100	BC000730 calpain 6	Homo sapiens
255	AJ000388	3439	99	calpain-like protease, CANPX	Homo sapiens
255	AL031117	3448	100	dJ914P14.1 (calpain-like protease CANPX)	Homo sapiens
256	AAH03143	1980	100	BC003143 dual specificity phosphatase 6	Homo sapiens
256	AAH03562	1980	100	BC003562 dual specificity phosphatase 6	Homo sapiens
256	X93920	1980	100	protein-tyrosine-phosphatase	Homo sapiens
257	AB023194	6006	100	KIAA0977 protein	Homo sapiens
257	AK052533	3549	61	unnamed protein product	Mus musculus
257	AL049939	1823	99	hypothetical protein	Homo sapiens
258	AAH15031	4447	100	BC015031 Unknown (protein for MGC:9105)	Homo sapiens
258	AB018266	4447	100	KIAA0723 protein	Homo sapiens
258	BC029070	4375	98	Similar to matrin 3	Mus musculus
259	AAH18726	1229	100	BC018726 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Homo sapiens
259	M13560	1229	100	cell surface glycoprotein	Homo sapiens
259	X00497	1229	100	putative p33	Homo sapiens
260	AF114262_3	2305	88	AF114260 forkhead protein AFXH	Mus musculus
260	X93996	2624	100	AFX	Homo sapiens
260	Y11284	2489	97	AFX1	Homo sapiens
261	AAH09409	1688	100	BC009409 Unknown (protein for MGC:10655)	Homo sapiens
261	X13425	1688	100	GA733-1 protein (AA 1-323)	Homo sapiens
261	X77754	1688	100	gp50/TROP-2	Homo sapiens
262	AAH02532	795	100	BC002532 epididymal secretory protein (19.5kD)	Homo sapiens
262	X67698	795	100	orf	Homo sapiens
262	X78134	795	100	epididymal secretory protein 14.6	Macaca fascicularis
263	AK075092	233	100	unnamed protein product	Homo sapiens
264	AAH16692	1163	100	BC016692 progesterone receptor membrane component 2	Homo sapiens
264	AJ002030	1163	100	progesterone binding protein	Homo sapiens
264	AY069921	525	60	membrane progesterone receptor-like protein	Oncorhynchus mykiss
265	AAH16041	1441	100	BC016041 insulin-like growth factor-binding protein 4	Homo sapiens
265	M62403	1441	100	IGF-BP 4	Homo sapiens
265	Y12508	1441	100	insulin-like growth factor binding protein 4	Homo sapiens
266	AK000575	734	100	unnamed protein product	Homo sapiens
266	AK013438	484	72	unnamed protein product	Mus musculus
266	AY116892	734	100	HCF-1 beta-propeller interacting protein	Homo sapiens
267	AAH14410	2273	100	BC014410 Similar to EGF-containing fibulin-like extracellular matrix protein 1	Homo sapiens
267	AK077302	2156	93	unnamed protein product	Mus musculus
267	AY004330	2273	100	EGF-containing fibulin-like extracellular matrix protein 1	Homo sapiens
268	AF102552	11066	84	270 kDa ankyrin G isoform	Rattus norvegicus
268	L40632	7184	95	ankyrin 3	Mus musculus
268	U13616	20107	99	ankyrin G	Homo sapiens
269	AC002073	3406	100	Lim Kinase	Homo sapiens
269	AL117466	3183	100	hypothetical protein	Homo sapiens
269	D45906	3406	100	LIMK-2	Homo sapiens
270	AAH00836	633	100	BC000836 CGI-127 protein	Homo sapiens
270	AF135161_1	633	100	AF135161 unknown	Homo sapiens
270	AF151885_1	633	100	AF151885 CGI-127 protein	Homo sapiens
271	A16768	356	79	kunitz type protease inhibitor	synthetic construct
271	BC033174	501	98	Similar to collagen, type VI,	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				alpha 3	
271	X52022	501	98	collagen type VI, alpha 3 chain	Homo sapiens
272	AAH04440	405	100	BC004440 Unknown (protein for MGC:4033)	Homo sapiens
272	AAH19336	424	98	BC019336 Unknown (protein for IMAGE:3617778)	Homo sapiens
272	U91512	399	98	ninjurin	Homo sapiens
273	AAH18127	1250	93	BC018127 Similar to Peptidylglycine alpha-amidating monooxygenase	Homo sapiens
273	AB095007	1250	93	peptidylglycine alpha-amidating monooxygenase	Homo sapiens
273	AF035320	1279	100	peptidylglycine alpha-amidating monooxygenase	Homo sapiens
274	AAH13398	6167	100	BC013398 pumilio (Drosophila) homolog 1	Homo sapiens
274	AF315592.1	6167	100	AF315592 Pumilio 1	Homo sapiens
274	D43951	6233	100	KIAA0099 protein	Homo sapiens
275	AAH00465	826	100	BC000465 growth arrest and DNA-damage-inducible, gamma	Homo sapiens
275	AAH19325	826	100	BC019325 growth arrest and DNA-damage-inducible, gamma	Homo sapiens
275	AF494037.1	826	100	AF494037 growth arrest and DNA-damage-inducible, gamma	Homo sapiens
276	AAH01955	883	100	BC001955 ribosomal protein S10	Homo sapiens
276	AAH04334	883	100	BC004334 ribosomal protein S10	Homo sapiens
276	AAH05012	883	100	BC005012 ribosomal protein S10	Homo sapiens
277	AAH12740	4687	99	BC012740 Similar to dystroglycan 1 (dystrophin-associated glycoprotein 1)	Homo sapiens
277	AAH14616	4687	99	BC014616 Unknown (protein for MGC:3618)	Homo sapiens
277	L19711	4703	100	dystroglycan	Homo sapiens
278	AAH20983	583	100	BC020983 pituitary tumor-transforming 1 interacting protein	Homo sapiens
278	BC031097	583	100	pituitary tumor-transforming 1 interacting protein	Homo sapiens
278	BC034250	583	100	pituitary tumor-transforming 1 interacting protein	Homo sapiens
279	AAH07082	185	100	BC007082 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Homo sapiens
279	AAH11017	185	100	BC011017 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Homo sapiens
279	AF035262	185	100	BAF57	Homo sapiens
281	AF099154	13656	86	von Willebrand factor	Canis familiaris
281	M25865	15510	99	von Willebrand factor	Homo sapiens
281	X04385	15515	100	VWF pre-pro-polypeptide (-22 to 2791)	Homo sapiens
282	AAH17692	1500	78	BC017692 Similar to quiescin Q6	Homo sapiens
282	AF361868	1492	78	sulfhydryl oxidase	Homo sapiens
282	U97276	2262	84	quiescin	Homo sapiens
284	AAH12123	1528	100	BC012123 golgi phosphoprotein 3	Homo sapiens
284	AJ296152	1528	100	Golgi protein	Homo sapiens
284	BC033725	1528	100	golgi phosphoprotein 3 (coat-protein)	Homo sapiens
285	AAH08726	2687	100	BC008726 oxidative-stress responsive 1	Homo sapiens
285	AB017642	2687	100	oxidative-stress responsive 1	Homo sapiens
285	AB029024	2355	100	KIAA1101 protein	Homo sapiens
286	AAH00478	3403	99	BC000478 heat shock 70kD protein 9B (mortalin-2)	Homo sapiens
286	BC024034	3403	99	heat shock 70kD protein 9B (mortalin-2)	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
286	BC030634	3399	99	heat shock 70kD protein 9B (mortalin-2)	Homo sapiens
287	BC006834	892	100	B-cell translocation gene 1, anti-proliferative	Mus musculus
287	BC018309	892	100	B-cell translocation gene 1, anti-proliferative	Mus musculus
287	Z16410	892	100	btgl	Mus musculus
288	AE003667	256	81	CG9318-PA	Drosophila melanogaster
288	AF026213	244	71	Hypothetical protein F08F1.7	Caenorhabditis elegans
288	AY069665	256	81	LD44273p	Drosophila melanogaster
289	A03736	3879	100	factor XIIIa	Homo sapiens
289	M14354	3879	100	clotting factor XIIIa precursor (EC 2.3.2.13)	Homo sapiens
289	M14539	4016	99	factor XIII precursor	Homo sapiens
290	AAH06541	969	99	BC006541 integrin, beta 5	Homo sapiens
290	J05633	962	98	integrin beta-5 subunit precursor	Homo sapiens
290	X53002	969	99	precursor polypeptide (AA -23 to 776)	Homo sapiens
291	D50929	7262	100	The KIAA0139 gene product is related to mouse centrosomin B.	Homo sapiens
291	U58046	7262	100	p167	Homo sapiens
291	U78311	7262	100	translation initiation factor 3 large subunit	Homo sapiens
292	AAH01571	2935	100	BC001571 eukaryotic translation initiation factor 3, subunit 8 (110kD)	Homo sapiens
292	AC002544	2935	100	Translation initiation factor eIF-p110	Homo sapiens
292	U46025	2935	100	translation initiation factor eIF-3 p110 subunit	Homo sapiens
293	AB019987	6513	99	chromosome-associated polypeptide-C	Homo sapiens
293	AF092564	6041	99	chromosome-associated protein-C	Homo sapiens
293	AL136877	6517	100	hypothetical protein	Homo sapiens
294	AAH01756	2880	99	BC001756 phosphoglucomutase 1	Homo sapiens
294	AAH19920	2873	99	BC019920 Unknown (protein for MGC:29909)	Homo sapiens
294	M83088	2880	99	PGM1	Homo sapiens
295	AB020664	3759	100	KIAA0857 protein	Homo sapiens
295	AF334812_1	3333	100	AF334812 Rab11 interacting protein Ripla	Homo sapiens
295	BC035013	3303	99	Similar to Rab coupling protein	Homo sapiens
296	AF356518_1	1637	100	AF356518 junctional adhesion molecule 3 precursor	Homo sapiens
296	AF448478_1	1637	100	AF448478 junctional adhesional molecule-3	Homo sapiens
296	AJ416101	1870	100	junction adhesion molecule 3	Homo sapiens
297	AF130117_48	239	76	AF130089 PRO2550	Homo sapiens
297	AK000385	240	76	unnamed protein product	Homo sapiens
297	AK090988	218	71	unnamed protein product	Homo sapiens
298	AAH01562	3284	100	BC001562 nuclear receptor coactivator 4	Homo sapiens
298	AL162047	3284	100	hypothetical protein	Homo sapiens
298	L49399	3284	100	ORF	Homo sapiens
299	AAH02356	2379	100	BC002356 nucleobindin 1	Homo sapiens
299	M96824	2326	98	nucleobindin	Homo sapiens
299	U31342	2357	99	nucleobindin	Homo sapiens
300	AAH17180	4694	100	BC017180 Unknown (protein for MGC:790)	Homo sapiens
300	AK088028	4597	97	unnamed protein product	Mus musculus
300	BC007126	4597	97	Unknown (protein for MGC:5677)	Mus musculus
301	AAH08099	378	100	BC008099 Unknown (protein for IMAGE:4183312)	Homo sapiens
301	AAH18427	214	100	BC018427 Unknown (protein for IMAGE:4515233)	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
302	AF137053_1	2310	99	AF137053 mutant desmin	Homo sapiens
302	BC032116	2313	99	desmin	Homo sapiens
302	U59167	2325	100	desmin	Homo sapiens
303	AL445795	23376	99	heparan sulfate proteoglycan perlecan	Homo sapiens
303	M85289	23477	99	heparan sulfate proteoglycan	Homo sapiens
303	X62515	23627	99	Human basement membrane heparan sulfate proteoglycan core protein	Homo sapiens
304	AK025116	206	48	unnamed protein product	Homo sapiens
304	AK057830	227	49	unnamed protein product	Homo sapiens
304	AK090511	194	51	unnamed protein product	Homo sapiens
305	AAH00429	309	100	BC000429 chromosome 14 open reading frame 2	Homo sapiens
305	AAH01944	309	100	BC001944 chromosome 14 open reading frame 2	Homo sapiens
305	AF054175	309	100	mitochondrial proteolipid 68MP homolog	Homo sapiens
306	AAH01263	2152	100	BC001263 serum/glucocorticoid regulated kinase	Homo sapiens
306	AF153609_1	2152	100	AF153609 serine/threonine protein kinase sgk	Homo sapiens
306	AX553549	2152	100	unnamed protein product	Homo sapiens
307	AAH07103	710	100	BC007103 small acidic protein	Homo sapiens
307	AAH16352	710	100	BC016352 small acidic protein	Homo sapiens
307	AAH20937	710	100	BC020937 small acidic protein	Homo sapiens
309	AY043487	412	100	selenoprotein SelM	Homo sapiens
309	AY043488	367	85	selenoprotein SelM	Mus musculus
309	BC019742	345	85	Unknown (protein for MGC:30803)	Mus musculus
310	AF124719_1	1018	100	AF124719 GM2 activator protein	Homo sapiens
310	X61095	1039	97	GM2-activator protein	Homo sapiens
310	X62078	1018	100	GM2 activator protein	Homo sapiens
311	AB028974	1802	100	KIAA1051 protein	Homo sapiens
311	AX082622	1995	100	unnamed protein product	Homo sapiens
311	AX082622	2129	100	unnamed protein product	Homo sapiens
312	BC026690	3964	100	CD97 antigen	Homo sapiens
312	U76764	3796	87	CD97	Homo sapiens
312	X84700	3951	99	leucocyte antigen CD97	Homo sapiens
313	K03195	2422	99	glucose transporter glycoprotein	Homo sapiens
313	M13979	2367	97	glucose-transporter protein	Rattus norvegicus
313	M22063	2367	97	glucose transporter protein	Rattus norvegicus
314	AAH19297	1801	100	BC019297 Unknown (protein for MGC:4111)	Homo sapiens
314	AK021655	1801	100	unnamed protein product	Homo sapiens
314	AK022757	1801	100	unnamed protein product	Homo sapiens
315	AC005943	1522	100	methyl-CpG binding protein MBD3	Homo sapiens
315	AF072247	1522	100	methyl-CpG binding domain-containing protein MBD3	Homo sapiens
315	AF072248	1427	95	methyl-CpG binding domain-containing protein MBD3	Mus musculus
316	AB018009	2602	100	L-type amino acid transporter 1	Homo sapiens
316	AB018542	2602	100	CD98 light chain	Homo sapiens
316	AF104032	2602	100	L-type amino acid transporter subunit LAT1	Homo sapiens
318	AAH10737	1911	100	BC010737 Similar to reticulon 4	Homo sapiens
318	AAH12619	1911	100	BC012619 Unknown (protein for MGC:13655)	Homo sapiens
318	BC026788	1911	100	reticulon 4	Homo sapiens
319	AAH02412	3766	99	BC002412 inner membrane protein, mitochondrial (mitofilin)	Homo sapiens
319	D21094	3766	99	motor protein	Homo sapiens
319	L42572	3771	100	transmembrane protein	Homo sapiens
320	AAH01925	573	100	BC001925 FK506-binding protein 1A (12kD)	Homo sapiens
320	AAH05147	573	100	BC005147 FK506-binding protein 1A (12kD)	Homo sapiens
320	M93060	573	100	FK506-binding protein 12	Homo sapiens

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321	AF116721_20	391	100	AF116620 PRO1068	Homo sapiens
322	AK075023	1335	99	unnamed protein product	Homo sapiens
322	AL117442	1344	100	hypothetical protein	Homo sapiens
322	BC002138	1302	96	Unknown (protein for IMAGE:3484538)	Mus musculus
323	AAH07674	382	100	BC007674 CD24 antigen (small cell lung carcinoma cluster 4 antigen)	Homo sapiens
323	L33930	382	100	signal transducer CD24	Homo sapiens
323	M58664	382	100	signal transducer CD24	Homo sapiens
324	AAH12181	4260	100	BC012181 Similar to paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein)	Homo sapiens
324	U20436	4060	95	furin endoprotease	Cricetulus griseus
324	X17094	4260	100	furin (AA 1-794)	Homo sapiens
325	AAH15236	876	100	BC015236 hypothetical protein	Homo sapiens
325	AF335324_1	876	100	AF335324 RTP801	Homo sapiens
325	AY090097	876	100	REDD-1	Homo sapiens
326	AK000496	332	66	unnamed protein product	Homo sapiens
326	AK025116	327	69	unnamed protein product	Homo sapiens
326	AK057830	358	69	unnamed protein product	Homo sapiens
327	AAH10058	3813	100	BC010058 exostoses (multiple) 2	Homo sapiens
327	U62740	3813	100	EXT2	Homo sapiens
327	U67368	3813	100	multiple exostosis 2	Homo sapiens
328	AAH08301	1967	100	BC008301 tuftelin 1	Homo sapiens
328	AF254260_1	1967	100	AF254260 tuftelin 1	Homo sapiens
328	AF254860	1967	100	tuftelin 1	Homo sapiens
330	AF272662_1	6961	80	AF272662 alpha 1 type V collagen	Rattus norvegicus
330	D90279	7452	86	collagen alpha 1(V) chain precursor	Homo sapiens
330	M76729	7422	85	pro-alpha-1 type V collagen	Homo sapiens
331	AAH03155	1193	76	BC003155 coatomer protein complex, subunit epsilon	Homo sapiens
331	AAH07250	1193	76	BC007250 coatomer protein complex, subunit epsilon	Homo sapiens
331	AAH17285	1193	76	BC017285 Unknown (protein for MGC:29652)	Homo sapiens
332	AX354381	347	100	unnamed protein product	Homo sapiens
333	AF202636_1	2164	100	AF202636 angiopoietin-like protein PP1158	Homo sapiens
333	AX079971	2164	100	unnamed protein product	Homo sapiens
333	BC023647	2164	100	angiopoietin-like 4	Homo sapiens
334	AAH12777	162	100	BC012777 Unknown (protein for MGC:16395)	Homo sapiens
334	AK056767	1189	100	unnamed protein product	Homo sapiens
334	AL831913	713	85	hypothetical protein	Homo sapiens
335	AAH01270	1896	100	BC001270 SH3-domain GRB2-like 1	Homo sapiens
335	U65999	1896	100	SH3-containing protein EEN	Homo sapiens
335	X99656	1896	100	SH3-containing Grb-2-like 1	Homo sapiens
336	AAH00385	4505	100	BC000385 Unknown (protein for MGC:8429)	Homo sapiens
336	AF102803	4505	100	alphaE-catenin	Homo sapiens
336	D13866	4505	100	alpha-catenin	Homo sapiens
337	AAH07564	601	90	BC007564 annexin A11	Homo sapiens
337	AJ278464	601	90	annexin A11	Homo sapiens
337	AJ278465	601	90	annexin A11	Homo sapiens
338	AAH01491	1470	99	BC001491 heme oxygenase (decycling) 1	Homo sapiens
338	X06985	1475	100	heme oxygenase (AA 1 - 288)	Homo sapiens
338	Z82244	1475	100	bK286B10.2 (Heme Oxygenase (decycling) 1 (HO-1 EC 1.14.99.3))	Homo sapiens
340	AAH13910	1671	100	BC013910 Similar to death effector domain-containing	Homo sapiens
340	AAH16724	1671	100	BC016724 death effector domain-containing	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
340	AJ010973	1671	100	DEDD protein	Homo sapiens
341	A16794	881	95	cDNA isolated for this protein using a monoclonal antibody directed against the p27k prosomal protein	Homo sapiens
341	BC022354	956	97	proteasome (prosome, macropain) subunit, alpha type 6	Homo sapiens
341	D10755	956	97	proteasome subunit R-IOTA	Rattus sp.
342	AAH09581	2041	100	BC009581 hydroxysteroid (17-beta) dehydrogenase 2	Homo sapiens
342	L11708	2041	100	17 beta hydroxysteroid dehydrogenase type 2	Homo sapiens
342	L40802	2041	100	17-hydroxysteroid dehydrogenase	Homo sapiens
343	AAH08452	586	100	BC008452 ATPase, H+ transporting, lysosomal (vacuolar proton pump), member J	Homo sapiens
343	AF038954	586	100	vacuolar H(+)-ATPase subunit	Homo sapiens
343	S82464	573	96	vacuolar H(+)-ATPase subunit; V-ATPase subunit; M16	Bos taurus
344	AE003452	193	35	CG9350-PB	Drosophila melanogaster
344	AJ510148	571	72	mitochondrial NADH:ubiquinone oxidoreductase B14.7 subunit	Bos taurus
344	AK008201	532	65	unnamed protein product	Mus musculus
345	AB020685	3216	100	KIAA0878 protein	Homo sapiens
345	AK006650	2065	93	unnamed protein product	Mus musculus
345	BC041337	3212	99	Rho-related BTB domain containing 3	Homo sapiens
346	AB058749	1868	100	KIAA1846 protein	Homo sapiens
346	AK092295	1868	100	unnamed protein product	Homo sapiens
346	AL035661	1868	100	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	Homo sapiens
347	AF009242	1168	100	proline-rich Gla protein 1	Homo sapiens
347	AF419154	577	52	mitotic phosphoprotein 77	Xenopus laevis
347	BC030786	1169	84	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	Homo sapiens
348	AF000652	1503	99	syntenin	Homo sapiens
348	AF006636	1508	100	melanoma differentiation associated protein-9	Homo sapiens
348	U83463	1503	99	scaffold protein Pbp1	Homo sapiens
349	AF312032	5200	99	ephrin type-B receptor 4 precursor	Homo sapiens
349	AY056047	5200	99	receptor protein tyrosine kinase EphB4	Homo sapiens
349	U07695	5196	99	tyrosine kinase	Homo sapiens
350	AF015553	4955	99	TFII-I protein	Homo sapiens
350	AF038969	4949	99	general transcription factor 2-I	Homo sapiens
350	Y14946	4949	99	SPIN protein	Homo sapiens
351	AAH07452	1442	100	BC007452 Similar to WW domain binding protein 2	Homo sapiens
351	AAH10616	1442	100	BC010616 Unknown (protein for MGC:18269)	Homo sapiens
351	U79458	1458	100	WW domain binding protein-2	Homo sapiens
352	AB097511	3996	93	hypothetical protein	Macaca fascicularis
352	AL359292	7373	99	dJ448K1.1.1 (absent in melanoma 1, isoform 1)	Homo sapiens
352	U83115	8577	100	non-lens beta gamma-crystallin like protein	Homo sapiens
353	AAH05921	357	86	BC005921 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
353	AAH20756	357	86	BC020756 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
353	AAH22044	357	86	BC022044 chorionic somatomammotropin hormone 2	Homo sapiens
354	AY158924	650	100	histone protein Hist2h2aa2	Mus musculus
354	AY158925	650	100	histone protein Hist2h2aa1	Mus musculus
354	AY158953	650	100	histone protein Hist2h3c2	Mus musculus
355	AF226614_1	2929	100	AF226614 ferroportin1	Homo sapiens
355	AF231121_1	2929	100	AF231121 iron-regulated transporter IREG1	Homo sapiens
355	BC037733	2929	100	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	Homo sapiens
356	AAH01693	709	100	BC001693 lectin, galactoside-binding, soluble, 1 (galectin 1)	Homo sapiens
356	AAH20675	709	100	BC020675 lectin, galactoside-binding, soluble, 1 (galectin 1)	Homo sapiens
356	X14829	709	100	beta-galactoside-binding lectin (AA 1-135)	Homo sapiens
357	AF151794	521	39	pol protein	Phascolarctos cinereus
357	AJ293657	496	37	polymerase	Porcine endogenous type C retrovirus
357	M26927	517	39	pol polyprotein	Gibbon ape leukemia virus
358	AAD18076	689	99	AF129756 G6c	Homo sapiens
358	AJ012008	689	99	Ly6-C protein	Homo sapiens
358	AJ315533	689	99	LY6G6C protein	Homo sapiens
359	AAH11682	2559	100	BC011682 Similar to cathepsin F	Homo sapiens
359	AF132894_1	2559	100	AF132894 cathepsin F	Homo sapiens
359	AJ007331	2559	100	cysteine proteinase	Homo sapiens
360	AF151048_1	407	87	AF151048 HSPC214	Homo sapiens
360	AF247565_1	423	91	AF247565 anaphase promoting complex subunit 11	Homo sapiens
360	AF247789_1	423	91	AF247789 putative anaphase-promoting complex subunit APC11	Homo sapiens
361	AAH11811	559	92	BC011811 Unknown (protein for MGC:20260)	Homo sapiens
361	AF218016_1	432	76	AF218016 unknown	Homo sapiens
362	AAH17201	634	98	BC017201 insulin-like growth factor binding protein 7	Homo sapiens
362	L19182	634	98	MAC25	Homo sapiens
362	S75725	634	98	prostacyclin-stimulating factor; PGI2-stimulating factor; PSF	Homo sapiens
364	AF126110_1	643	96	AF126110 fibulin-1 isoform D precursor	Homo sapiens
364	BC022497	643	96	fibulin 1	Homo sapiens
364	U01244	643	96	fibulin-1D	Homo sapiens
365	AAH05839	414	97	BC005839 follistatin-like 3 (secreted glycoprotein)	Homo sapiens
365	BC033119	414	97	follistatin-like 3 (secreted glycoprotein)	Homo sapiens
365	U76702	414	97	follistatin-related protein FLRG	Homo sapiens
366	AAH00163	601	99	BC000163 vimentin	Homo sapiens
366	BC030573	601	99	Unknown (protein for MGC:16183)	Homo sapiens
366	X56134	601	99	vimentin	Homo sapiens
367	AB018265	5555	100	KIAA0722 protein	Homo sapiens
367	AF045458	5460	100	serine/threonine kinase ULK1	Homo sapiens
367	AF072370_1	4865	89	AF072370 UNC51.1 serine/threonine kinase	Mus musculus
368	AAH00865	227	100	BC000865 Unknown (protein for IMAGE:3460093)	Homo sapiens
369	AAH02978	279	91	BC002978 CD81 antigen (target of antiproliferative antibody 1)	Homo sapiens
369	AF116600	279	91	CD81	Pan troglodytes
369	M33680	279	91	26-kDa cell surface protein TAPA-	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				1	
370	AAH15156	678	100	BC015156 ferritin, heavy polypeptide 1	Homo sapiens
370	AAH16009	678	100	BC016009 ferritin, heavy polypeptide 1	Homo sapiens
370	AAH16857	678	100	BC016857 ferritin, heavy polypeptide 1	Homo sapiens
371	AAH08012	298	67	BC008012 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
371	AAH09907	298	67	BC009907 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
371	AAH12819	298	67	BC012819 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
372	AAH20756	470	83	BC020756 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
372	AAH22044	470	83	BC022044 chorionic somatomammotropin hormone 2	Homo sapiens
372	M15894	461	92	chorionic somatomammotropin precursor	Homo sapiens
373	A65264	705	100	unnamed protein product	unidentified
373	AAH01288	574	93	BC001288 Similar to decay accelerating factor for complement (CD55, Cromer blood group system)	Homo sapiens
373	M31516	574	93	decay-accelerating factor	Homo sapiens
374	AF289553 1	193	75	AF289553 unknown	Homo sapiens
374	AK096998	202	64	unnamed protein product	Homo sapiens
374	AK097342	207	78	unnamed protein product	Homo sapiens
375	AAH05326	499	98	BC005326 ribosomal protein L27a	Homo sapiens
375	AAH20169	499	98	BC020169 Unknown (protein for IMAGE:3543815)	Homo sapiens
375	U14968	499	98	ribosomal protein L27a	Homo sapiens
377	AAH21297	282	91	BC021297 Similar to Dynein heavy chain 64C	Homo sapiens
377	AB002323	282	91	KIAA0325	Homo sapiens
377	AY004877	267	94	cytoplasmic dynein heavy chain	Mus musculus
378	BC026018	643	100	Similar to laminin, beta 1	Homo sapiens
378	M20206	643	100	laminin B1	Homo sapiens
378	M55370	643	100	laminin B1	Homo sapiens
379	AF061658	585	91	cytidine deaminase	Homo sapiens
379	AJ000474	585	91	cytidine deaminase	Homo sapiens
379	L27943	585	91	cytidine deaminase	Homo sapiens
380	AAH18986	412	73	BC018986 Unknown (protein for MGC:20092)	Homo sapiens
380	AF229830	412	73	prostaglandin dehydrogenase	Papio hamadryas
380	U63296	412	73	15-hydroxyprostaglandin dehydrogenase	Homo sapiens
381	AAH00749	507	100	BC000749 lactate dehydrogenase A	Homo sapiens
381	AAH01829	507	100	BC001829 lactate dehydrogenase A	Homo sapiens
381	X03077	507	100	lactate dehydrogenase-A	Homo sapiens
382	AAH00903	749	84	BC000903 high-mobility group (nonhistone chromosomal) protein 2	Homo sapiens
382	AAH01063	749	84	BC001063 high-mobility group (nonhistone chromosomal) protein 2	Homo sapiens
382	X62534	749	84	HMG-2	Homo sapiens
383	AK075214	338	91	unnamed protein product	Homo sapiens
383	AX417526	338	91	unnamed protein product	Homo sapiens
383	AX417528	338	91	unnamed protein product	Homo sapiens
384	AF135060	735	96	fibrillin-2	Rattus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
					norvegicus
384	U03272	745	99	fibrillin-2	Homo sapiens
384	X62009	745	98	fibrillin 5	Homo sapiens
385	AAH13083	478	100	BC013083 Similar to cystatin C (amyloid angiopathy and cerebral hemorrhage)	Homo sapiens
385	X12763	478	100	ompA - cystatin C fusion preprotein (AA -21 to 120)	synthetic construct
385	X61681	478	100	cystatin C	Homo sapiens
387	AF135060	523	89	fibrillin-2	Rattus norvegicus
387	L39790	532	90	fibrillin 2	Mus musculus
387	U03272	597	100	fibrillin-2	Homo sapiens
388	M65149	1200	85	CELF	Rattus norvegicus
388	M83667	1430	100	NF-IL6-beta protein	Homo sapiens
388	S63168	1418	99	CCAAT/enhancer-binding protein delta; C/EBP delta	Homo sapiens
389	AF186111_1	228	52	AF186111 NOTCH4-like protein	Homo sapiens
389	AL512735	228	52	hypothetical protein	Homo sapiens
389	AX133831	228	52	unnamed protein product	Homo sapiens
390	M13452	641	90	lamin A protein	Homo sapiens
390	X03444	631	95	put. lamin A precursor (aa 1-702)	Homo sapiens
390	X66870	629	84	lamin A	Rattus norvegicus
391	U14631	244	100	11 beta-hydroxysteroid dehydrogenase type II	Homo sapiens
391	U26726	244	100	11-beta-hydroxysteroid dehydrogenase type 2	Homo sapiens
391	U27317	244	100	11 beta-hydroxysteroid dehydrogenase 2	Homo sapiens
392	AB049946	666	100	mitochondrial ribosomal protein S15	Homo sapiens
392	AF265439_1	415	100	AF265439 DC37	Homo sapiens
392	BC031336	666	100	mitochondrial ribosomal protein S15	Homo sapiens
393	AAH13733	333	92	BC013733 px19-like protein	Homo sapiens
393	AAH13748	333	92	BC013748 px19-like protein	Homo sapiens
393	AF201925_1	333	92	AF201925 PRELI	Homo sapiens
394	AAH02362	694	100	BC002362 lactate dehydrogenase B	Homo sapiens
394	AAH15122	694	100	BC015122 lactate dehydrogenase B	Homo sapiens
394	Y00711	694	100	lactate dehydrogenase B (AA 1 - 334)	Homo sapiens
395	AAH03070	427	76	BC003070 GATA-binding protein 3	Homo sapiens
395	AAH06793	427	76	BC006793 GATA-binding protein 3	Homo sapiens
395	X55037	427	76	GATA-3	Homo sapiens
396	AF269289_1	287	94	AF269289 unknown	Homo sapiens
397	AAH07728	376	80	BC007728 Unknown (protein for MGC:12671)	Homo sapiens
397	AL080102	376	80	hypothetical protein	Homo sapiens
397	U49436	376	80	translation initiation factor 5	Homo sapiens
398	AAH03190	472	94	BC003190 p75NTR-associated cell death executor; ovarian granulosa cell protein (13kD)	Homo sapiens
398	AF187064_1	472	94	AF187064 p75NTR-associated cell death executor; NADE	Homo sapiens
398	M38188	472	94	unknown	Homo sapiens
399	AB037767	5427	99	KIAA1346 protein	Homo sapiens
399	AF207664_1	5274	100	AF207664 matrix metalloprotease	Homo sapiens
399	AP001697	5274	100	metalloprotease with thrombospondin type 1 motifs	Homo sapiens
400	U90938	213	76	Fc gamma receptor IIc1	Homo sapiens
400	X17652	213	76	IgG Fc receptor	Homo sapiens
400	X17652	213	76	IgG Fc receptor	Homo sapiens
401	AAH01768	390	93	BC001768 neuronatin	Homo sapiens
401	AL109614	390	93	ba425M5.3.1 (neuronatin (isoform 1))	Homo sapiens
401	U31767	390	93	neuronatin alpha	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
402	AF151373_1	328	82	AF151373 nucleolin-related protein NRP	Rattus norvegicus
402	M15825	281	73	nucleolin, C23	Cricetulus griseus
402	M55022	286	75	nucleolin	Rattus norvegicus
403	AAH13428	558	86	BC013428 PP1201 protein	Homo sapiens
403	AF193045_1	558	86	AF193045 unknown	Homo sapiens
403	BC026348	558	86	PP1201 protein	Homo sapiens
404	AF393832_1	721	94	AF393832 beta-actin	Morulus calbasu
404	AY039657	721	94	beta-actin	Chrysophrys auratus
404	AY148350	721	94	actin	Dicentrarchus labrax
405	AK055593	370	98	unnamed protein product	Homo sapiens
406	AAH21233	1036	100	BC021233 ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	Homo sapiens
406	BC022865	1036	100	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	Homo sapiens
406	X83218	1036	100	ATP synthase, oligomycin sensitivity conferring protein	Homo sapiens
407	AAH04368	1221	99	BC004368 proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	Homo sapiens
407	AAH19885	1221	99	BC019885 proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	Homo sapiens
407	D45248	1226	100	proteasome activator hPA28 suunit beta	Homo sapiens
408	AF090306	2306	100	retinoblastoma binding protein	Rattus norvegicus
408	U35143	2306	100	retinoblastoma-binding protein RbAp46	Homo sapiens
408	X72841	2306	100	IEF 7442	Homo sapiens
409	AAH00413	1748	100	BC000413 eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	Homo sapiens
409	AAH03140	1748	100	BC003140 eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	Homo sapiens
409	U39067	1748	100	translation initiation factor eIF3 p36 subunit	Homo sapiens
410	AF042166	13721	100	beta-filamin	Homo sapiens
410	AF043045	13709	99	actin-binding protein homolog ABP-278	Homo sapiens
410	AF191633	13721	100	filamin	Homo sapiens
411	AF165515_1	1862	100	AF165515 ancient ubiquitous protein 1 precursor	Homo sapiens
411	AK023983	1935	100	unnamed protein product	Homo sapiens
411	BC033646	1862	100	ancient ubiquitous protein 1	Homo sapiens
412	AB009865	1347	100	Angiopoietin-2	Homo sapiens
412	AF187858_1	1335	99	AF187858 angiopoietin-2 isoform-1	Homo sapiens
412	AF218015_1	1347	100	AF218015 unknown	Homo sapiens
413	AF035718	914	99	mesoderm-specific basic-helix-loop-helix protein; Pod-1	Homo sapiens
413	AL356109	917	100	bA373A10.1 (transcription factor 21)	Homo sapiens
413	BC025697	917	100	transcription factor 21	Homo sapiens
414	M38690	1200	100	CD9 antigen	Homo sapiens
414	S60489	1200	100	CD9 antigen	Homo sapiens
414	X60111	1200	100	MRP-1 (motility related protein)	Homo sapiens
415	AAH02368	4629	99	BC002368 proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
415	AAH02997	4629	99	BC002997 proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Homo sapiens
415	D78151	4637	100	human 26S proteasome subunit p97	Homo sapiens
416	AAH00182	1622	100	BC000182 annexin A4	Homo sapiens
416	AAH11659	1622	100	BC011659 Similar to annexin A4	Homo sapiens
416	D78152	1622	100	annexin IV (carbohydrate-binding protein p33/41)	Homo sapiens
417	AAH03064	4016	99	BC003064 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	Homo sapiens
417	AF205890	4028	100	disabled-2	Homo sapiens
417	U39050	4028	100	DOC-2	Homo sapiens
418	AAH07075	780	100	BC007075 hemoglobin, beta	Homo sapiens
418	U01317	780	100	beta-globin	Homo sapiens
418	V00499	780	100	beta globin	Homo sapiens
419	AAH21557	4093	99	BC021557 transmembrane protein 8 (five membrane-spanning domains)	Homo sapiens
419	AB045292	4100	100	M83 protein	Homo sapiens
419	AE006463_7	4088	99	AE006463 M83	Homo sapiens
420	AF193048_1	946	100	AF193048 unknown	Homo sapiens
421	AF151980_1	2009	100	AF151980 connexin 43	Homo sapiens
421	BC026329	2009	100	gap junction protein, alpha 1, 43kD (connexin 43)	Homo sapiens
421	X52947	2009	100	gap junction protein (AA 1-382)	Homo sapiens
422	AJ313463	1258	100	adipsin/complement factor D precursor	Homo sapiens
422	BC034529	1249	100	Unknown (protein for IMAGE:4780594)	Homo sapiens
422	M84526	1198	98	adipsin/complement factor D	Homo sapiens
423	AF258549_1	533	100	AF258549 PP1292	Homo sapiens
424	AF217963_1	4215	99	AF217963 NRAGE	Homo sapiens
424	AF258554_1	4223	100	AF258554 PP2250	Homo sapiens
424	BC032473	4223	100	melanoma antigen, family D, 1	Homo sapiens
425	AAH14635	635	100	BC014635 Similar to SH3-domain, GRB2-like, endophilin B2	Homo sapiens
425	AF257319_1	635	100	AF257319 SH3-containing protein SH3GLB2	Homo sapiens
425	AF258589_1	635	100	AF258589 PP578	Homo sapiens
426	AAH03390	707	100	BC003390 hypothetical protein	Homo sapiens
426	AAH14334	707	100	BC014334 Unknown (protein for MGC:22874)	Homo sapiens
426	AF275807_1	822	100	AF275807 PNAS-110	Homo sapiens
427	AAH05238	469	100	BC005238 FXD domain-containing ion transport regulator 3	Homo sapiens
427	U28249	411	75	11kD protein	Homo sapiens
427	X93036	469	100	MAT8 protein	Homo sapiens
428	AF014402	1500	100	type-2 phosphatidic acid phosphatase alpha-1	Homo sapiens
428	BC039847	1500	100	Similar to phosphatidic acid phosphatase type 2A	Homo sapiens
428	Y14436	1500	100	phosphatidic acid phosphatase type 2	Homo sapiens
429	AL163249	2729	99	T-complex protein 1 theta subunit	Homo sapiens
429	D13627	2730	99	KIAA0002	Homo sapiens
429	D42052	2734	100	predicted protein of 548 amino acids	Homo sapiens
430	AAH01312	2306	100	BC001312 protein disulfide isomerase-related protein	Homo sapiens
430	BC006865	2220	95	Similar to protein disulfide isomerase-related protein	Mus musculus
430	D49489	2306	100	human P5	Homo sapiens
431	AF439513_1	7917	91	AF439513 pregnancy-associated plasma protein-A	Mus musculus
431	U28727	8980	100	pregnancy-associated plasma protein-A preproform	Homo sapiens
431	X68280	8574	100	unnamed protein product	Homo sapiens
432	AAH01936	1357	100	BC001936 Similar to BCL2-	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				associated athanogene	
432	AAH14774	1357	100	BC014774 Unknown (protein for MGC:17086)	Homo sapiens
432	AF022224	1357	100	Bcl-2-binding protein	Homo sapiens
433	AAH04490	1953	100	BC004490 v-fos FBJ murine osteosarcoma viral oncogene homolog	Homo sapiens
433	AF111167	1953	100	cfos	Homo sapiens
433	V01512	1953	100	c-fos	Homo sapiens
434	AAH20235	3282	99	BC020235 Unknown (protein for MGC:31939)	Homo sapiens
434	M19645	3314	100	GRP78 precursor	Homo sapiens
434	X87949	3314	100	BiP	Homo sapiens
435	AAH14433	2640	100	BC014433 Unknown (protein for MGC:2159)	Homo sapiens
435	BC036000	2640	100	Unknown (protein for IMAGE:4712175)	Homo sapiens
435	U42068	2640	100	P58	Homo sapiens
436	BC032722	1478	100	tumor necrosis factor (ligand) superfamily, member 10	Homo sapiens
436	U37518	1478	100	TNF-related apoptosis inducing ligand TRAIL	Homo sapiens
436	U57059	1478	100	Apo-2 ligand	Homo sapiens
437	AAH01022	1591	100	BC001022 pyrophosphatase (inorganic)	Homo sapiens
437	AF119665_1	1591	100	AF119665 inorganic pyrophosphatase	Homo sapiens
437	AF217186_1	1591	100	AF217186 inorganic pyrophosphatase 1	Homo sapiens
438	AAH08743	3145	100	BC008743 zyxin	Homo sapiens
438	AAH09360	3145	100	BC009360 zyxin	Homo sapiens
438	AAH10031	3145	100	BC010031 zyxin	Homo sapiens
439	AAH05901	919	100	BC005901 Microfibril-associated glycoprotein-2	Homo sapiens
439	AF084927	919	100	microfibril-associated glycoprotein 2	Homo sapiens
439	U37283	919	100	microfibril-associated glycoprotein-2 MAGP-2	Homo sapiens
440	AAH00933	2015	100	BC000933 isocitrate dehydrogenase 3 (NAD+) gamma	Homo sapiens
440	Z68129	2015	100	NAD(H)-specific isocitrate dehydrogenase gamma-subunit precursor	Homo sapiens
440	Z68907	2015	100	NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	Homo sapiens
441	AAH12265	846	100	BC012265 Similar to cofilin 1, non-muscle	Homo sapiens
441	AAH12318	846	100	BC012318 Similar to cofilin 1, non-muscle	Homo sapiens
441	AAH18256	846	100	BC018256 Similar to cofilin 1, non-muscle	Homo sapiens
442	AB069964	861	100	ubiquitin-conjugating enzyme 9	Gallus gallus
442	AF461016_1	861	100	AF461016 ubiquitin-conjugating enzyme	Gallus gallus
442	U88561	861	100	E2 ubiquitin conjugating enzyme	Xenopus laevis
443	AAH06249	989	100	BC006249 guanylate kinase 1	Homo sapiens
443	AAH09914	989	100	BC009914 guanylate kinase 1	Homo sapiens
443	U66895	989	100	guanylate kinase	Homo sapiens
445	AAH01120	1369	99	BC001120 lectin, galactoside-binding, soluble, 3 (galectin 3)	Homo sapiens
445	AF031425	1369	99	galectin 3	Homo sapiens
445	M35368	1377	100	galactose-specific lectin	Homo sapiens
446	AAH00877	615	88	BC000877 hypothetical protein PP5395	Homo sapiens
446	AF218019_1	615	88	AF218019 unknown	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
446	AF241786_1	1125	100	AF241786 NPDP013	Homo sapiens
447	AAH02503	547	70	BC002503 spermidine/spermine N1-acetyltransferase	Homo sapiens
447	AAH08424	547	70	BC008424 spermidine/spermine N1-acetyltransferase	Homo sapiens
447	AF251292_1	1059	100	AF251292 DC21	Homo sapiens
448	AF135157_1	745	69	AF135157 complement C1q A chain precursor	Homo sapiens
448	AF260332_1	1550	100	AF260332 DC33	Homo sapiens
448	BC030153	745	69	complement component 1, q subcomponent, alpha polypeptide	Homo sapiens
449	AAH00589	770	100	BC000589 CGI-39 protein; cell death-regulatory protein GRIM19	Homo sapiens
449	AAH09189	770	100	BC009189 CGI-39 protein; cell death-regulatory protein GRIM19	Homo sapiens
449	AF261134_1	1196	100	AF261134 CDA016	Homo sapiens
450	AAH12296	1135	99	BC012296 hypothetical protein FLJ21174	Homo sapiens
450	AF271783_1	1141	100	AF271783 NPDP017	Homo sapiens
450	AF314542_1	1141	100	AF314542 B lymphocyte activation-related protein	Homo sapiens
451	AK090427	13940	99	FLJ00343 protein	Homo sapiens
451	L44140	14011	100	filamin	Homo sapiens
451	X53416	14004	99	actin-binding protein	Homo sapiens
452	AAH12341	1492	100	BC012341 Similar to M5-14 protein	Homo sapiens
452	AL136622	1492	100	hypothetical protein	Homo sapiens
452	AL390090	1492	100	c3orf1 hypothetical protein, M5-14 similar to (AE003703)140up gene product Drosophila melanogaster	Homo sapiens
453	AC005624	824	100	MY18 HUMAN	Homo sapiens
453	AF078077	824	100	growth arrest and DNA-damage-inducible protein GADD45beta	Homo sapiens
453	AF087853_1	824	100	AF087853 growth arrest and DNA damage inducible protein beta	Homo sapiens
454	AF020185	478	100	protein inhibitor of nitric oxide synthase	Mus musculus
454	BC008106	478	100	dynein, cytoplasmic, light polypeptide	Mus musculus
454	BC034258	478	100	dynein, cytoplasmic, light polypeptide	Mus musculus
455	AAH01539	1466	100	BC001539 dickkopf (Xenopus laevis) homolog 1	Homo sapiens
455	AF177394_1	1466	100	AF177394 dickkopf-1	Homo sapiens
455	AF261158	1466	100	dickkopf homolog 1	Homo sapiens
456	AAC33279	1396	100	AC005559 basigin	Homo sapiens
456	AAH09040	1396	100	BC009040 basigin (OK blood group)	Homo sapiens
456	AF042855	1396	100	EMMPRIN	Homo sapiens
457	L47125	3057	100	glypican	Homo sapiens
457	L47176	3057	100	GTR2-2 gene product	Homo sapiens
457	Z37987	3057	100	MXR7	Homo sapiens
458	D83476	4306	77	Xtld protein	Xenopus laevis
458	L24755	4948	92	bone morphogenetic protein	Mus musculus
458	U50330	5416	100	procollagen C-proteinase	Homo sapiens
459	AAH01287	669	100	BC001287 histidine triad nucleotide-binding protein	Homo sapiens
459	AAH07090	669	100	BC007090 histidine triad nucleotide-binding protein	Homo sapiens
459	U51004	669	100	protein kinase C inhibitor	Homo sapiens
460	AB003306	1280	94	PSMB5	Mus musculus
460	AF060091_1	1280	94	AF060091 proteasome subunit X	Mus musculus
460	X95586	1370	100	proteasome	Homo sapiens
461	AF102848_1	2178	100	AF102848 keratin 23	Homo sapiens
461	AK002047	2151	98	unnamed protein product	Homo sapiens
461	BC028356	2155	99	type I intermediate filament cytokeratin	Homo sapiens
462	AAH00097	3483	100	BC000097 transforming growth	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				factor, beta-induced, 68kD	
462	AAH04972	3483	100	BC004972 transforming growth factor, beta-induced, 68kD	Homo sapiens
462	AY149344	3483	100	transforming growth factor, beta-induced, 68kDa	Homo sapiens
463	AF414110_1	635	100	AF414110 histone variant H2A.F/Z	Danio rerio
463	AF414111_1	635	100	AF414111 histone variant H2A.F/Z	Danio rerio
463	V00414	635	100	histone H2A	Gallus gallus
464	BC011457	957	100	Unknown (protein for MGC:7976)	Mus musculus
464	BC019761	957	100	putative membrane protein	Mus musculus
464	BC020098	957	100	putative membrane protein	Mus musculus
465	AAH00140	3579	100	BC000140 propionyl Coenzyme A carboxylase, alpha polypeptide	Homo sapiens
465	AF385926_1	3579	100	AF385926 propionyl-CoA carboxylase alpha subunit	Homo sapiens
465	AY035808	3579	100	propionyl-CoA carboxylase alpha polypeptide precursor	Homo sapiens
466	AF372216_1	562	99	AF372216 tropomyosin alpha isoform	Rattus norvegicus
466	M19267	565	100	tropomyosin	Homo sapiens
466	M19715	565	100	skeletal muscle tropomyosin	Homo sapiens
467	AAH00191	704	100	BC000191 hypothetical protein	Homo sapiens
467	AAH14329	704	100	BC014329 Unknown (protein for MGC:22862)	Homo sapiens
467	AF212248_1	704	100	AF212248 CDA09	Homo sapiens
468	AAH00255	783	100	BC000255 Unknown (protein for MGC:2495)	Homo sapiens
468	AF320778_1	783	100	AF320778 cervical cancer oncogene 3	Homo sapiens
468	AY032594	783	100	hepatitis C virus core-binding protein 6	Homo sapiens
469	AAH00271	799	100	BC000271 Unknown (protein for MGC:3204)	Homo sapiens
469	AAH01434	799	100	BC001434 Unknown (protein for MGC:2477)	Homo sapiens
469	AK007390	449	82	unnamed protein product	Mus musculus
470	AAH00421	1243	100	BC000421 lysosomal-associated protein transmembrane 4 alpha	Homo sapiens
470	AAH03158	1240	99	BC003158 lysosomal-associated protein transmembrane 4 alpha	Homo sapiens
470	D14696	1243	100	KIAA0108	Homo sapiens
471	AAH00461	1738	100	BC000461 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	Homo sapiens
471	AAH00934	1735	99	BC000934 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	Homo sapiens
471	AL031668	1738	100	dJ64K7.2 (eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD))	Homo sapiens
472	AAH00466	1059	100	BC000466 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1)	Homo sapiens
472	AAH19276	1059	100	BC019276 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1)	Homo sapiens
472	AF044958	1059	100	NADH:ubiquinone oxidoreductase ASH1 subunit	Homo sapiens
473	AAH00490	1821	100	BC000490 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	Homo sapiens
473	AK095574	1774	98	unnamed protein product	Homo sapiens
473	U94855	1821	100	translation initiation factor 3 47 kDa subunit	Homo sapiens
474	AAH00502	970	100	BC000502 ribosomal protein L17	Homo sapiens
474	AAH17831	970	100	BC017831 ribosomal protein L17	Homo sapiens
474	X53777	970	100	putative ribosomal protein (AA 1-184)	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
475	AAH00505	808	100	BC000505 microsomal glutathione S-transferase 3	Homo sapiens
475	AAH03034	808	100	BC003034 microsomal glutathione S-transferase 3	Homo sapiens
475	AAH05964	808	100	BC005964 microsomal glutathione S-transferase 3	Homo sapiens
476	AAH00509	1425	100	BC000509 proteasome (prosome, macropain) subunit, beta type, 7	Homo sapiens
476	AAH17116	1393	100	BC017116 proteasome (prosome, macropain) subunit, beta type, 7	Homo sapiens
476	D38048	1421	99	proteasome subunit z	Homo sapiens
477	BC033015	4539	100	RAS p21 protein activator (GTPase activating protein) 1	Homo sapiens
477	M23379	4539	100	GTPase-activating protein	Homo sapiens
477	M23612	4555	100	GTPase-activating protein	Homo sapiens
478	BC003860	2254	100	protease (prosome, macropain) 26S subunit, ATPase 1	Mus musculus
478	D50696	2254	100	proteasomal ATPase (S4)	Rattus norvegicus
478	U39302	2254	100	P26s4	Mus musculus
479	AAH00522	2131	100	BC000522 Similar to serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor). member 1	Homo sapiens
479	AF400442_1	2125	99	AF400442 pigment epithelium-derived factor	Homo sapiens
479	M76979	2119	99	pigment epithelial-differentiating factor	Homo sapiens
480	AAH00529	1616	100	BC000529 prostate differentiation factor	Homo sapiens
480	AAH08962	1616	100	BC008962 Unknown (protein for MGC:4145)	Homo sapiens
480	AF003934	1613	99	prostate differentiation factor	Homo sapiens
481	AAH00548	806	100	BC000548 receptor (calcitonin) activity modifying protein 1	Homo sapiens
481	AF181550_1	596	71	AF181550 receptor activity modifying protein 1	Rattus norvegicus
481	AJ001014	806	100	RAMP1	Homo sapiens
482	AAH00554	1409	100	BC000554 Similar to integral membrane protein 2B	Homo sapiens
482	AF136973_1	1409	100	AF136973 putative transmembrane protein E3-16	Homo sapiens
482	AF152462_1	1409	100	AF152462 transmembrane protein BRI	Homo sapiens
483	AAH00601	479	100	BC000601 DKFZP564K247 protein	Homo sapiens
483	AAH09583	479	100	BC009583 DKFZP564K247 protein	Homo sapiens
483	AAH09594	479	100	BC009594 DKFZP564K247 protein	Homo sapiens
484	AAH00691	906	100	BC000691 brain specific protein	Homo sapiens
484	AF132972_1	902	99	AF132972 CGI-38 protein	Homo sapiens
484	BC010788	888	96	RIKEN cDNA 2700055K07 gene	Mus musculus
485	AAH00720	798	100	BC000720 ubiquitously-expressed transcript	Homo sapiens
485	AAH08890	798	100	BC008890 ubiquitously-expressed transcript	Homo sapiens
485	AF092737_1	798	100	AF092737 ubiquitously expressed transcript	Homo sapiens
486	AAH01016	958	100	BC001016 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV)	Homo sapiens
486	AF044953_1	958	100	AF044953 NADH:ubiquinone oxidoreductase PGIV subunit	Homo sapiens
486	X59697	866	88	19 kDa subunit of NADH:ubiquinone oxidoreductase complex (complex I)	Bos taurus
487	AAH01066	763	100	BC001066 hypothetical protein	Homo sapiens
487	AAH21986	763	100	BC021986 mitochondrial ribosomal protein L27	Homo sapiens
487	AB049647	763	100	mitochondrial ribosomal protein	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				L27 (L27mt)	
488	AAH01101	2975	100	BC001101 HSPC025	Homo sapiens
488	AAH07510	2975	100	BC007510 HSPC025	Homo sapiens
488	BC029265	2975	100	eukaryotic translation initiation factor 3, subunit 6 interacting protein	Homo sapiens
489	AAH01150	2803	100	BC001150 metalloprotease 1 (pitrilysin family)	Homo sapiens
489	AAH05025	2802	99	BC005025 Similar to metalloprotease 1 (pitrilysin family)	Homo sapiens
489	AB029027	2803	100	KIAA1104 protein	Homo sapiens
490	AAH01288	2064	100	BC001288 Similar to decay accelerating factor for complement (CD55, Cromer blood group system)	Homo sapiens
490	M30142	2064	100	decay-accelerating factor A	Homo sapiens
490	M31516	2064	100	decay-accelerating factor	Homo sapiens
491	AAH01387	833	100	BC001387 similar to rat HREV107	Homo sapiens
491	AB030814	833	100	H-REV107 protein homolog	Homo sapiens
491	AF317086	833	100	HREV107-3	Homo sapiens
492	AAH01420	800	100	BC001420 HN1 protein	Homo sapiens
492	AF177862_1	800	100	AF177862 HN1 protein	Homo sapiens
492	AF348672	800	100	hematological and neurological expressed 1 protein	Homo sapiens
493	AAH01426	482	100	BC001426 Similar to ubiquinol-cytochrome c reductase hinge protein	Homo sapiens
493	AAH01934	482	100	BC001934 Similar to ubiquinol-cytochrome c reductase hinge protein	Homo sapiens
493	AAH15177	482	100	BC015177 Unknown (protein for MGC:10149)	Homo sapiens
494	AAH21173	429	100	BC021173 normal mucosa of esophagus specific 1	Homo sapiens
494	AB026707	429	100	FOAP-11 protein	Homo sapiens
494	AF228422_1	429	100	AF228422 normal mucosa of esophagus specific 1	Homo sapiens
495	AAH15173	608	100	BC015173 ribosomal protein, large, P0	Homo sapiens
495	AAH15690	608	100	BC015690 ribosomal protein, large, P0	Homo sapiens
495	AF274958_1	737	100	AF274958 PNAS-101	Homo sapiens
496	AAH14908	1453	100	BC014908 stem-loop (histone) binding protein	Homo sapiens
496	AAH15703	1453	100	BC015703 stem-loop (histone) binding protein	Homo sapiens
496	Z71188	1453	100	histone RNA hairpin-binding protein	Homo sapiens
497	AB000491	2046	100	proteasome p45/SUG	Rattus norvegicus
497	D83521	2046	100	proteasomal ATPase (rat SUG1)	Rattus norvegicus
497	Z54219	2046	100	mSUG1 protein	Mus musculus
498	AK075215	831	100	unnamed protein product	Homo sapiens
499	AAH02481	480	100	BC002481 HSPC162 protein	Homo sapiens
499	AF132750_1	480	100	AF132750 bithoraxoid-like protein	Homo sapiens
499	AF178431_1	480	100	AF178431 BITH	Homo sapiens
500	AAH02559	3087	100	BC002559 high-glucose-regulated protein 8	Homo sapiens
500	AK083882	3077	99	unnamed protein product	Mus musculus
500	BC014797	3077	99	Unknown (protein for MGC:11691)	Mus musculus
501	AAH02589	2230	100	BC002589 proteasome (prosome, macropain) 26S subunit, ATPase, 2	Homo sapiens
501	BC005462	2226	99	proteasome (prosome, macropain) 26S subunit, ATPase 2	Mus musculus
501	D11094	2230	100	MSS1 protein	Homo sapiens
502	AAH02634	1769	100	BC002634 Unknown (protein for	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				MGC:4272)	
502	AK003354	1732	96	unnamed protein product	Mus musculus
502	BC002128	1725	96	Unknown (protein for MGC:6737)	Mus musculus
503	AAH02803	843	100	BC002803 hypothetical protein	Homo sapiens
503	AF151072.1	843	100	AF151072 HSPC238	Homo sapiens
503	BC005559	711	78	RIKEN cDNA 2500002L14 gene	Mus musculus
504	AAH02911	856	100	BC002911 Unknown (protein for MGC:11276)	Homo sapiens
504	AK003237	722	84	unnamed protein product	Mus musculus
504	BC031732	722	84	DNA segment, Chr 7, Wayne State University 86, expressed	Mus musculus
505	AAH02945	2197	100	BC002945 Similar to hypothetical protein FLJ10101	Homo sapiens
505	AAH21095	1290	100	BC021095 Unknown (protein for MGC:31800)	Homo sapiens
505	AK027586	1290	100	unnamed protein product	Homo sapiens
506	AAH02954	2552	100	BC002954 UDP-glucose pyrophosphorylase 2	Homo sapiens
506	BC023810	2524	98	UDP-glucose pyrophosphorylase 2	Mus musculus
506	U27460	2542	99	uridine diphosphoglucose pyrophosphorylase	Homo sapiens
507	AAH03005	886	100	BC003005 unactive progesterone receptor, 23 kD	Homo sapiens
507	BC003708	876	98	telomerase binding protein, p23	Mus musculus
507	L24804	886	100	p23	Homo sapiens
508	AAH03056	2132	100	BC003056 HSPC028 protein	Homo sapiens
508	AAH08453	2132	100	BC008453 HSPC028 protein	Homo sapiens
508	AAH09597	2132	100	BC009597 HSPC028 protein	Homo sapiens
510	AAH01773	591	100	BC001773 Similar to ribosomal protein L34	Homo sapiens
510	AB061832	591	100	ribosomal protein L34	Homo sapiens
510	BC028517	587	99	Unknown (protein for MGC:41239)	Mus musculus
511	AAH01882	533	100	BC001882 Similar to ribosomal protein L5	Homo sapiens
511	D10737	512	100	ribosomal protein L5	Gallus gallus
511	X57016	512	100	ribosomal protein L5	Gallus gallus
512	AAH01884	589	100	BC001884 NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)	Homo sapiens
512	AF020352	589	100	NADH:ubiquinone oxidoreductase 15 kDa IP subunit	Homo sapiens
512	AF047434	589	100	NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein	Homo sapiens
513	AAH01926	2197	100	BC001926 creatine kinase, mitochondrial 1 (ubiquitous)	Homo sapiens
513	AAH06467	2197	100	BC006467 creatine kinase, mitochondrial 1 (ubiquitous)	Homo sapiens
513	J04469	2197	100	creatine kinase	Homo sapiens
514	AAH03373	763	100	BC003373 prefoldin 5	Homo sapiens
514	AB055803	763	100	MM-1 alpha	Homo sapiens
514	D89667	763	100	c-myc binding protein	Homo sapiens
515	AAH05939	998	100	BC005939 prostaglandin D2 synthase (21kD, brain)	Homo sapiens
515	AY026356	998	100	prostaglandin D synthase	Homo sapiens
515	M98539	998	100	prostaglandin D2 synthase	Homo sapiens
516	AAH00045	1388	100	BC000045 TONDU	Homo sapiens
516	AAH03362	1388	100	BC003362 TONDU	Homo sapiens
516	Z97632	1388	100	dJ196E23.1.1 (novel protein) (isoform 1)	Homo sapiens
517	AAH03366	796	100	BC003366 calcium-regulated heat-stable protein (24kD)	Homo sapiens
517	AF115345_1	787	99	AF115345 calcium-regulated heat stable protein CRHSP-24	Homo sapiens
517	AF115346_1	785	97	AF115346 calcium-regulated heat stable protein CRHSP-24	Rattus sp.

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
518	AAH03369	581	100	BC003369 ribosomal protein, large, P1	Homo sapiens
518	AAH07590	581	100	BC007590 ribosomal protein, large, P1	Homo sapiens
518	AB061836	581	100	ribosomal protein P1	Homo sapiens
519	AAH03377	550	100	BC003377 Similar to thioredoxin	Homo sapiens
519	AF313911_1	550	100	AF313911 thioredoxin	Homo sapiens
519	AY004872	550	100	thioredoxin	Homo sapiens
520	BC032493	1086	100	cysteine and glycine-rich protein 1	Homo sapiens
520	M33146	1086	100	cysteine-rich protein	Homo sapiens
520	M76378	1086	100	cysteine-rich protein	Homo sapiens
521	AAH03382	2620	100	BC003382 sorting nexin 2	Homo sapiens
521	AF065482	2612	99	sorting nexin 2	Homo sapiens
521	AK075929	2564	98	unnamed protein product	Mus musculus
522	AAH03394	1485	100	BC003394 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
522	AAH08364	1478	99	BC008364 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
522	AAH08423	1461	95	BC008423 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
523	AAH03501	2155	100	BC003501 Similar to RIKEN cDNA 2310001A20 gene	Homo sapiens
523	AB033767	2155	100	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	Homo sapiens
523	AL035661	2155	100	dJ568C11.2 (chromosome 20 open reading frame 3)	Homo sapiens
524	AAH03512	3204	100	BC003512 mesothelin	Homo sapiens
524	AE006464_21	3189	99	AE006464 pre-pro-megakaryocyte potentiating factor precursor	Homo sapiens
524	D49441	3192	99	pre-pro-megakaryocyte potentiating factor	Homo sapiens
525	AAH03077	5288	100	BC003077 Similar to ATPase, Na+K+ transporting, alpha 1 polypeptide	Homo sapiens
525	D00099	5288	100	Na,K-ATPase alpha-subunit	Homo sapiens
525	X04297	5288	100	ATPase alpha subunit (aa 1-1023)	Homo sapiens
526	AAH03079	786	100	BC003079 16.7Kd protein	Homo sapiens
526	AAH15639	786	100	BC015639 16.7Kd protein	Homo sapiens
526	AF078845	786	100	16.7Kd protein	Homo sapiens
527	AAH00161	1827	100	BC000161 secretory carrier membrane protein 3	Homo sapiens
527	AAH05135	1827	100	BC005135 secretory carrier membrane protein 3	Homo sapiens
527	AF005039	1817	99	secretory carrier membrane protein	Homo sapiens
528	AAH08704	887	100	BC008704 cytochrome c oxidase subunit IV	Homo sapiens
528	AAH21236	887	100	BC021236 cytochrome c oxidase subunit IV isoform 1	Homo sapiens
528	X54802	887	100	cytochrome-c oxidase subunit IV	Homo sapiens
529	AAH00915	1731	100	BC000915 PDZ and LIM domain 1 (elfin)	Homo sapiens
529	AAH18755	1731	100	BC018755 PDZ and LIM domain 1 (elfin)	Homo sapiens
529	AJ310549	1731	100	CLP-36 protein	Homo sapiens
530	AF236636	1302	98	uridine-cytidine kinase 2	Mus musculus
530	AF236637	1333	100	uridine-cytidine kinase 2	Homo sapiens
530	BC023789	1302	98	uridine-cytidine kinase 2	Mus musculus
531	AAH00176	940	100	BC000176 RAP1B, member of RAS oncogene family	Homo sapiens
531	AF493913_1	940	100	AF493913 Ras family small GTP binding protein RAP1B	Homo sapiens
531	BC033382	952	87	RAP1B, member of RAS oncogene family	Mus musculus
532	D63519	870	100	leptin	Homo sapiens
532	D63710	870	100	ob protein	Homo sapiens
532	U43653	870	100	obese protein	Homo sapiens

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533	BC002088	637	100	ribosomal protein S25	Mus musculus
533	BC027208	637	100	ribosomal protein S25	Mus musculus
533	X62482	637	100	ribosomal protein S25	Rattus rattus
534	AAH03662	2092	100	BC003662 KIAA0111 gene product	Homo sapiens
534	AAH04386	2092	100	BC004386 KIAA0111 gene product	Homo sapiens
534	AAH11151	2092	100	BC011151 Similar to KIAA0111 gene product	Homo sapiens
535	AF349038_1	1780	100	AF349038 TFIID subunit TAFII55	Homo sapiens
535	BC032737	1780	100	similar to TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD	Homo sapiens
535	X97999	1780	100	transcription factor IID	Homo sapiens
536	AAH02601	1673	100	BC002601 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Homo sapiens
536	AAH04983	1673	100	BC004983 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Homo sapiens
536	AY033600	1673	100	NFKBIA	Homo sapiens
537	AF211480_1	2102	100	AF211480 CD001	Homo sapiens
537	AK002102	2086	100	unnamed protein product	Homo sapiens
537	AX191505	2086	100	unnamed protein product	Homo sapiens
538	AAH05110	4609	100	BC005110 Unknown (protein for MGC:13217)	Homo sapiens
538	AK049371	4473	93	unnamed protein product	Mus musculus
538	AY044865	4609	100	sorting nexin 14	Homo sapiens
539	AAH05118	592	100	BC005118 Similar to putative translation initiation factor	Homo sapiens
539	AAH08710	592	100	BC008710 putative translation initiation factor	Homo sapiens
539	AF083441_1	592	100	AF083441 SUI1 isolog	Homo sapiens
540	AAH05127	2190	100	BC005127 adipose differentiation-related protein	Homo sapiens
540	AF443203_1	2190	100	AF443203 adipose differentiation-related protein	Homo sapiens
540	AX025098	2181	99	unnamed protein product	Homo sapiens
541	AAH05143	964	100	BC005143 vitamin A responsive; cytoskeleton related	Homo sapiens
541	AAH20797	964	100	BC020797 vitamin A responsive; cytoskeleton related	Homo sapiens
541	AY102608	964	100	JWA protein	Homo sapiens
542	AAH05228	360	100	BC005228 Unknown (protein for MGC:12250)	Homo sapiens
543	AF072506	2871	100	envelope protein precursor	Homo sapiens
543	AF208161	2868	99	syncytin precursor	Homo sapiens
543	AF513360_1	2868	99	AF513360 enverin	Homo sapiens
544	AAH05322	1866	100	BC005322 decorin	Homo sapiens
544	AF138300	1866	100	decorin variant A	Homo sapiens
544	AF491944_1	1866	100	AF491944 decorin	Homo sapiens
545	AAH01392	827	100	BC001392 ribosomal protein S27a	Homo sapiens
545	D83209	827	100	ubiquitin extention protein	Cavia porcellus
545	M24507	827	100	ubiquitin	synthetic construct
546	AAH05330	1306	100	BC005330 tissue factor pathway inhibitor 2	Homo sapiens
546	AF217542	1306	100	tissue factor pathway inhibitor 2	Homo sapiens
546	D29992	1306	100	placental protein 5 (PP5)	Homo sapiens
547	AAH05361	1334	100	BC005361 proteasome (prosome, macropain) subunit, alpha type, 4	Homo sapiens
547	BC022445	1334	100	proteasome (prosome, macropain) subunit, alpha type, 4	Homo sapiens
547	D00763	1334	100	proteasome subunit C9	Homo sapiens
548	AAH05366	1298	100	BC005366 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Homo sapiens
548	AAH16350	1298	100	BC016350 Unknown (protein for	Homo sapiens

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				MGC:24431)	
548	AL390195	1298	100	bA552M11.3 (ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1)	Homo sapiens
549	AAH05390	1993	100	BC005390 Unknown (protein for MGC:12520)	Homo sapiens
549	AF006305	1993	100	26S proteasome regulatory subunit	Homo sapiens
549	U36395	1993	100	conserved ATPase domain protein 44	Spermophilus tridecemlineatus
550	AAH10370	1800	99	BC010370 Putative prostate cancer tumor suppressor	Homo sapiens
550	U42349	1826	100	39 kDa encoded by N33	Homo sapiens
550	U42360	1808	99	N33 protein form 1	Homo sapiens
551	AAH05839	1492	100	BC005839 follistatin-like 3 (secreted glycoprotein)	Homo sapiens
551	BC033119	1492	100	follistatin-like 3 (secreted glycoprotein)	Homo sapiens
551	U76702	1492	100	follistatin-related protein FLRG	Homo sapiens
552	AAH05354	564	100	BC005354 ribosomal protein, large P2	Homo sapiens
552	AAH05920	564	100	BC005920 ribosomal protein, large P2	Homo sapiens
552	AAH07573	564	100	BC007573 ribosomal protein, large P2	Homo sapiens
553	AAH17660	414	100	BC017660 Unknown (protein for MGC:14608)	Homo sapiens
553	AJ249731	414	100	putative G8.2 protein	Homo sapiens
553	AJ249732	307	79	G8 protein	Homo sapiens
554	AAH05966	647	100	BC005966 ring finger protein 7	Homo sapiens
554	AAH08627	647	100	BC008627 ring finger protein 7	Homo sapiens
554	AF092878_1	647	100	AF092878 zinc RING finger protein SAG	Homo sapiens
555	AAH05975	1163	100	BC005975 calcyclin binding protein	Homo sapiens
555	AF314752_1	1163	100	AF314752 calcyclin binding protein	Homo sapiens
555	BC022352	1163	100	Siah-interacting protein	Homo sapiens
556	AAH06337	739	100	BC006337 Unknown (protein for MGC:12798)	Homo sapiens
556	M37194	739	100	clathrin-associated protein 17	Rattus norvegicus
556	X97074	729	98	clathrin-associated protein	Homo sapiens
557	AAH01928	3365	100	BC001928 protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Homo sapiens
557	AAH06344	3365	100	BC006344 protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Homo sapiens
557	AAH11754	3365	100	BC011754 Similar to protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Homo sapiens
558	AF453478_1	1155	100	AF453478 phosphopantetheine adenylyltransferase / dephosphocoenzyme A kinase	Homo sapiens
558	AY094602	1155	100	bifunctional phosphopantetheine adenylyl transferase / dephospho CoA kinase	Homo sapiens
558	BC020985	1155	100	Unknown (protein for MGC:9724)	Homo sapiens
559	AAH06393	2797	100	BC006393 Similar to carboxypeptidase Z	Homo sapiens
559	AF017638	2419	86	carboxypeptidase Z	Rattus norvegicus
559	U83411	2787	99	carboxypeptidase Z precursor	Homo sapiens
560	AF126110_1	3913	100	AF126110 fibulin-1 isoform D precursor	Homo sapiens

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560	U01244	3913	100	fibulin-1D	Homo sapiens
560	X70854	3392	84	BM-90/fibulin	Mus musculus
561	AAH02343	2494	100	BC002343 Similar to nucleolin	Homo sapiens
561	AAH06494	2494	100	BC006494 Unknown (protein for MGC:1440)	Homo sapiens
561	AAH06516	2494	100	BC006516 Unknown (protein for MGC:3588)	Homo sapiens
562	AAH20515	772	100	BC020515 ribosomal protein S14	Homo sapiens
562	M11241	772	100	ribosomal protein S14	Cricetulus griseus
562	M35008	772	100	ribosomal protein S14	Cricetulus griseus
563	AAH08926	645	100	BC008926 ribosomal protein L29	Homo sapiens
563	U10248	645	100	ribosomal protein L29	Homo sapiens
563	U49083	645	100	HIP	Homo sapiens
564	AAH06791	1105	100	BC006791 ribosomal protein L10a	Homo sapiens
564	AAH11366	1105	100	BC011366 Similar to ribosomal protein L10a	Homo sapiens
564	X93352	1105	100	ribosomal protein L10a	Rattus norvegicus
565	AAH01418	1132	100	BC001418 Similar to RIKEN cDNA 1810017F10 gene	Homo sapiens
565	AAH13953	1132	100	BC013953 Unknown (protein for MGC:2853)	Homo sapiens
565	AY027543	1132	100	beta-casein-like protein	Homo sapiens
566	AAH07038	1762	100	BC007038 lumican	Homo sapiens
566	BC035997	1762	100	lumican	Homo sapiens
566	U21128	1762	100	lumican	Homo sapiens
567	AAH03609	1441	100	BC003609 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
567	AAH07107	1441	100	BC007107 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
567	AAH16770	1441	100	BC016770 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
568	AAH07282	952	100	BC007282 Unknown (protein for MGC:15626)	Homo sapiens
568	AK014338	909	97	unnamed protein product	Mus musculus
568	M83751	937	98	arginine-rich protein	Homo sapiens
569	AAH07402	1005	100	BC007402 apolipoprotein D	Homo sapiens
569	J02611	1005	100	apolipoprotein D precursor	Homo sapiens
569	M16696	1005	100	apolipoprotein D precursor	Homo sapiens
570	AAH01603	849	100	BC001603 Similar to ribosomal protein L21	Homo sapiens
570	AAH07505	849	100	BC007505 Unknown (protein for MGC:4136)	Homo sapiens
570	X89401	849	100	ribosomal protein L21	Homo sapiens
571	AAH07507	605	100	BC007507 ribosomal protein S20	Homo sapiens
571	BC011323	605	100	Similar to ribosomal protein S20	Mus musculus
571	X51537	605	100	ribosomal protein S20 (AA 1-119)	Rattus rattus
572	AAH14459	791	100	BC014459 Similar to ribosomal protein L23a	Homo sapiens
572	BC029892	791	100	ribosomal protein L23a	Mus musculus
572	X65228	791	100	ribosomal protein L23a	Rattus rattus
573	AJ420896	2114	99	SPPL2a protein	Homo sapiens
573	AK027446	2126	100	unnamed protein product	Homo sapiens
573	BC025740	2114	99	Similar to hypothetical protein FLJ14540	Homo sapiens
574	AF036548	554	82	RGC-32	Rattus norvegicus
574	AF036549.1	569	100	AF036549 RGC32	Homo sapiens
574	AL354833	607	91	ba157L14.2 (RGC32, a novel gene induced by complement activation in oligodendrocytes)	Homo sapiens
575	AAH01024	2749	99	BC001024 putative nucleotide binding protein, estradiol-induced	Homo sapiens

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575	AK027514	2756	100	unnamed protein product	Homo sapiens
575	AK027516	2753	99	unnamed protein product	Homo sapiens
576	AAH07834	563	100	BC007834 Unknown (protein for MGC:14141)	Homo sapiens
577	AAH03061	2338	99	BC003061 protease, cysteine, 1 (legumain)	Homo sapiens
577	D55696	2335	99	cysteine protease	Homo sapiens
577	Y09862	2339	100	legumain	Homo sapiens
578	AAH08081	1095	100	BC008081 Similar to KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Homo sapiens
578	AAH14568	1095	100	BC014568 Similar to KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Homo sapiens
578	X63745	1095	100	KDEL receptor	Homo sapiens
579	AF004877	7574	99	pro-alpha 2(I) collagen	Homo sapiens
579	J03464	7554	99	pre-pro-alpha-2 type I collagen	Homo sapiens
579	Z74616	7596	100	prepro-alpha2(I) collagen	Homo sapiens
580	AAH08188	946	100	BC008188 Unknown (protein for MGC:5243)	Homo sapiens
580	AF021819	946	100	RNA-binding protein regulatory subunit	Homo sapiens
580	AL034417	946	100	bK215D11.1 (RNA-binding protein regulatory subunit)	Homo sapiens
581	AAH08283	594	100	BC008283 cholecystokinin	Homo sapiens
581	L00354	594	100	cholecystokinin	Homo sapiens
581	M60458	569	95	cholecystokinin	Macaca fascicularis
582	AAH06794	693	99	BC006794 Similar to interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
582	AAH08417	698	100	BC008417 Similar to interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
582	BC022439	698	100	interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
583	AAH05993	1421	100	BC005993 Unknown (protein for MGC:14796)	Homo sapiens
583	AAH08691	1421	100	BC008691 Unknown (protein for MGC:8886)	Homo sapiens
583	AAH15644	1421	100	BC015644 Ras suppressor protein 1	Homo sapiens
584	AAH08938	1942	100	BC008938 Similar to histocompatibility 13	Homo sapiens
584	AAH08959	1942	100	BC008959 Similar to histocompatibility 13	Homo sapiens
584	AF483215_1	1934	99	AF483215 minor histocompatibility antigen H13 isoform 1	Homo sapiens
585	AAH16320	2150	100	BC016320 cathepsin D (lysosomal aspartyl protease)	Homo sapiens
585	M11233	2150	100	preprocathepsin D	Homo sapiens
585	X05344	2150	100	precursor polypeptide (AA -20 to 392)	Homo sapiens
586	AAH08983	1364	100	BC008983 complement component 1, q subcomponent, beta polypeptide	Homo sapiens
586	X03084	1240	100	Clq B-chain precursor	Homo sapiens
586	X16874	1075	79	precursor polypeptide (AA -25 to 228)	Mus musculus
587	AAH09177	1014	100	BC009177 ras homolog gene family, member C	Homo sapiens
587	AF498972_1	1014	100	AF498972 small GTP binding protein RhoC	Homo sapiens
587	BC004627	1014	100	ras homolog gene family, member C	Mus musculus
588	AAH09200	1068	100	BC009200 Rho GDP dissociation inhibitor (GDI) beta	Homo sapiens
588	AF498927_1	1068	100	AF498927 Rho GDP dissociation inhibitor beta	Homo sapiens
588	X69549	1068	100	Human rho GDP-dissociation	Homo sapiens

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				Inhibitor 2 (IEF 8120)	
589	AAH09201	1137	100	BC009201 clathrin, light polypeptide (Lca)	Homo sapiens
589	AAH19287	1137	100	BC019287 clathrin, light polypeptide (Lca)	Homo sapiens
589	AL158830	1137	100	bA421H8.4.2 (clathrin, light polypeptide (LCA))	Homo sapiens
590	AAH09232	596	100	BC009232 Similar to G antigen 8	Homo sapiens
590	AJ318880	596	100	XAGE-2 protein	Homo sapiens
590	AJ318891	596	100	XAGE-2 protein	Homo sapiens
591	AAH03378	1149	100	BC003378 high-mobility group (nonhistone chromosomal) protein 1	Homo sapiens
591	BC030981	1149	100	high-mobility group (nonhistone chromosomal) protein 1	Homo sapiens
591	X12597	1149	100	HMG-1 protein (AA 1-215)	Homo sapiens
592	AB002368	5586	100	KIAA0370	Homo sapiens
592	AY026388	5765	100	ran binding protein RanBP20	Homo sapiens
592	AY029528	5663	97	RANBP20	Mus musculus
593	AAH09799	1308	100	BC009799 amphiregulin (schwannoma-derived growth factor)	Homo sapiens
593	M30703	1308	100	amphiregulin	Homo sapiens
593	M30704	1308	100	amphiregulin	Homo sapiens
594	AAH09869	511	100	BC009869 Unknown (protein for MGC:16406)	Homo sapiens
594	AAH15491	511	100	BC015491 Unknown (protein for MGC:8965)	Homo sapiens
594	BC022326	511	100	Unknown (protein for MGC:22741)	Homo sapiens
595	AAH09898	1921	100	BC009898 spermine synthase	Homo sapiens
595	AD001528	1921	100	spermidine aminopropyltransferase	Homo sapiens
595	Z49099	1916	100	spermine synthase	Homo sapiens
596	AL365410	1055	100	hypothetical protein	Homo sapiens
596	L32162	294	70	transcription factor	Homo sapiens
597	AAH10016	1542	100	BC010016 Similar to CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Homo sapiens
597	AAH12884	1542	100	BC012884 Unknown (protein for MGC:9240)	Homo sapiens
597	Z25521	1542	100	integrin associated protein	Homo sapiens
598	AAH10055	784	100	BC010055 hypothetical protein PRO2605	Homo sapiens
598	AF116721_109	642	100	AF116709 PRO2605	Homo sapiens
599	AAH04976	634	100	BC004976 Unknown (protein for IMAGE:2958115)	Homo sapiens
599	AAH10076	634	100	BC010076 Unknown (protein for MGC:19576)	Homo sapiens
599	AY061855	634	100	mitochondrial ribosomal protein S6	Homo sapiens
600	AAH10129	907	100	BC010129 Similar to hypothetical protein R33729_1	Homo sapiens
600	AAH14655	907	100	BC014655 Unknown (protein for MGC:20383)	Homo sapiens
600	AL365374	894	100	R33729_1 hypothetical protein	Homo sapiens
601	AB028894	824	100	ribosomal protein S11	Mus musculus
601	BC012641	824	100	ribosomal protein S11	Mus musculus
601	U93864	824	100	ribosomal protein S11	Mus musculus
602	BC002077	1058	100	RAB1, member RAS oncogene family	Mus musculus
602	X15744	1058	100	GTP-binding protein	Mus musculus
602	Y00094	1058	100	Ypt1 protein (AA 1-205)	Mus musculus
603	AAH02947	1482	100	BC002947 folate receptor 1 (adult)	Homo sapiens
603	U20391	1482	100	folate receptor	Homo sapiens
603	X62753	1482	100	adult folate binding protein	Homo sapiens
604	U65932	3016	100	extracellular matrix protein 1	Homo sapiens
604	U65938	3016	100	extracellular matrix protein 1	Homo sapiens
604	U68186	3016	100	extracellular matrix protein 1	Homo sapiens
605	AAH10897	541	100	BC010897 Similar to JM27 protein	Homo sapiens

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605	AF275258_1	541	100	AF275258 PAGE-4	Homo sapiens
605	AJ005894	541	100	JM27	Homo sapiens
606	AAH11171	2528	100	BC011171 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1	Homo sapiens
606	AF435921_1	2524	99	AF435921 C1 esterase inhibitor	Homo sapiens
606	X07427	2524	99	C1 inhibitor	Homo sapiens
607	D38112	1781	93	cytochrome b	Homo sapiens
607	U09500	1780	93	cytochrome b	Homo sapiens
607	V00662	1785	93	cytochrome B	Homo sapiens
608	AAH11514	696	100	BC011514 Similar to ribosomal protein L32	Homo sapiens
608	K02060	696	100	ribosomal protein L32-3A	Mus musculus
608	X06483	696	100	ribosomal protein L32	Rattus norvegicus
609	AAH11786	645	100	BC011786 Unknown (protein for MGC:19839)	Homo sapiens
609	AF318382_1	645	100	AF318382 unknown	Homo sapiens
609	X07868	456	100	1.8 kb mRNA (AA 1-84)	Homo sapiens
610	AAH11792	1649	100	BC011792 Unknown (protein for MGC:19561)	Homo sapiens
610	AAH17408	1643	99	BC017408 Unknown (protein for MGC:27221)	Homo sapiens
610	U16660	1603	97	peroxisomal enoyl-CoA hydratase-like protein	Homo sapiens
611	AAH00159	2163	100	BC000159 keratin 17	Homo sapiens
611	AAH11901	2163	100	BC011901 Similar to keratin 17	Homo sapiens
611	X62571	2163	100	keratin related product	Homo sapiens
612	AAH12132	3933	100	BC012132 Similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	Homo sapiens
612	BC010624	3872	97	Unknown (protein for MGC:11570)	Mus musculus
612	X70649	3933	100	member of DEAD box protein family	Homo sapiens
613	AF157623_1	2466	100	AF157623 HTRA serine protease	Homo sapiens
613	D87258	2466	100	serin protease with IGF-binding motif	Homo sapiens
613	Y07921	2466	100	novel serine protease, PRSS11	Homo sapiens
614	AF242550_1	1030	100	AF242550 cellular nucleic acid binding protein	Rattus norvegicus
614	AF389887	1030	100	zinc finger protein 9	Homo sapiens
614	D45254	1030	100	Cellular Nucleic Acid Binding Protein	Rattus norvegicus
615	AAH14277	1191	100	BC014277 Similar to tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	Homo sapiens
615	U33114	1191	100	tissue inhibitor of metalloproteinases-3	Homo sapiens
615	X76227	1191	100	tissue inhibitor of metalloproteinases-3	Homo sapiens
616	AAH12384	1017	100	BC012384 Similar to programmed cell death 6	Homo sapiens
616	AF035606	1017	100	calcium binding protein	Homo sapiens
616	U58773_1	1017	100	U58773 calcium binding protein	Homo sapiens
617	AAH12464	755	100	BC012464 prefoldin 2	Homo sapiens
617	AF117237_1	755	100	AF117237 prefoldin subunit 2	Homo sapiens
617	BC026839	729	96	Similar to prefoldin 2	Mus musculus
618	AAH08230	849	100	BC008230 ribosomal protein L12	Homo sapiens
618	BC018321	848	99	ribosomal protein L12	Mus musculus
618	L06505	849	100	ribosomal protein L12	Homo sapiens
619	AAH12606	1665	100	BC012606 Similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	Homo sapiens
619	D50063	1637	98	proteasome subunit p40 / Mov34 protein	Homo sapiens
619	M64640	1597	96	36 kD protein	Mus musculus
620	AAH11835	1485	100	BC011835 Similar to ATPase, Na+/K+ transporting, beta 3	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				polypeptide	
620	AF005896	1485	100	Na K-ATPase beta-3 subunit	Homo sapiens
620	U51478	1485	100	sodium/potassium-transporting ATPase beta-3 subunit	Homo sapiens
621	AAH13041	5526	100	BC013041 Unknown (protein for MGC:4781)	Homo sapiens
621	M58028	5526	100	ubiquitin-activating enzyme E1	Homo sapiens
621	X56976	5516	99	ubiquitin activating enzyme E1	Homo sapiens
622	AAH13162	491	100	BC013162 Similar to heat shock protein, 30 kDa	Homo sapiens
622	AF085359	491	100	HSPC030	Homo sapiens
622	AF537132	491	100	selenoprotein K	Homo sapiens
623	AAH13175	992	100	BC013175 Similar to novel RGD-containing protein	Homo sapiens
623	BC029249	958	96	dynactin 6	Mus musculus
623	D84145	992	100	WS-3	Homo sapiens
624	BC003825	2344	100	tubulin, beta 5	Mus musculus
624	X04663	2344	100	beta-tubulin AA 1-444 (79 is 1st base in codon)	Mus musculus
624	X07011	2344	100	c(beta)7 tubulin (AA 1 - 444)	Gallus gallus
625	A47413	3336	96	CALPASTATINE HUMAINE	Homo sapiens
625	AAH13579	3420	100	BC013579 Similar to calpastatin	Homo sapiens
625	D16217	3340	93	calpastatin	Homo sapiens
626	BC024378	567	100	defender against cell death 1	Mus musculus
626	Y13335	567	100	DAD-1	Mus musculus
626	Y13336	567	100	DAD-1	Rattus norvegicus
627	AAH13975	3963	100	BC013975 Similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	Homo sapiens
627	BC024220	3963	100	Unknown (protein for MGC:1483)	Homo sapiens
627	U28369	3951	99	semaphorin V	Homo sapiens
628	AAH14142	3503	100	BC014142 Similar to glucuronidase, beta	Homo sapiens
628	AX147652	3496	99	unnamed protein product	Homo sapiens
628	M15182	3496	99	beta-glucuronidase precursor (EC 3.2.1.31)	Homo sapiens
629	AB022163	2024	92	mouse ortholog of the zebrafish hagoromo gene	Mus musculus
629	AF281859	2217	100	dactylin	Homo sapiens
629	BC027031	2024	92	f-box and WD-40 domain protein 4	Mus musculus
630	AAH01377	1114	100	BC001377 DKFZP586G1722 protein	Homo sapiens
630	AAH06514	1114	100	BC006514 DKFZP586G1722 protein	Homo sapiens
630	AAH14391	1114	100	BC014391 DKFZP586G1722 protein	Homo sapiens
631	AF159256_1	1147	100	AF159256 Lps/Ran GTPase	Mus musculus
631	AF306457_1	1147	100	AF306457 GTPase	Rattus norvegicus
631	BC014829	1147	100	RAN, member RAS oncogene family	Mus musculus
632	AAH15000	1347	100	BC015000 Similar to major histocompatibility complex, class II, DP beta 1	Homo sapiens
632	M57466	1306	96	light chain	Homo sapiens
632	X01426	1301	96	SB-2-beta precursor polypeptide (aa -29 to 229)	Homo sapiens
633	AAH15039	1006	100	BC015039 microfibrillar-associated protein 2	Homo sapiens
633	AL049569	1006	100	dJ37C10.4 (microfibrillar-associated protein 2 (microfibril-associated glycoprotein precursor, MGAP1))	Homo sapiens
633	U19718	1006	100	microfibril-associated glycoprotein	Homo sapiens
634	AF117383_1	746	100	AF117383 placental protein 13; PPI3	Homo sapiens
634	AY055826	746	100	placenta protein 13	Homo sapiens
634	BC022257	510	69	Similar to placental protein 13-	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				like protein	
635	AAH02387	2063	100	BC002387 nucleosome assembly protein 1-like 1	Homo sapiens
635	AAH15599	2063	100	BC015599 nucleosome assembly protein 1-like 1	Homo sapiens
635	AL162068	2063	100	hypothetical protein	Homo sapiens
636	A03911	2017	99	glia-derived neurite-promoting factor (GdNPF)	Homo sapiens
636	AAH15663	2040	100	BC015663 Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	Homo sapiens
636	M17783	2016	99	glia-derived nexin precursor	Homo sapiens
637	AAH02403	3107	100	BC002403 lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	Homo sapiens
637	AAH02998	3107	100	BC002998 lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	Homo sapiens
637	AAH15761	3107	100	BC015761 lectin, galactoside-binding, soluble, 3 binding protein	Homo sapiens
638	AAH15032	2122	100	BC015032 ribosomal protein L3	Homo sapiens
638	AAH15767	2122	100	BC015767 ribosomal protein L3	Homo sapiens
638	BC008003	2122	100	ribosomal protein L3	Homo sapiens
639	AF052694	2391	100	alpha-tubulin	Meriones unguiculatus
639	BC002219	2391	100	Similar to tubulin alpha 1	Mus musculus
639	BC008117	2391	100	tubulin alpha 1	Mus musculus
640	AK054840	169	67	unnamed protein product	Homo sapiens
640	AK097965	163	64	unnamed protein product	Homo sapiens
640	AX400008	150	58	unnamed protein product	Homo sapiens
641	AAH02449	1196	99	BC002449 Similar to CG10641 gene product	Homo sapiens
641	AAH04128	1331	99	BC004128 Unknown (protein for IMAGE:3940060)	Homo sapiens
641	AK023674	1199	100	unnamed protein product	Homo sapiens
642	AAH01537	2971	100	BC001537 Unknown (protein for MGC:786)	Homo sapiens
642	AB021743	2968	99	PR65	Mus musculus
642	BC006606	2968	99	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Mus musculus
643	AAH09642	939	100	BC009642 FXYP domain-containing ion transport regulator 5	Homo sapiens
643	AB072911	939	100	dysadherin	Homo sapiens
643	AF161462.1	923	98	AF161462 HSPEC113	Homo sapiens
644	AAH09687	869	100	BC009687 epithelial membrane protein 2	Homo sapiens
644	AY057060	869	100	epithelial membrane protein 2	Homo sapiens
644	U52100	869	100	XMP	Homo sapiens
645	AB012214	6727	78	DNA cytosine 5 methyltransferase	Rattus rattus
645	AF180682	6869	100	DNA (cytosine-5)-methyltransferase	Homo sapiens
645	X63692	8587	100	DNA (cytosine-5)-methyltransferase	Homo sapiens
646	AAH15961	961	100	BC015961 adrenomedullin	Homo sapiens
646	D14874	961	100	adrenomedullin precursor	Homo sapiens
646	S73906	961	100	adrenomedullin; AM	Homo sapiens
647	AAH15973	514	100	BC015973 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	Homo sapiens
647	M38591	514	100	cellular ligand of annexin II	Homo sapiens
647	M81457	514	100	calpactin I light chain	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
648	AAH16056	1137	100	BC016056 claudin 3	Homo sapiens
648	AB000714	1137	100	RVPI	Homo sapiens
648	AF007189	1137	100	claudin 3	Homo sapiens
649	AAH16142	1432	100	BC016142 Similar to RIKEN cDNA 2310032N20 gene	Homo sapiens
649	AAH20773	1432	100	BC020773 Unknown (protein for MGC:22685)	Homo sapiens
649	AX405824	1432	100	unnamed protein product	Homo sapiens
650	AF315378_1	1955	98	AF315378 suppressor of profilin/p41 of actin-related complex 2/3	Rattus norvegicus
650	BC039594	1964	99	actin related protein 2/3 complex, subunit 1A, 41kDa	Homo sapiens
650	Y08999	1980	100	Sop2p-like protein	Homo sapiens
651	AF492677_1	383	100	AF492677 odd homeobox 1 protein isoform A	Homo sapiens
651	AF492680_1	383	100	AF492680 odd homeobox 1 protein isoform A	Homo sapiens
651	AF492681_1	383	100	AF492681 odd homeobox 1 protein isoform A	Homo sapiens
652	AK056992	2163	100	unnamed protein product	Homo sapiens
652	AX392121	2155	99	unnamed protein product	Homo sapiens
652	AY033237	2155	99	alcohol dehydrogenase 8	Homo sapiens
653	AAH16748	485	100	BC016748 ribosomal protein L37a	Homo sapiens
653	X14069	485	100	ribosomal protein L37a (AA 1 - 92)	Rattus rattus
653	X73331	485	100	ribosomal protein L37a	Mus musculus
654	AAH12807	3702	100	BC012807 Unknown (protein for MGC:3483)	Homo sapiens
654	AAH14485	3702	100	BC014485 Unknown (protein for MGC:23206)	Homo sapiens
654	AAH16753	3702	100	BC016753 Unknown (protein for MGC:1138)	Homo sapiens
655	AAH15834	1724	100	BC015834 annexin A2	Homo sapiens
655	AAH16774	1724	100	BC016774 annexin A2	Homo sapiens
655	AAH21114	1724	100	BC021114 annexin A2	Homo sapiens
656	AAH17343	644	100	BC017343 ribosomal protein L31	Homo sapiens
656	BC008223	644	100	ribosomal protein L31	Mus musculus
656	X04809	644	100	ribosomal protein L31 (AA 1-125)	Rattus norvegicus
657	AAH17378	2955	100	BC017378 hexosaminidase B (beta polypeptide)	Homo sapiens
657	AF378118_1	2955	100	AF378118 cervical cancer proto-oncogene 7	Homo sapiens
657	M23294	2955	100	beta-hexosaminidase beta-subunit	Homo sapiens
658	AAH12168	1373	100	BC012168 Similar to proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
658	AAH17451	1373	100	BC017451 proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
658	AAH17486	1373	100	BC017486 proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
659	AAH06124	2618	100	BC006124 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
659	AAH12840	2618	100	BC012840 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
659	AAH15567	2618	100	BC015567 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
660	AAH07457	1103	100	BC007457 hypothetical protein	Homo sapiens
660	AAH20796	1103	100	BC020796 hypothetical protein HSPC177	Homo sapiens
660	AAH21168	1103	100	BC021168 hypothetical protein HSPC177	Homo sapiens
661	AAH04904	2894	99	BC004904 nuclear RNA export factor 1	Homo sapiens
661	BC028041	2894	99	nuclear RNA export factor 1	Homo sapiens
661	U80073	2905	100	tip associating protein	Homo sapiens
662	AF064238_1	4503	97	AF064238 smoothelin large isoform	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				L2	
662	AY061971	4653	100	smoothelin-B2	Homo sapiens
662	AY061972	4533	96	smoothelin-B3	Homo sapiens
663	AAH17773	1214	100	BC017773 triggering receptor expressed on myeloid cells 1	Homo sapiens
663	AF196329_1	1214	100	AF196329 triggering receptor expressed on monocytes 1	Homo sapiens
663	AF287008_1	1214	100	AF287008 triggering receptor expressed on monocytes 1	Homo sapiens
664	AAH17891	579	100	BC017891 vesicle-associated membrane protein 5 (myobrevin)	Homo sapiens
664	AF054825	579	100	VAMP5	Homo sapiens
664	AF077197	579	100	VAMP5-like protein	Homo sapiens
665	AAH17931	819	100	BC017931 Similar to RIKEN cDNA 1110055A02 gene	Homo sapiens
665	AF400652_1	819	100	AF400652 thyroid hormone receptor interacting protein 3	Homo sapiens
665	L40410	806	100	thyroid receptor interactor	Homo sapiens
666	AAH18732	1606	100	BC018732 Unknown (protein for MGC:31847)	Homo sapiens
666	AF125533_1	1606	100	AF125533 NADH-cytochrome b5 reductase isoform	Homo sapiens
666	AX083421	1606	100	unnamed protein product	Homo sapiens
667	AAH02453	3263	100	BC002453 heat shock 70kD protein 1A	Homo sapiens
667	AAH09322	3263	100	BC009322 heat shock 70kD protein 1A	Homo sapiens
667	AAH18740	3263	100	BC018740 heat shock 70kD protein 1A	Homo sapiens
668	1680052_1	2856	100	S62076 lysosomal enzyme beta-N-acetylhexosaminidase A	Homo sapiens
668	AAH18927	2856	100	BC018927 hexosaminidase A (alpha polypeptide)	Homo sapiens
668	M16424	2856	100	beta-hexosaminidase alpha chain	Homo sapiens
669	AAH12992	2115	99	BC012992 Similar to RNA binding motif, single stranded interacting protein 1	Homo sapiens
669	AAH12993	2115	99	BC012993 Similar to RNA binding motif, single stranded interacting protein 1	Homo sapiens
669	AAH18951	2142	100	BC018951 RNA binding motif, single stranded interacting protein 1	Homo sapiens
670	AAH16346	908	100	BC016346 Unknown (protein for MGC:24392)	Homo sapiens
670	AAH16354	908	100	BC016354 Unknown (protein for MGC:24480)	Homo sapiens
670	AAH18990	908	100	BC018990 Unknown (protein for MGC:20176)	Homo sapiens
671	AAH01206	2235	99	BC001206 Unknown (protein for MGC:3208)	Homo sapiens
671	AK025822	3505	99	unnamed protein product	Homo sapiens
671	AL833865	3414	100	hypothetical protein	Homo sapiens
672	AAH06772	769	100	BC006772 ribosomal protein S13	Homo sapiens
672	BC029732	769	100	ribosomal protein S13	Homo sapiens
672	X53378	769	100	ribosomal protein S13	Rattus rattus
673	J05192	1982	100	alpha-actin	Homo sapiens
673	X06801	1968	99	alpha-actin (AA 1-377)	Rattus rattus
673	X13297	1968	99	alpha-actin (AA 1-377)	Mus musculus
674	AAH00260	1675	99	BC000260 aldo-keto reductase family 1, member B1 (aldose reductase)	Homo sapiens
674	AAH10391	1675	99	BC010391 aldo-keto reductase family 1, member B1 (aldose reductase)	Homo sapiens
674	J05017	1677	100	aldose reductase	Homo sapiens
675	M22246	2623	100	aromatase precursor (EC	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				1.14.14.1)	
675	X13589	2623	100	aromatase (AA 1-503)	Homo sapiens
675	Y07508	2620	99	aromatase (AA 1-503)	Homo sapiens
676	M59916	3466	100	acid sphingomyelinase	Homo sapiens
676	M81780	3450	99	acid sphingomyelinase	Homo sapiens
676	X63600	3461	99	acid sphingomyelinase	Homo sapiens
677	AAH21993	1707	100	BC021993 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	Homo sapiens
677	M24193	1707	100	MHC B complex protein 12.3	Gallus gallus
677	X75313	1707	100	B complex protein mRNA 12-3	Mus musculus
678	AAH05358	642	100	BC005358 non-histone chromosome protein 2 (S. cerevisiae)-like 1	Homo sapiens
678	AAH19282	642	100	BC019282 non-histone chromosome protein 2 (S. cerevisiae)-like 1	Homo sapiens
678	BC026755	642	100	Similar to sperm specific antigen 1	Mus musculus
679	AAH19296	2747	100	BC019296 chaperonin containing TCP1, subunit 7 (eta)	Homo sapiens
679	AF026292	2747	100	chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta	Homo sapiens
679	BC008255	2628	95	chaperonin subunit 7 (eta)	Mus musculus
680	BC035220	3879	99	similar to complement component	Homo sapiens
680	M14058	3885	100	human complement C1r	Homo sapiens
680	X04701	3879	99	precursor of C1r (AA -17 to 688)	Homo sapiens
681	J04080	3789	100	complement component C1s	Homo sapiens
681	M18767	3789	100	complement subcomponent C1s precursor	Homo sapiens
681	X06596	3789	100	complement protein C1s precursor	Homo sapiens
682	AAH03175	2072	100	BC003175 N-myc downstream regulated	Homo sapiens
682	AF004162	2072	100	nickel-specific induction protein	Homo sapiens
682	D87953	2072	100	RTP	Homo sapiens
683	AF085250	759	100	calmodulin	Perca flavescens
683	D83350	759	100	calmodulin	Anas platyrhynchos
683	K01945	759	100	calmodulin (cDNA clone 71)	Xenopus laevis
684	AAH07911	2282	100	BC007911 calreticulin	Homo sapiens
684	AAH20493	2282	100	BC020493 calreticulin	Homo sapiens
684	AY047586	2282	100	calreticulin	Homo sapiens
685	AAH16300	533	100	BC016300 S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	Homo sapiens
685	Z18950	533	100	CAPL	Homo sapiens
685	Z33457	533	100	mtsl	Homo sapiens
686	AAH01506	710	100	BC001506 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	Homo sapiens
686	X16447	710	100	precursor polypeptide (AA -25 to 103)	Homo sapiens
686	X17198	710	100	CD59 antigen precursor	Homo sapiens
687	AAH06290	898	100	BC006290 chorionic gonadotropin, beta polypeptide	Homo sapiens
687	BC022796	898	100	Unknown (protein for MGC:39080)	Homo sapiens
687	BC030994	898	100	chorionic gonadotropin, beta polypeptide	Homo sapiens
688	J03225	1674	100	lipoprotein-associated coagulation inhibitor precursor	Homo sapiens
688	M58650	1674	100	lipoprotein associated coagulation inhibitor	Homo sapiens
688	M59499	1674	100	lipoprotein-associated	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				coagulation inhibitor	
689	AAH14167	1072	100	BC014167 Unknown (protein for MGC:20892)	Homo sapiens
689	AAH20804	1072	100	BC020804 ribosomal protein L13	Homo sapiens
689	BC027463	1072	100	ribosomal protein L13	Homo sapiens
690	AAH21136	1333	100	BC021136 Unknown (protein for MGC:32056)	Homo sapiens
690	AF097362_1	1333	100	AF097362 gamma-interferon inducible lysosomal thiol reductase	Homo sapiens
690	BC031020	1329	99	interferon, gamma-inducible protein 30	Homo sapiens
691	AAH07008	929	100	BC007008 crystallin, alpha B	Homo sapiens
691	M28638	929	100	alpha-B2-crystallin	Homo sapiens
691	S45630	929	100	alpha B-crystallin	Homo sapiens
692	BC003775	1169	99	casein kinase II, beta subunit	Mus musculus
692	M30448	1174	100	casein kinase II beta subunit	Homo sapiens
692	M59458	1169	99	casein kinase II beta subunit	Gallus gallus
693	M77820	6209	50	fibronectin	Xenopus laevis
693	X02761	12570	99	fibronectin precursor	Homo sapiens
693	X15906	7305	65	precursor polypeptide (AA -32 to 2445)	Rattus norvegicus
694	BC032329	2740	99	cytochrome P450, subfamily XIA (cholesterol side chain cleavage)	Homo sapiens
694	M14565	2753	100	cholesterol side-chain cleavage enzyme P450scc (EC 1.14.15.67)	Homo sapiens
694	X05367	2734	99	desmolase	Homo sapiens
695	AF318372_1	592	99	AF318372 unknown	Homo sapiens
695	AJ318881	601	100	XAGE-3 protein	Homo sapiens
695	AJ318893	601	100	XAGE-3 protein	Homo sapiens
696	AAH18641	2406	100	BC018641 eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
696	AAH21686	2406	100	BC021686 eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
696	BC028674	2406	100	eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
697	AAH07044	2377	100	BC007044 fibrinogen, gamma polypeptide	Homo sapiens
697	AAH21674	2377	100	BC021674 fibrinogen, gamma polypeptide	Homo sapiens
697	AF350254_1	2377	100	AF350254 fibrinogen gamma chain, isoform gamma-A precursor	Homo sapiens
698	AAH07785	2357	100	BC007785 Unknown (protein for IMAGE:2819608)	Homo sapiens
698	AAH21565	2387	100	BC021565 Unknown (protein for MGC:31904)	Homo sapiens
698	AF121858_1	2387	100	AF121858 sorting nexin 8	Homo sapiens
699	AAH05929	1222	100	BC005929 proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	Homo sapiens
699	X14088	1222	100	major basic protein precursor (AA 1-222)	Homo sapiens
699	Y00809	1222	100	major basic preproprotein (AA -15 to 207)	Homo sapiens
700	AL050169	951	100	hypothetical protein	Homo sapiens
700	M34046	951	100	placental protein 14 precursor (PP14)	Homo sapiens
700	M61886	951	100	pregnancy-associated endometrial alpha2-globulin	Homo sapiens
701	AAH15641	2224	100	BC015641 enolase 1, (alpha)	Homo sapiens
701	BC022545	2224	100	enolase 1, (alpha)	Homo sapiens
701	BC027725	2224	100	enolase 1, (alpha)	Homo sapiens
702	AF272142	2649	100	cytochrome P450	Homo sapiens
702	BC032594	2649	100	cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase)	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				polypeptide 2	
702	U37143	2649	100	cytochrome P450 monooxygenase CYP2J2	Homo sapiens
703	AAH17123	1367	100	BC017123 ribosomal protein S3A	Homo sapiens
703	AAH19072	1367	100	BC019072 ribosomal protein S3A	Homo sapiens
703	BC030161	1367	100	ribosomal protein S3A	Homo sapiens
704	AB042200	2004	88	low-density lipoprotein receptor-related protein 9	Mus musculus
704	AL834518	2154	99	hypothetical protein	Homo sapiens
704	AX359701	2268	99	unnamed protein product	Homo sapiens
705	BC040431	5104	99	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	Homo sapiens
705	M34424	5105	100	acid alpha-glucosidase	Homo sapiens
705	X55080	5105	100	acid alpha-glucosidase	Homo sapiens
706	AAH10914	768	100	BC010914 Similar to hemoglobin, gamma G	Homo sapiens
706	BC029387	768	100	hemoglobin, gamma G	Homo sapiens
706	M91037	768	100	G-gamma globin	Homo sapiens
707	AY148100	4568	100	colony stimulating factor 3 receptor (granulocyte)	Homo sapiens
707	M59818	4568	100	granulocyte colony-stimulating factor receptor	Homo sapiens
707	X55721	4568	100	granulocyte colony stimulating factor receptor 25-1	Homo sapiens
708	AAH00013	1579	100	BC000013 insulin-like growth factor binding protein 3	Homo sapiens
708	AAH18962	1579	100	BC018962 insulin-like growth factor binding protein 3	Homo sapiens
708	M35878	1579	100	growth factor-binding protein-3 precursor	Homo sapiens
709	M23595	1413	100	insulin-like growth factor binding protein 1	Homo sapiens
709	M59316	1413	100	insulin-like growth factor binding protein-1	Homo sapiens
709	X12385	1413	100	PP12 precursor (AA -25 to 234)	Homo sapiens
710	BC041218	676	100	H3 histone, family 3B	Xenopus laevis
710	M11393	676	100	histone 3.3	Gallus gallus
710	Y00392	676	100	histone H3.3B (AA 1 - 136)	Gallus gallus
711	AF523281	1916	99	MHC class Ib antigen	Homo sapiens
711	AF523283	1916	99	MHC class Ib antigen	Homo sapiens
711	M20022	1922	100	HLA-E class I protein precursor	Homo sapiens
712	AAH03569	1980	100	BC003569 E74-like factor 3 (ets domain transcription factor, epithelial-specific)	Homo sapiens
712	AF017307	1980	100	Ets-related transcription factor	Homo sapiens
712	AF110184_1	1980	100	AF110184 epithelium-restricted Ets protein ESX	Homo sapiens
713	AF523305	1810	100	MHC class Ib antigen	Homo sapiens
713	AF523306	1810	100	MHC class Ib antigen	Homo sapiens
713	AF523309	1810	100	MHC class Ib antigen	Homo sapiens
714	AAH09507	836	99	BC009507 Unknown (protein for MGC:3945)	Homo sapiens
714	AY168648	836	99	ubiquitin-like protein ISG15	Homo sapiens
714	M13755	839	100	17-kDa protein	Homo sapiens
715	AB033054	2549	95	KIAA1228 protein	Homo sapiens
715	AF099138	1351	51	GLUT4 vesicle protein	Rattus norvegicus
715	BC011482	1358	50	Similar to membrane bound C2 domain containing protein	Mus musculus
716	AAH10853	1129	100	BC010853 Similar to integral type I protein	Homo sapiens
716	AAH17495	1129	100	BC017495 integral type I protein	Homo sapiens
716	BC022232	1129	100	integral type I protein	Homo sapiens
717	AF357203_1	1832	97	AF357203 MAP kinase phosphatase-1	Rattus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
					norvegicus
717	BC022463	1886	100	dual specificity phosphatase 1	Homo sapiens
717	X68277	1886	100	protein-tyrosine phosphatase	Homo sapiens
718	AAH09407	687	100	BC009407 ribosomal protein S17	Homo sapiens
718	AAH19899	687	100	BC019899 ribosomal protein S17	Homo sapiens
718	BC022370	687	100	ribosomal protein S17	Homo sapiens
719	AAH15105	1370	100	BC015105 proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
719	AAH15356	1370	100	BC015356 proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
719	BC022372	1370	100	proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
720	AAH03352	723	100	BC003352 tumor protein, translationally-controlled 1	Homo sapiens
720	BC022436	723	100	Similar to tumor protein, translationally-controlled 1	Homo sapiens
720	X16064	723	100	tumor protein (AA 1 - 172)	Homo sapiens
721	BC023006	3271	100	Unknown (protein for MGC:30059)	Homo sapiens
721	M27024	3271	100	heat shock protein	Homo sapiens
721	X15183	3271	100	90 kDa heat-shock protein (AA 1-732)	Homo sapiens
722	AAH08064	2806	100	BC008064 monoamine oxidase A	Homo sapiens
722	M68857	2806	100	monoamine oxidase A	Homo sapiens
722	M69226	2806	100	monoamine oxidase A	Homo sapiens
723	M84378	1952	100	lymphocyte antigen	Homo sapiens
723	M84379	1945	99	MHC class I lymphocyte antigen	Homo sapiens
723	Z27120	1946	99	HLA-A2 SLU	Homo sapiens
724	BC032350	1338	100	major histocompatibility complex, class II, DR alpha	Homo sapiens
724	M60334	1338	100	cell surface glycoprotein	Homo sapiens
724	Z84814	1338	100	dJ172K2.4.1 (major histocompatibility complex, class II, DR alpha, isoform 1)	Homo sapiens
725	AAH02476	803	100	BC002476 non-metastatic cells 2, protein (NM23B) expressed in	Homo sapiens
725	L16785	803	100	c-myc transcription factor	Homo sapiens
725	X58965	803	100	NM23-H2 protein	Homo sapiens
726	AAH11645	1585	100	BC011645 Similar to Ras-related associated with diabetes	Homo sapiens
726	L24564	1585	100	Rad	Homo sapiens
726	U46165	1565	99	Rad GTPase	Homo sapiens
727	AAH03358	1151	100	BC003358 ribosomal protein L10	Homo sapiens
727	BC026276	1151	100	ribosomal protein L10	Homo sapiens
727	L44140	1151	100	QM	Homo sapiens
728	A84527	2912	100	unnamed protein product	unidentified
728	AX024042	2912	100	fusion between Aequorea victoria and human	synthetic construct
728	M62399	2912	100	NF-kappa-B transcription factor	Homo sapiens
729	AAH10860	2071	100	BC010860 serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	Homo sapiens
729	AF386492_1	2071	100	AF386492 serine-cysteine proteinase inhibitor clade E member 1	Homo sapiens
729	X04429	2071	100	precursor polypeptide	Homo sapiens
730	AAH00491	1316	100	BC000491 proliferating cell nuclear antigen	Homo sapiens
730	AF347680_1	1316	100	AF347680 proliferating cell nuclear antigen	Macaca fascicularis
730	AL121924	1316	100	dJ746J20.2 (proliferating cell nuclear antigen)	Homo sapiens
731	AC007165	2130	100	interleukin-1 receptor type II	Homo sapiens
731	AY124010	2130	100	interleukin 1 receptor, type II	Homo sapiens
731	X59770	2130	100	type II interleukin-1 receptor	Homo sapiens
732	BC041071	2366	100	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Homo sapiens

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732	M64929	2366	100	protein phosphatase-2A subunit-alpha	Homo sapiens
732	U09356	2366	100	protein phosphatase 2A1 B alpha subunit	Oryctolagus cuniculus
733	M34421	2279	99	pregnancy-specific beta-1 glycoprotein precursor	Homo sapiens
733	M34481	2279	99	pregnancy-specific beta-1-glycoprotein 11	Homo sapiens
733	M58591	2291	100	PSG11	Homo sapiens
734	BC018254	703	97	retinol binding protein 1, cellular	Mus musculus
734	M11433	724	100	retinol-binding protein	Homo sapiens
734	X07437	724	100	cellular retinol binding protein	Homo sapiens
735	J03149	4237	83	M-CSF receptor	Felis catus
735	U63963	5158	100	CSF-1 receptor	Homo sapiens
735	X03663	5150	99	put. c-fms precursor	Homo sapiens
736	BC005580	902	100	polymerase (RNA) II (DNA directed) polypeptide G	Mus musculus
736	U52427	902	100	RNA polymerase II seventh subunit	Homo sapiens
736	Z71925	902	100	RNA polymerase II RPB7 subunit-like protein	Rattus norvegicus
737	AAH11601	658	100	BC011601 interferon, alpha-inducible protein (clone IFI-6-16)	Homo sapiens
737	AAH15603	658	100	BC015603 interferon, alpha-inducible protein (clone IFI-6-16)	Homo sapiens
737	D11384	652	98	ORF	Pan troglodytes
738	AF147083	1683	100	gamma-glutamyl hydrolase	Homo sapiens
738	BC025025	1683	100	gamma-glutamyl hydrolase (conjugase, folylpolyglutamyl hydrolase)	Homo sapiens
738	U55206	1683	100	human gamma-glutamyl hydrolase	Homo sapiens
739	AAH10418	1552	100	BC010418 laminin receptor 1 (67kD, ribosomal protein SA)	Homo sapiens
739	AAH13827	1552	100	BC013827 laminin receptor 1 (67kD, ribosomal protein SA)	Homo sapiens
739	U43901	1552	100	37 kD laminin receptor precursor/p40 ribosome associated protein	Homo sapiens
740	BC026033	4101	100	gelsolin (amyloidosis, Finnish type)	Homo sapiens
740	X04412	4101	100	plasma gelsolin	Homo sapiens
740	X13871	3849	94	gelsolin	Sus scrofa
741	AF304463_1	2813	100	AF304463 calcium transport protein CaT1	Homo sapiens
741	AF365927_1	2813	100	AF365927 calcium transport protein CaT1	Homo sapiens
741	AF365928_1	2946	100	AF365928 calcium transport protein CaT1	Homo sapiens
742	AY040542	2353	100	sialic acid binding immunoglobulin-like lectin 6	Homo sapiens
742	D86358	2353	100	CD33L1	Homo sapiens
742	U71382	2246	97	OB binding protein-1	Homo sapiens
743	AF286534_1	1115	100	AF286534 GTP-binding protein RAB11B	Rattus norvegicus
743	AF498947_1	1115	100	AF498947 small GTP binding protein RAB11B	Homo sapiens
743	X79780	1110	99	YPT3	Homo sapiens
744	BC010604	1253	99	ribosomal protein S6	Mus musculus
744	BC027620	1256	100	ribosomal protein S6	Homo sapiens
744	Z54209	1253	99	rpS6	Mus musculus
745	AJ005654	703	100	secondary lymphoid tissue chemokine	Homo sapiens
745	BC027918	703	100	small inducible cytokine subfamily A (Cys-Cys), member 21	Homo sapiens
745	U88320	703	100	beta chemokine Exodus-2	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
746	AF148856 2	6613	98	AF148856 unknown	Homo sapiens
746	AF149422 2	6615	98	AF149422 unknown	Homo sapiens
746	U93564	6714	100	putative p150	Homo sapiens
747	AK012013	1608	100	unnamed protein product	Mus musculus
747	BC003742	1608	100	26S proteasome-associated pad1 homolog	Mus musculus
747	U86782	1608	100	26S proteasome-associated pad1 homolog	Homo sapiens
748	AK011431	484	100	unnamed protein product	Mus musculus
748	BC041218	676	100	H3 histone, family 3B	Xenopus laevis
748	Y00392	676	100	histone H3.3B (AA 1 - 136)	Gallus gallus
749	AAH11262	2716	99	BC011262 Unknown (protein for MGC:18226)	Homo sapiens
749	AF006043	2719	100	3-phosphoglycerate dehydrogenase	Homo sapiens
749	AF171237_1	2719	100	AF171237 3-phosphoglycerate dehydrogenase	Homo sapiens
750	AF109197 1	1254	100	AF109197 nuclear chloride channel	Homo sapiens
750	AJ012008	1251	99	RNCC protein	Homo sapiens
750	U93205	1254	100	nuclear chloride ion channel protein	Homo sapiens
751	BC029402	1311	100	proteasome (prosome, macropain) subunit, alpha type, 3	Homo sapiens
751	BC038990	1307	99	Similar to proteasome (prosome, macropain) subunit, alpha type, 3	Homo sapiens
751	D00762	1307	99	proteasome subunit C8	Homo sapiens
752	AB062400	671	100	Similar to ribosomal protein S15a	Homo sapiens
752	BC030569	671	100	ribosomal protein S15a	Homo sapiens
752	X77953	671	100	ribosomal protein S15a	Rattus norvegicus
753	AB062438	1926	100	OK/SW-CL.30	Homo sapiens
753	BC025832	1581	90	Unknown (protein for MGC:37936)	Mus musculus
753	BC036872	1912	99	Unknown (protein for IMAGE:5225889)	Homo sapiens
754	AAH16706	2319	100	BC016706 eukaryotic translation initiation factor 3, subunit 6 (48kD)	Homo sapiens
754	AAH21679	2319	100	BC021679 eukaryotic translation initiation factor 3, subunit 6 (48kD)	Homo sapiens
754	BC029177	2319	100	eukaryotic translation initiation factor 3, subunit 6 (48kD)	Mus musculus
755	AAH04138	1465	99	BC004138 ribosomal protein L6	Homo sapiens
755	BC031009	1475	100	ribosomal protein L6	Homo sapiens
755	BC032299	1465	99	ribosomal protein L6	Homo sapiens
756	AAH15813	2331	100	BC015813 eukaryotic translation elongation factor 1 gamma	Homo sapiens
756	BC028179	2331	100	eukaryotic translation elongation factor 1 gamma	Homo sapiens
756	BC031012	2331	100	eukaryotic translation elongation factor 1 gamma	Homo sapiens
757	AAH04927	1051	100	BC004927 Unknown (protein for MGC:10432)	Homo sapiens
757	AF013711	1051	100	22 kDa actin-binding protein	Homo sapiens
757	D84342	1051	100	SM22 alpha	Homo sapiens
758	AB007510	12543	100	PRP8 protein	Homo sapiens
758	AB047391	12461	99	pre-mRNA processing 8 protein	Mus musculus
758	AF092565	12477	99	splicing factor Prp8	Homo sapiens
759	AAH10034	3127	100	BC010034 thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
759	AAH12154	3127	100	BC012154 Similar to thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
759	AAH18259	3127	100	BC018259 thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
760	AL050369	2492	99	hypothetical protein	Homo sapiens
760	AY040822	2500	100	U4/U6 snRNP-associated 61 kDa protein	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
760	BC018376	2479	98	Unknown (protein for MGC:19247)	Mus musculus
761	AF343440_1	454	98	AF343440 lysosomal H+ transporting-ATPase subunit M9.2	Canis familiaris
761	AX400012	459	100	unnamed protein product	Homo sapiens
761	Y15286	459	100	vacuolar proton-ATPase subunit M9.2	Homo sapiens
762	AAH01273	1831	99	BC001273 galactose-4-epimerase, UDP-	Homo sapiens
762	AF022382	1835	100	UDP-galactose 4' epimerase	Homo sapiens
762	L41668	1835	100	UDP-galactose-4-epimerase	Homo sapiens
763	AAH05270	900	99	BC005270 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	Homo sapiens
763	AF020351	904	100	NADH:ubiquinone oxidoreductase 18 kDa IP subunit	Homo sapiens
763	X63215	839	90	NADH dehydrogenase	Bos taurus
764	AAH04963	674	100	BC004963 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Homo sapiens
764	AL080089	674	100	hypothetical protein	Homo sapiens
764	X69907	674	100	P1 gene for c subunit of human mitochondrial ATP synthase	Homo sapiens
765	AF100620_1	1492	100	AF100620 transcription factor-like protein MRGX	Homo sapiens
765	AF167174_1	1492	100	AF167174 MSL3-2 protein	Homo sapiens
765	AL049610	1492	100	dJ1055C14.2 (KIAA0026 (transcription factor-like protein MRGX))	Homo sapiens
766	AAH15557	1854	99	BC015557 Unknown (protein for MGC:1567)	Homo sapiens
766	BC021637	1140	66	CD68 antigen	Mus musculus
766	S57235	1858	100	CD68	Homo sapiens
767	L27631	4010	100	amyloid precursor-like protein 2	Homo sapiens
767	S60099	4010	100	APPH	Homo sapiens
767	Z22572	4010	100	CDEI binding protein	Homo sapiens
768	AAH08850	1273	99	BC008850 Unknown (protein for MGC:14308)	Homo sapiens
768	AAH09599	1273	99	BC009599 Unknown (protein for MGC:14690)	Homo sapiens
768	L16558	1276	100	ribosomal protein L7	Homo sapiens
769	AF062482	845	99	SDP3	Mus musculus
769	AF062483	852	100	SDP3	Homo sapiens
769	AF520420	838	98	sorting nexin 3	Mus musculus
770	AF063657	6995	100	vascular endothelial growth factor receptor	Homo sapiens
770	D28498	5882	82	Fit-1 tyrosine kinase receptor	Rattus norvegicus
770	X51602	6989	99	flt gene product (AA 1-1338)	Homo sapiens
771	AF081112	239	34	ORF2	Mus musculus domesticus
771	U83119	244	34	ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH	Rattus norvegicus
771	U93572	336	42	putative p150	Homo sapiens
772	AF029729	3066	100	neuralized	Homo sapiens
772	BC026336	3041	99	neuralized-like (Drosophila)	Homo sapiens
772	U87864	3066	100	neuralized homolog	Homo sapiens
773	AAH20782	643	100	BC020782 glycoprotein hormones, alpha polypeptide	Homo sapiens
773	J00152	643	100	glycoprotein alpha subunit	Homo sapiens
773	V00518	643	100	chorionic gonadotropin	Homo sapiens
774	AAH02722	2070	100	BC002722 guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1	Homo sapiens
774	AF493897_1	2070	100	AF493897 guanine nucleotide	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				binding protein alpha s long	
774	X04408	2070	100	alpha-S2 (aa 1-394)	Homo sapiens
775	BC033714	1724	100	heterogeneous nuclear ribonucleoprotein A1	Homo sapiens
775	D86729	1724	100	TIS	Mus musculus
775	M99167	1724	100	RNA binding protein	Mus musculus
776	AF072836	1827	100	Sox-like transcriptional factor	Homo sapiens
776	AF146223_1	620	100	AF146223 HMG domain protein HMGX2	Homo sapiens
776	AF288679	620	100	smarcel-related protein	Homo sapiens
777	AAH21979	1360	100	BC021979 ribosomal protein L7a	Homo sapiens
777	BC032533	1360	100	ribosomal protein L7a	Homo sapiens
777	X15013	1360	100	ribosomal protein L7a (AA 1-266)	Rattus rattus
778	X51538	693	100	ribosomal protein S24 (AA 1-133)	Rattus rattus
778	X52445	693	100	ribosomal protein S24	Rattus norvegicus
778	X52658	693	100	ribosomal protein S19 (AA 1 - 133)	Mesocricetus auratus
779	AAH01503	2789	100	BC001503 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
779	AAH04275	2789	100	BC004275 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
779	AAH07612	2789	100	BC007612 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
780	AAH11776	1369	100	BC011776 Similar to tropomyosin 2 (beta)	Homo sapiens
780	M74817	1369	100	tropomyosin-1	Homo sapiens
780	M75165	1369	100	tropomyosin	Homo sapiens
781	AL023883	1173	99	dJ404K8.1 (prolactin)	Homo sapiens
781	BC015850	1185	100	similar to prolactin precursor	Homo sapiens
781	V00566	1185	100	reading frame prolactin	Homo sapiens
782	AK012601	247	64	unnamed protein product	Mus musculus
782	AK021409	286	69	unnamed protein product	Mus musculus
782	AK075801	246	64	unnamed protein product	Mus musculus
783	AF300943_1	9468	94	AF300943 tyrosine phosphatase LAR	Mus musculus
783	L11586	9484	95	leukocyte common antigen-related phosphatase	Rattus norvegicus
783	Y00815	9953	100	put. LAR preprotein (AA -16 to 1881)	Homo sapiens
784	AAH16046	2739	100	BC016046 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Homo sapiens
784	AAH19310	2739	100	BC019310 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Homo sapiens
784	X65460	2739	100	ATP synthase alpha subunit	Homo sapiens
785	AF237581_1	613	100	AF237581 migration inhibitory factor-related protein 14 variant P	Homo sapiens
785	M26311	613	100	cystic fibrosis antigen	Homo sapiens
785	X06233	613	100	MRP-14 (AA 1-114)	Homo sapiens
786	AAH15492	523	96	BC015492 Unknown (protein for MGC:8967)	Homo sapiens
786	BC032626	280	64	TLH29 protein precursor	Homo sapiens
786	X67325	556	100	ISG12	Homo sapiens
787	L00160	2135	100	phosphoglycerate kinase	Homo sapiens
787	M11968	2135	100	phosphoglycerate kinase	Homo sapiens
787	V00572	2135	100	coding sequence	Homo sapiens
788	AF075575	11112	100	dysferlin	Homo sapiens
788	AF188290_1	10355	93	AF188290 dysferlin	Mus musculus
788	AK074104	7939	98	FLJ00175 protein	Homo sapiens
789	AB052229	10414	100	RNA polymerase II largest subunit	Cricetulus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
					griseus
789	D87294	10414	100	RNA polymerase II largest subunit	Cricetus griseus
789	X63564	10414	100	RNA polymerase II largest subunit	Homo sapiens
790	AF070650	844	100	F1F0-type ATP synthase subunit d	Homo sapiens
790	AF087135	844	100	F1F0-type ATPase subunit d	Homo sapiens
790	BC038092	844	100	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Homo sapiens
791	U01153	4046	97	GRP94	Canis familiaris
791	X15187	4112	100	precursor polypeptide (AA -21 to 782)	Homo sapiens
791	Y09136	4038	97	gp96/GRP94	Sus scrofa
792	AF297036_1	670	100	AF297036 ubiquitin fusion protein	Ophiophagus hannah
792	BC014772	670	100	ubiquitin A-52 residue ribosomal protein fusion product 1	Mus musculus
792	M24508	670	100	ubiquitin	synthetic construct
793	AB047600	167	67	hypothetical protein	Macaca fascicularis
793	AK097085	208	48	unnamed protein product	Homo sapiens
793	X92485	165	68	pval	Plasmodium vivax
794	AF100956	782	100	ribosomal protein subunit S18	Mus musculus
794	AF110520	782	100	RPS18	Mus musculus
794	M76763	782	100	ribosomal protein	Mus musculus
795	BC025077	930	100	RIKEN cDNA 2010203J19 gene	Mus musculus
795	L05092	930	100	ribosomal protein L11	Homo sapiens
795	X62146	930	100	ribosomal protein L11	Rattus rattus
796	AB037890	6795	99	pre-mRNA splicing factor SF3b 155 kDa subunit	Mus musculus
796	AF054284	6808	100	spliceosomal protein SAP 155	Homo sapiens
796	Y08997	6566	96	146kDa nuclear protein	Xenopus laevis
797	AF072097	624	100	beta-2 microglobulin	Homo sapiens
797	AY007153	624	100	similar to Homo sapiens mRNA for beta 2-microglobulin with GenBank Accession Number AB021288	
797	BC032589	624	100	beta-2-microglobulin	Homo sapiens
798	AAH17839	1602	100	BC017839 caspase 4, apoptosis-related cysteine protease	Homo sapiens
798	U28976	1602	100	Mih1/TX isoform alpha	Homo sapiens
798	U28977	1769	100	Mih1/TX isoform beta	Homo sapiens
799	AAH07967	974	100	BC007967 Unknown (protein for MGC:14460)	Homo sapiens
799	AAH12149	974	100	BC012149 Unknown (protein for MGC:20365)	Homo sapiens
799	BC031906	974	100	similar to ribosomal protein L9; 60S ribosomal protein L9	Homo sapiens
800	BC002145	745	100	ribosomal protein S23	Mus musculus
800	D14530	745	100	ribosomal protein	Homo sapiens
800	X77398	745	100	ribosomal protein S23	Rattus norvegicus
801	AF227256_1	405	100	AF227256 NEDD8	Bos taurus
801	BC004625	398	98	neural precursor cell expressed, developmentally down-regulated gene 8	Mus musculus
801	D23662	405	100	ubiquitin-like protein	Homo sapiens
802	U46034	2076	83	stromelysin 3	Rattus norvegicus
802	X57766	2679	100	stromelysin-3 precursor	Homo sapiens
802	Z12604	2164	81	stromelysin-3	Mus musculus
803	AAH01734	499	100	BC001734 protein translocation complex beta	Homo sapiens
803	AL137067	499	100	bA13B9.2 (novel protein similar	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				to the beta subunit of transport protein SEC61)	
803	L25085	499	100	Sec61-complex beta-subunit	Homo sapiens
804	AF165522_1	360	100	AF165522 ras-related GTP-binding protein 4b	Homo sapiens
804	AF217985_1	360	100	AF217985 unknown	Homo sapiens
804	AF498935_1	360	100	AF498935 small GTP binding protein RAB4B	Homo sapiens
805	AF006602	5436	94	histone deacetylase mHDA1	Mus musculus
805	AF132608_1	5784	100	AF132608 histone deacetylase 5	Homo sapiens
805	AF207748_1	5431	94	AF207748 histone deacetylase 5	Mus musculus
806	AL050259	4009	100	hypothetical protein	Homo sapiens
806	BC032681	4009	100	RAB2, member RAS oncogene family-like	Homo sapiens
806	Z97184	4009	100	c1CF0811.4.1 (RAB2, member RAS oncogene family-like, isoform 1)	Homo sapiens
807	AF151855_1	1278	100	AF151855 CGI-97 protein	Homo sapiens
807	AK001779	1214	96	unnamed protein product	Homo sapiens
807	BC003849	1200	94	RIKEN cDNA 4733401P19 gene	Mus musculus
808	AAH00234	1377	100	BC000234 nicotinamide N-methyltransferase	Homo sapiens
808	U08021	1377	100	nicotinamide N-methyltransferase	Homo sapiens
808	U20971	1377	100	nicotinamide N-methyltransferase	Homo sapiens
809	AAH03137	1240	100	BC003137 ribosomal protein S3	Homo sapiens
809	BC034149	1240	100	ribosomal protein S3	Homo sapiens
809	U14992	1240	100	ribosomal protein S3	Homo sapiens
810	AF090891_1	3913	99	AF090891 PRO0105	Homo sapiens
810	AF268075_1	3913	99	AF268075 TRAF6-binding protein T6BP	Homo sapiens
810	U33821	3924	100	tax1-binding protein TXBP151	Homo sapiens
811	AF186112_1	619	100	AF186112 neurokinin B-like protein ZNEUROK1	Homo sapiens
811	AF216586_1	619	100	AF216586 neurokinin B	Homo sapiens
811	BC032145	619	100	tachykinin 3 (neuromedin K, neurokinin beta)	Homo sapiens
812	AAH08405	2044	90	BC008405 Unknown (protein for MGC:14528)	Homo sapiens
812	M94891	2042	90	pregnancy-specific beta-1 glycoprotein	Homo sapiens
812	U18467	2252	100	pregnancy-specific beta 1-glycoprotein 7 precursor	Homo sapiens
813	AK002989	980	93	unnamed protein product	Mus musculus
813	D38076	1041	99	Ran-BP1(Ran-binding protein 1)	Homo sapiens
813	X83617	1057	100	RanBP1	Homo sapiens
814	AF152604	3398	100	bromodomain-containing protein	Homo sapiens
814	AF213969	3369	99	bromodomain protein CELTIX1	Homo sapiens
814	AJ271881	3398	100	bromodomain containing protein	Homo sapiens
815	AK000496	327	65	unnamed protein product	Homo sapiens
815	AK090511	328	65	unnamed protein product	Homo sapiens
815	AX399963	319	62	unnamed protein product	Homo sapiens
816	AK000917	2276	100	unnamed protein product	Homo sapiens
816	BC025560	2156	94	Similar to hypothetical protein FLJ10055	Mus musculus
816	BC039867	2259	99	hypothetical protein FLJ10055	Homo sapiens
817	AB039886	1071	100	down-regulated in gastric cancer	Homo sapiens
817	AY139182	995	100	18 kDa antrum mucosa protein	Homo sapiens
817	AY139184	995	100	18 kDa antrum mucosa protein	Homo sapiens
818	BC033721	3540	99	Unknown (protein for MGC:45264)	Homo sapiens
818	X82157	3543	100	hevin	Homo sapiens
818	X86693	3504	99	Hevin-like protein	Homo sapiens
819	M84472	1675	100	17-beta-hydroxysteroid dehydrogenase	Homo sapiens
819	U34879	1675	100	17-beta-hydroxysteroid dehydrogenase	Homo sapiens
819	X13440	1675	100	17-HSD protein (AA 1 - 328)	Homo sapiens
820	AAH12612	1812	99	BC012612 Similar to cathepsin L	Homo sapiens
820	M20496	1816	100	preprocathepsin L precursor	Homo sapiens
820	X12451	1816	100	pro-(cathepsin L)	Homo sapiens

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821	AAH12355	3449	100	BC012355 Similar to solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Homo sapiens
821	U36341	3449	100	creatine transporter	Homo sapiens
821	Z66539	3449	100	creatine transporter	Homo sapiens
822	AF267852_1	749	100	AF267852 placental protein 13-like protein	Homo sapiens
822	AF367430	571	100	placental protein 13-like	Homo sapiens
822	BC022257	731	98	Similar to placental protein 13-like protein	Homo sapiens
823	AB001636	4072	99	ATP-dependent RNA helicase #46	Homo sapiens
823	AF279891_1	4162	100	AF279891 dead box protein 15	Homo sapiens
823	BC035974	4162	100	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	Homo sapiens
824	AAH17321	687	100	BC017321 Unknown (protein for MGC:29768)	Homo sapiens
824	BC002079	687	100	Similar to ribosomal protein S12	Mus musculus
824	BC018362	687	100	Unknown (protein for MGC:19264)	Mus musculus
825	AAH20619	1123	99	BC020619 glutathione S-transferase A3	Homo sapiens
825	AF508266_1	1127	100	AF508266 glutathione transferase A3-3	Homo sapiens
825	AL121969	1127	100	dJ214M20.1 (glutathione S-transferase A3)	Homo sapiens
826	AAH00359	923	100	BC000359 signal peptidase complex (18kD)	Homo sapiens
826	AAH14508	923	100	BC014508 Similar to signal peptidase complex (18kD)	Homo sapiens
826	AF061737	923	100	microsomal signal peptidase	Homo sapiens
827	AF179890_1	598	100	AF179890 DNA polymerase delta smallest subunit p12	Homo sapiens
827	AF515709_1	492	83	AF515709 small subunit DNA polymerase delta p12	Mus musculus
827	BC028520	492	83	Unknown (protein for MGC:41275)	Mus musculus
828	AC005067_2	1340	73	AC005067 Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan	Homo sapiens
828	AF226732_1	2286	100	AF226732 NPD007	Homo sapiens
828	BC018360	1199	68	Unknown (protein for MGC:18730)	Mus musculus
829	AAH19040	897	100	BC019040 Unknown (protein for MGC:20769)	Homo sapiens
829	D11428	826	100	PMP-22 (PAS-II/SR13/Gas-3)	Homo sapiens
829	L03203	826	100	peripheral myelin protein 22	Homo sapiens
830	AK023767	960	100	unnamed protein product	Homo sapiens
830	AL080169	979	100	hypothetical protein	Homo sapiens
830	BC016647	960	100	Unknown (protein for MGC:16844)	Homo sapiens
831	AF309646_1	1144	88	AF309646 Rab6-like protein WTH3	Homo sapiens
831	AF498941_1	1058	100	AF498941 small GTP binding protein RAB6C	Homo sapiens
831	AL136727	1144	88	hypothetical protein	Homo sapiens
832	AC005095_1	1373	100	AC005095 pantophysin	Homo sapiens
832	S72481	1373	100	pantophysin	Homo sapiens
832	X68194	1373	100	h-Spl	Homo sapiens
833	D14665	3850	99	KIAA0021 protein	Homo sapiens
833	U41765	3814	83	metalloprotease/disintegrin/cysteine rich protein precursor	Mus musculus
833	U41766	4476	100	metalloprotease/disintegrin/cysteine-rich protein precursor	Homo sapiens
834	U20770	1412	100	cell surface glycoprotein	Homo sapiens
834	U67274	1412	100	metastasis suppressor	Homo sapiens
834	X53795	1412	100	inducible membrane protein	Homo sapiens
835	AF517934_1	2980	100	AF517934 interleukin 2 receptor, beta	Homo sapiens
835	AL022314	2980	100	dJ1170K4.3 (Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen))	Homo sapiens

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835	BC025691	2980	100	interleukin 2 receptor, beta	Homo sapiens
836	AF072242	2167	100	methyl-CpG binding protein MBD2	Homo sapiens
836	AF120994	2167	100	methyl-CpG binding protein 2	Homo sapiens
836	BC032638	2167	100	methyl-CpG binding domain protein 2	Homo sapiens
837	AAH00486	607	100	BC000486 small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	Homo sapiens
837	AAH01930	607	100	BC001930 small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	Homo sapiens
837	AC007191_1	607	100	AC007191 SMD2 HUMAN; SNRNP CORE PROTEIN D2; SM-D2	Homo sapiens
838	AAH18180	870	100	BC018180 CGI-121 protein	Homo sapiens
838	AF151879_1	870	100	AF151879 CGI-121 protein	Homo sapiens
838	BC029492	870	100	CGI-121 protein	Homo sapiens
839	U52373	4063	99	MNB	Homo sapiens
839	U58497	4037	99	mp86	Mus musculus
839	X79769	4052	99	Dual Specificity Yak1-related Kinase (Dyrk)	Rattus norvegicus
853	AF090949	1710	97	HBV-X associated protein 2	Cercopithecus aethiops
853	U31913	1736	99	HBV-X associated protein	Homo sapiens
853	U78521	1740	100	immunophilin homolog ARA9	Homo sapiens
854	AAH12333	1168	100	BC012333 Unknown (protein for MGC:2084)	Homo sapiens
854	AF187981_1	1168	100	AF187981 delta7-sterol-C5-desaturase	Homo sapiens
854	D85181	1273	100	fungus sterol-C5-desaturase homolog	Homo sapiens
856	A84511	1017	99	unnamed protein product	unidentified
856	AF498970_1	1016	100	AF498970 small GTP binding protein RhoA	Homo sapiens
856	AX427410	1017	99	unnamed protein product	unidentified
857	AAH04312	563	94	BC004312 insulin-like growth factor binding protein 2 (36kD)	Homo sapiens
857	AAH09902	563	94	BC009902 Unknown (protein for MGC:2339)	Homo sapiens
857	AAH12769	563	94	BC012769 Unknown (protein for MGC:16256)	Homo sapiens
858	AAH02434	430	100	BC002434 p8 protein (candidate of metastasis 1)	Homo sapiens
858	AF069074	430	100	P8 protein	Homo sapiens
858	AF135266_1	430	100	AF135266 p8 protein homolog	Homo sapiens
859	AB047892	301	84	hypothetical protein	Macaca fascicularis
860	AAH01199	833	99	BC001199 Similar to glucose regulated protein, 58 kDa	Homo sapiens
860	AJ440721	833	99	thioredoxin related protein	Homo sapiens
860	AL834423	833	99	hypothetical protein	Homo sapiens
861	AAH00866	1124	100	BC000866 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	Homo sapiens
861	M59906	1124	100	collagenase inhibitor	Homo sapiens
861	X03124	1124	100	precursor	Homo sapiens
862	AAH00518	1120	98	BC000518 Similar to brain acid-soluble protein 1	Homo sapiens
862	AF039656	1105	96	neuronal tissue-enriched acidic protein	Homo sapiens
862	U92535	818	75	neuronal axonal membrane protein	Bos taurus
863	AAH05931	733	100	BC005931 hemoglobin, alpha 2	Homo sapiens
863	AAH08572	733	100	BC008572 hemoglobin, alpha 2	Homo sapiens
863	BC032122	733	100	hemoglobin, alpha 2	Homo sapiens
864	AF347006	2436	91	cytochrome c oxidase subunit I	Homo sapiens
864	AF382012	2424	92	cytochrome c oxidase subunit I	Homo sapiens
864	AF382013	2424	92	cytochrome c oxidase subunit I	Homo sapiens
865	AF242729_1	1242	100	AF242729 HT022	Homo sapiens

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865	AJ245874	1242	100	putative ATG/GTP binding protein	Homo sapiens
865	AJ250344	1242	100	hypothetical protein	Homo sapiens
866	AAH17050	1367	100	BC017050 2,3-bisphosphoglycerate mutase	Homo sapiens
866	M23068	1367	100	2,3-bisphosphoglycerate	Homo sapiens
866	X04327	1367	100	2,3 biphosphoglycerated mutase (AA 1 - 259)	Homo sapiens
867	AAH02334	921	100	BC002334 DAZ associated protein 2	Homo sapiens
867	AAH07900	921	100	BC007900 DAZ associated protein 2	Homo sapiens
867	D31767	921	100	KIAA0058	Homo sapiens
868	AAH09571	308	98	BC009571 Similar to stimulated by retinoic acid 13	Homo sapiens
868	U95006	309	98	D9 splice variant A	Homo sapiens
868	U95007	273	98	D9 splice variant B	Homo sapiens
869	AAH11674	753	92	BC011674 Similar to procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Homo sapiens
869	AC004876 4	753	92	AC004876 lysyl hydroxylase 3	Homo sapiens
869	AF207069	753	92	lysyl hydroxylase 3	Homo sapiens
870	AAH16765	1778	99	BC016765 Unknown (protein for MGC:22663)	Homo sapiens
870	AF153882_1	1785	100	AF153882 reversion-induced LIM protein	Homo sapiens
870	AF154335_1	1785	100	AF154335 reversion-induced LIM protein	Homo sapiens
871	AF023268	1546	95	metaxin	Homo sapiens
871	BC023071	1424	87	metaxin	Mus musculus
871	U46920	1546	95	metaxin	Homo sapiens
872	AF193053 1	575	100	AF193053 unknown	Homo sapiens
873	AF318351 1	3211	100	AF318351 unknown	Homo sapiens
873	AF318377 1	3211	100	AF318377 unknown	Homo sapiens
873	AX106709	3211	100	unnamed protein product	Homo sapiens
874	AL357374	2678	100	bA353C18.3.2 (splicing factor CC1.3, isoform 2 (CC1.4))	Homo sapiens
874	AY061882	2663	99	transcription coactivator CAPER	Mus musculus
874	L10911	2678	100	splicing factor	Homo sapiens
875	AAH08807	2806	98	BC008807 keratin 6A	Homo sapiens
875	AAH14152	2809	98	BC014152 Similar to keratin 6A	Homo sapiens
875	L42583	2806	98	keratin type II	Homo sapiens
876	AK000496	301	72	unnamed protein product	Homo sapiens
876	AK025116	271	67	unnamed protein product	Homo sapiens
876	AK090511	282	60	unnamed protein product	Homo sapiens
877	AAH16842	2431	99	BC016842 Unknown (protein for MGC:10135)	Homo sapiens
877	AK027643	2435	100	unnamed protein product	Homo sapiens
877	AL834398	2529	99	hypothetical protein	Homo sapiens
878	AAH02563	1624	100	BC002563 Similar to zinc/iron regulated transporter-like	Homo sapiens
878	AAH07886	1624	100	BC007886 Unknown (protein for MGC:14180)	Homo sapiens
878	AAH14303	1624	100	BC014303 Unknown (protein for MGC:16418)	Homo sapiens
879	AF056732	3342	100	prostaglandin transporter	Homo sapiens
879	BC041140	3478	99	solute carrier family 21 (prostaglandin transporter), member 2	Homo sapiens
879	U70867	3342	100	prostaglandin transporter hPGT	Homo sapiens
880	AAH15206	335	100	BC015206 guanine nucleotide binding protein 10	Homo sapiens
880	AAH16319	335	100	BC016319 guanine nucleotide binding protein 10	Homo sapiens
880	AF493877_1	335	100	AF493877 guanine nucleotide binding protein gamma 10	Homo sapiens
881	BC010572	1333	79	Jun proto-oncogene related gene dl	Mus musculus
881	X51346	1517	99	jun-D gene product (AA 1-303)	Homo sapiens
881	X56681	1716	98	junD protein	Homo sapiens
882	AY081680	693	100	chlorophyll a/b-binding protein	Arabidopsis

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				CP29	thaliana
882	AY133566	693	100	At5g01530/F7A7_50	Arabidopsis thaliana
882	BT000363	693	100	chlorophyll a/b-binding protein CP29	Arabidopsis thaliana
883	AY086905	622	100	photosystem II type I chlorophyll a /b binding protein, putative	Arabidopsis thaliana
883	AY128345	622	100	photosystem II type I chlorophyll a/b binding protein, putative	Arabidopsis thaliana
883	BT000726	622	100	putative photosystem II type I chlorophyll a /b binding protein	Arabidopsis thaliana
884	AK074519	1524	97	unnamed protein product	Homo sapiens
884	AK074523	1524	97	unnamed protein product	Homo sapiens
884	AX118867	1543	100	unnamed protein product	Homo sapiens
885	AY050935	572	100	putative photosystem II type I chlorophyll a/b binding protein	Arabidopsis thaliana
885	AY058180	572	100	At1g29930/F1N18_23	Arabidopsis thaliana
885	AY091169	572	100	putative chlorophyll a/b-binding protein	Arabidopsis thaliana
886	AF178954	2149	88	monocarboxylate transporter 4	Mus musculus
886	U81800	2399	100	monocarboxylate transporter	Homo sapiens
886	U87627	2164	88	putative monocarboxylate transporter	Rattus norvegicus
887	AAH18345	173	100	BC018345 Unknown (protein for MGC:8802)	Homo sapiens
887	AF237776_1	173	100	AF237776 MAP kinase-interacting kinase 2b	Homo sapiens
887	AL137565	173	100	hypothetical protein	Homo sapiens
888	AF006013	3773	99	dishevelled 3	Homo sapiens
888	BC032459	3784	99	dishevelled, dsh homolog 3 (Drosophila)	Homo sapiens
888	U75651	3806	100	dishevelled 3	Homo sapiens
889	AK000268	2659	100	unnamed protein product	Homo sapiens
889	AK053678	1598	71	unnamed protein product	Mus musculus
889	L00193	1342	58	epidermal keratin subunit I	Mus musculus
890	AX354357	840	100	unnamed protein product	Homo sapiens
890	BC002198	243	42	Similar to hypothetical protein FLJ20093	Mus musculus
890	BC039642	658	75	Unknown (protein for IMAGE:5352548)	Mus musculus
891	AF012348	962	92	smooth muscle gamma actin	Gallus gallus
891	BC002042	962	92	Similar to actin, gamma 2, smooth muscle, enteric	Mus musculus
891	S63494	962	92	gamma-actin	Gallus gallus
892	AAH13867	2057	100	BC013867 Similar to palladin	Homo sapiens
892	AB023209	2064	99	KIAA0992 protein	Homo sapiens
892	AF151909_1	2161	100	AF151909 CGI-151 protein	Homo sapiens
893	AF287271_1	714	100	AF287271 ribosomal protein L23	Mus musculus
893	AF401577_1	714	100	AF401577 ribosomal protein L23	Ictalurus punctatus
893	BC025918	714	100	ribosomal protein L23	Mus musculus
894	U43916	817	100	TMP	Homo sapiens
894	Y07909	817	100	progression associated protein	Homo sapiens
894	Z50751	817	100	B4B	Homo sapiens
895	AAH09647	2778	99	BC009647 Unknown (protein for MGC:5096)	Homo sapiens
895	M13078	2773	99	alkaline phosphatase precursor	Homo sapiens
895	M19159	2780	100	placental alkaline phosphatase-1	Homo sapiens
896	AF326591	2240	100	fenestrated-endothelial linked structure protein	Homo sapiens
896	AF348827	2232	99	PV1 protein	Homo sapiens
896	AL834363	2304	99	hypothetical protein	Homo sapiens
897	AAH11686	5877	100	BC011686 damage-specific DNA binding protein 1 (127kD)	Homo sapiens

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897	L40326	5877	100	X-associated protein 1	Homo sapiens
897	U18299	5877	100	DDBa p127	Homo sapiens
898	U66661	1330	100	GABA-A receptor epsilon subunit	Homo sapiens
898	Y07637	1330	100	putative GABA-gated chloride channel	Homo sapiens
898	Y09765	1330	100	GABA receptor epsilon subunit	Homo sapiens
899	AF380181_1	11506	99	AF380181 SON DNA binding protein isoform C	Homo sapiens
899	AF380184_1	12193	99	AF380184 SON DNA binding protein isoform F	Homo sapiens
899	AY026895	11871	97	NREBP	Homo sapiens
900	A20470	2142	99	preA-PAI-2	synthetic construct
900	AAH12609	2148	100	BC012609 Similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	Homo sapiens
900	Y00630	2139	99	PAI-2 precursor (AA -22 to 393)	Homo sapiens
901	AB037819	7936	100	KIAA1398 protein	Homo sapiens
901	AL132765	5785	95	bA462D18.3.2 (ribosome binding protein 1 (dog 180 kDa homolog) (KIAA1398) (isoform 2))	Homo sapiens
901	X87224	6518	84	ribosome receptor	Canis familiaris
902	AAH00716	2646	98	BC000716 seryl-tRNA synthetase	Homo sapiens
902	D49914	2646	98	Seryl tRNA Synthetase	Homo sapiens
902	X91257	2649	98	seryl-tRNA synthetase	Homo sapiens
903	D29640	4698	57	KIAA0051	Homo sapiens
903	L33075	4698	57	ras GTPase-activating-like protein	Homo sapiens
903	U51903	8003	100	RasGAP-related protein	Homo sapiens
904	AAH17338	2576	99	BC017338 fucosidase, alpha-L- 1, tissue	Homo sapiens
904	M29877	2581	100	alpha-L-fucosidase precursor (EC 3.2.1.5)	Homo sapiens
904	M80815	2576	99	alpha-L-fucosidase	Homo sapiens
905	AAH03067	3601	100	BC003067 growth arrest and DNA-damage-inducible 34	Homo sapiens
905	AK001361	3568	99	unnamed protein product	Homo sapiens
905	U83981	3601	100	apoptosis associated protein	Homo sapiens
906	AAH02717	379	77	BC002717 Similar to chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
906	AAH05921	379	77	BC005921 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
906	AAH20756	379	77	BC020756 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
907	M57939	2349	100	ribonucleoprotein antigen	Homo sapiens
907	X04654	3252	100	70 K protein (AA 1-614)	Homo sapiens
907	X84841	2349	100	68 kDa (U1) ribonucleoprotein	Homo sapiens
908	AAH09945	3737	99	BC009945 Unknown (protein for IMAGE:4123572)	Homo sapiens
908	AB018289	5502	100	KIAA0746 protein	Homo sapiens
908	AK030487	4620	87	unnamed protein product	Mus musculus
909	AJ422147	664	100	C15 protein	Homo sapiens
909	AX352692	664	100	unnamed protein product	Homo sapiens
909	AX357061	664	100	unnamed protein product	Homo sapiens
910	AF251294_1	375	90	AF251294 hCLA-iso	Homo sapiens
910	AL834432	375	90	hypothetical protein	Homo sapiens
910	AY037150	375	90	hypothetical protein SB138	Homo sapiens
911	AAH01501	1520	100	BC001501 Unknown (protein for MGC:2233)	Homo sapiens
911	AAH14078	1520	100	BC014078 cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Homo sapiens
911	BC025302	1520	100	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	Homo sapiens
912	BC036285	1936	100	protein kinase, cAMP-dependent,	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				regulatory, type I, alpha (tissue specific extinguisher 1)	
912	M18468	1936	100	cAMP-dependent protein kinase regulatory subunit type 1	Homo sapiens
912	M33336	1936	100	cAMP-dependent protein kinase type I-alpha subunit	Homo sapiens
913	BC024165	600	100	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Homo sapiens
913	X82385	600	100	RNA polymerase II subunit	Homo sapiens
913	X98433	600	100	RNA polymerase II subunit	Homo sapiens
914	AL138761	8033	99	ba16H23.2 (collagen, type XVII, alpha 1 (BP180))	Homo sapiens
914	M91669	8228	100	autoantigen	Homo sapiens
914	U76604	8037	99	180 kDa bullous pemphigoid antigen 2/type XVII collagen	Homo sapiens
915	AAH03575	2373	100	BC003575 mannosyl (alpha-1,3)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	Homo sapiens
915	M55621	2363	99	N-acetylglucosaminyltransferase I	Homo sapiens
915	M61829	2373	100	alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase	Homo sapiens
916	L13923	16639	99	fibrillin	Homo sapiens
916	L28748	16362	97	putative	Bos taurus
916	X63556	17359	100	fibrillin	Homo sapiens
917	AAH02576	3661	100	BC002576 matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)	Homo sapiens
917	J03210	3584	100	collagenase type IV precursor	Homo sapiens
917	M55593	3661	100	type IV collagenase	Homo sapiens
918	AAH22087	2466	99	BC022087 Similar to CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	Homo sapiens
918	AF467889_1	2380	86	AF467889 high density lipoprotein receptor SR-BI	Sus scrofa
918	Z22555	2684	100	CLA-1	Homo sapiens
919	AF106202_1	1249	100	AF106202 endothelial cell protein C receptor precursor	Homo sapiens
919	AF375468_1	1249	100	AF375468 endothelial protein C receptor	Homo sapiens
919	X89079	1249	100	centrocyclin	Homo sapiens
920	AF153603_1	666	100	AF153603 TSC-22 related protein	Homo sapiens
920	AF183393_1	666	100	AF183393 TSC-22-like Protein	Homo sapiens
920	AF228339	666	100	glucocorticoid-induced GILZ	Homo sapiens
921	AF111168	3586	99	unknown	Homo sapiens
921	AK075445	2876	99	unnamed protein product	Homo sapiens
921	AX136231	2876	99	unnamed protein product	Homo sapiens
922	AAH11234	1220	100	BC011234 Similar to splicing factor 30, survival of motor neuron-related	Homo sapiens
922	AF083385	1220	100	30kDa splicing factor; SPF 30	Homo sapiens
922	AF107463	1220	100	splicing factor	Homo sapiens
923	AAH10240	1921	100	BC010240 cathepsin B	Homo sapiens
923	L16510	1912	99	cathepsin B	Homo sapiens
923	M14221	1915	99	preprocathepsin B	Homo sapiens
924	AK056033	495	97	unnamed protein product	Homo sapiens
925	AE003588	205	22	CG2839-PA	Drosophila melanogaster
925	AE014836_21	231	26	AE014836 hypothetical protein	Plasmodium falciparum 3D7
925	AY052127	202	22	SD07741p	Drosophila melanogaster
926	AF222743_1	2415	100	AF222743 Sec61 alpha-1	Mus musculus
926	BC003707	2415	100	sec61 homolog	Mus musculus
926	M96630	2415	100	sec61-like protein	Rattus sp.
927	AF332086_1	3193	96	AF332086 Rad21	Mus musculus
927	D38551	3284	100	The ha1237 gene product is	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
				related to S.pombe rad21 gene product.	
927	X98294	3275	99	HR21spa	Homo sapiens
928	AAH16325	925	100	BC016325 ADP-ribosylation factor 4	Homo sapiens
928	AF493883_1	925	100	AF493883 ADP-ribosylation factor protein 4	Homo sapiens
928	BC022866	925	100	ADP-ribosylation factor 4	Homo sapiens
929	AAH18201	763	100	BC018201 Unknown (protein for MGC:21505)	Homo sapiens
929	AF217965_1	763	100	AF217965 unknown	Homo sapiens
929	AF217972_1	763	100	AF217972 unknown	Homo sapiens
930	AAH00211	1162	100	BC000211 eukaryotic translation elongation factor 1 beta 2	Homo sapiens
930	AAH04931	1162	100	BC004931 eukaryotic translation elongation factor 1 beta 2	Homo sapiens
930	X60489	1162	100	elongation factor-1-beta	Homo sapiens
931	D82984	1758	93	C/EBP alpha protein	Bos taurus
931	U34070	1857	96	CCAAT/enhancer binding protein alpha	Homo sapiens
931	Y11525	1927	100	CCAAT/enhancer binding protein alpha	Homo sapiens
932	AK025116	341	71	unnamed protein product	Homo sapiens
932	AK090511	358	72	unnamed protein product	Homo sapiens
932	AK096373	341	70	unnamed protein product	Homo sapiens
933	AAH13963	2458	100	BC013963 Similar to adenylyl cyclase-associated protein	Homo sapiens
933	AAH17196	2458	100	BC017196 adenylyl cyclase-associated protein	Homo sapiens
933	M98474	2458	100	CAP protein	Homo sapiens
934	AAH02464	2175	99	BC002464 coagulation factor II (thrombin) receptor	Homo sapiens
934	AF391809_1	2179	99	AF391809 coagulation factor II (thrombin) receptor	Homo sapiens
934	M62424	2187	100	thrombin receptor	Homo sapiens
935	AF085250	759	100	calmodulin	Perca flavescens
935	D83350	759	100	calmodulin	Anas platyrhynchos
935	K01945	759	100	calmodulin (cDNA clone 71)	Xenopus laevis
936	AL050265	2193	100	hypothetical protein	Homo sapiens
936	BC033475	2128	96	similar to TAR DNA-binding protein-43 (TDP-43)	Mus musculus
936	U23731	2193	100	TAR DNA-binding protein-43	Homo sapiens
937	AAH01495	1673	99	BC001495 chromosome 1 open reading frame 8	Homo sapiens
937	AAH16374	1697	100	BC016374 chromosome 1 open reading frame 8	Homo sapiens
937	AF290615_1	1673	99	AF290615 liver membrane-bound protein	Homo sapiens
938	AK000385	329	65	unnamed protein product	Homo sapiens
938	AK092450	360	69	unnamed protein product	Homo sapiens
938	AK097266	329	74	unnamed protein product	Homo sapiens
939	AAH00642	683	99	BC000642 MY047 protein	Homo sapiens
939	AF063605	688	100	brain my047 protein	Homo sapiens
939	AX136119	683	99	unnamed protein product	Homo sapiens
940	AF035947_1	1394	100	AF035947 cytokine-inducible inhibitor of signalling type 1b	Homo sapiens
940	AF132297_1	1332	99	AF132297 cytokine-inducible SH2-containing protein	Homo sapiens
940	BC031590	1321	100	cytokine inducible SH2-containing protein	Homo sapiens
941	AF151018_1	955	100	AF151018 HSPC184	Homo sapiens
941	AK012047	951	99	unnamed protein product	Mus musculus
941	AK075227	955	100	unnamed protein product	Homo sapiens
942	AK025116	322	70	unnamed protein product	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
942	AK090511	302	63	unnamed protein product	Homo sapiens
942	AK090929	308	71	unnamed protein product	Homo sapiens
943	AAH09357	1052	100	BC009357 transgelin 2	Homo sapiens
943	AY007127	1157	100	similar to Homo sapiens mRNA for KIAA0120 gene with GenBank Accession Number D21261.1	
943	D21261	1052	100	similar to human 22kDa, SM22 mRNA (HUM22SM).	Homo sapiens
945	AAH14006	260	89	BC014006 Similar to 6-phosphogluconolactonase	Homo sapiens
945	AJ243972	260	89	6-phosphogluconolactonase	Homo sapiens
945	BC006594	243	80	RIKEN cDNA 1110030K05 gene	Mus musculus
946	AAH03125	2055	99	BC003125 Unknown (protein for MGC:3222)	Homo sapiens
946	AK027877	2055	99	unnamed protein product	Homo sapiens
946	AL136916	2055	99	hypothetical protein	Homo sapiens
947	AAH03681	2956	100	BC003681 Unknown (protein for IMAGE:3453235)	Homo sapiens
947	AL096828	3008	100	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	Homo sapiens
947	AX400070	2878	96	unnamed protein product	Homo sapiens
948	AF161372_1	872	100	AF161372 HSPC254	Homo sapiens
949	AAH11714	476	100	BC011714 Similar to heterogeneous nuclear ribonucleoprotein D-like	Homo sapiens
949	AB017020	476	100	JKTBP	Mus musculus
949	BC021374	476	100	heterogeneous nuclear ribonucleoprotein D-like	Mus musculus
950	AAH02673	1063	100	BC002673 protein kinase H11; small stress protein-like protein HSP22	Homo sapiens
950	AF191017_1	1063	100	AF191017 E2IG1	Homo sapiens
950	AF250138_1	1063	100	AF250138 small stress protein-like protein HSP22	Homo sapiens
951	AAH05033	4718	99	BC005033 Unknown (protein for MGC:12692)	Homo sapiens
951	AJ289242	4654	97	alpha-actinin 4	Mus musculus
951	BC013616	4654	97	alpha actinin 4	Mus musculus
952	AAH11908	1787	100	BC011908 Unknown (protein for MGC:20321)	Homo sapiens
952	AAH14564	1787	100	BC014564 Unknown (protein for MGC:2063)	Homo sapiens
952	AAH18695	1787	100	BC018695 Unknown (protein for MGC:3838)	Homo sapiens
953	AAH12977	1363	100	BC012977 nuclear LIM interactor-interacting factor	Homo sapiens
953	AF229162_1	1363	100	AF229162 nuclear LIM interactor-interacting factor	Homo sapiens
953	AF229163	1363	100	nuclear LIM interactor-interacting factor	Homo sapiens
954	AAH09718	557	92	BC009718 epithelial membrane protein 3	Homo sapiens
954	U52101	557	92	YMP	Homo sapiens
954	U87947	557	92	hematopoietic neural membrane protein	Homo sapiens
955	AF162781_1	4986	94	AF162781 SH2-containing inositol 5-phosphatase 2	Mus musculus
955	L36818	6044	99	51C protein	Homo sapiens
955	Y14385	5270	98	inositol polyphosphate 5-phosphatase	Homo sapiens
956	AAH17369	1238	100	BC017369 splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
956	AAH17908	1238	100	BC017908 splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
956	BC022328	1238	100	splicing factor, arginine/serine-rich 7 (35kD)	Homo sapiens
957	AAH14323	1209	99	BC014323 Similar to accessory proteins BAP31/BAP29	Homo sapiens
957	X81109	1213	100	tumor-associated antigen	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
957	Z31696	1213	100	CDM	Homo sapiens
958	AAH15763	3102	100	BC015763 hypothetical protein FLJ20258	Homo sapiens
958	AK000265	3093	99	unnamed protein product	Homo sapiens
958	AK075098	2998	99	unnamed protein product	Homo sapiens
959	AAH07858	2250	100	BC007858 inhibin, beta A (activin A, activin AB alpha polypeptide)	Homo sapiens
959	M13436	2250	100	beta-A inhibin	Homo sapiens
959	X57578	2250	100	activin beta-A subunit	Homo sapiens
960	AK027598	3474	100	unnamed protein product	Homo sapiens
960	AX481758	3492	99	unnamed protein product	Homo sapiens
960	AX481760	3492	99	unnamed protein product	Homo sapiens
961	AAH15958	3278	100	BC015958 Unknown (protein for MGC:15290)	Homo sapiens
961	BC023520	3278	100	Unknown (protein for MGC:12727)	Homo sapiens
961	U68105	3278	100	poly(A)-binding protein	Homo sapiens
962	AAH10623	3729	96	BC010623 Similar to nuclear factor (erythroid-derived 2)-like 1	Homo sapiens
962	AK090459	4032	100	FLJ00380 protein	Homo sapiens
962	X77366	3926	100	hbZ17	Homo sapiens
963	AAH03177	3500	100	BC003177 KIAA1536 protein	Homo sapiens
963	AK027881	3480	99	unnamed protein product	Homo sapiens
963	AL136895	3500	100	hypothetical protein	Homo sapiens
964	AY054301	4981	94	type III procollagen alpha 1 chain	Homo sapiens
964	BC028178	6603	100	Similar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	Homo sapiens
964	X14420	4981	94	prepro-alpha-1 type 3 collagen	Homo sapiens
965	AAH11819	3473	99	BC011819 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	Homo sapiens
965	AF000982	3476	100	dead box, X isoform	Homo sapiens
965	AF000983	3476	100	dead box, X isoform	Homo sapiens
966	AAH14959	1160	100	BC014959 RING1 and YY1 binding protein	Homo sapiens
966	AF179286_1	1160	100	AF179286 death effector domain-associated factor	Homo sapiens
966	BC036459	1156	99	RING1 and YY1 binding protein	Homo sapiens
967	AAH17172	634	99	BC017172 hypothetical protein	Homo sapiens
967	AF110774_1	634	99	AF110774 adrenal gland protein AD-001	Homo sapiens
967	AX354355	634	99	unnamed protein product	Homo sapiens
968	AAH08442	1106	100	BC008442 Similar to transmembrane 4 superfamily member 1	Homo sapiens
968	AAH10166	1106	100	BC010166 Similar to transmembrane 4 superfamily member 1	Homo sapiens
968	M90657	1106	100	L6	Homo sapiens
969	AAH10354	1764	100	BC10354 PTD010 protein	Homo sapiens
969	AB009685	1764	100	DERP2	Homo sapiens
969	AF131820	1764	100	Unknown	Homo sapiens
970	AF217787	1172	99	extracellular glutathione peroxidase	Homo sapiens
970	D00632	1195	100	glutathione peroxidase	Homo sapiens
970	X58295	1195	100	glutathione peroxidase	Homo sapiens
971	AAH00531	939	97	BC000531 insulin-like growth factor 2 (somatomedin A)	Homo sapiens
971	AF517226_1	939	97	AF517226 insulin-like growth factor 2 (somatomedin A)	Homo sapiens
971	M17863	942	97	preproinsulin-like growth factor II, domains A-E	Homo sapiens
972	AJ310544	2183	100	EGLN2 protein	Homo sapiens
972	AX553864	2183	100	unnamed protein product	Homo sapiens
972	BC036051	2183	100	Similar to egl nine homolog 2 (C. elegans)	Homo sapiens
973	AAH00867	915	98	BC000867 PRO0659 protein	Homo sapiens
973	AL834135	1118	99	hypothetical protein	Homo sapiens
973	AX405861	1118	99	unnamed protein product	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
974	AL136890	1293	98	hypothetical protein	Homo sapiens
974	AL137798	878	80	dJ1182A14.5.2 (novel gene (isoform 2) KIAA1245 protein)	Homo sapiens
974	BC024011	1747	100	Similar to hypothetical protein DKFZp434D177	Homo sapiens
975	AB037755	4896	99	KIAA1334 protein	Homo sapiens
975	AF155135_1	4845	99	AF155135 novel retinal pigment epithelial cell protein	Homo sapiens
975	AF202315_1	4141	85	AF202315 ankycorbin	Mus musculus
976	AK097965	344	77	unnamed protein product	Homo sapiens
976	AX400008	283	62	unnamed protein product	Homo sapiens
976	BC033959	342	70	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
977	AAH12444	1319	100	BC012444 Similar to chloride intracellular channel 4	Homo sapiens
977	AF097330_1	1305	99	AF097330 H1 chloride channel; p64H1; CLIC4	Homo sapiens
977	AL117424	1319	100	hypothetical protein	Homo sapiens
978	AB034747	904	100	small integral membrane protein of lysosome/late endosome	Homo sapiens
978	AF171100	812	85	TBX1 protein	Mus musculus
978	BC018559	812	85	LPS-induced TNF-alpha factor	Mus musculus
979	AAH10645	1737	100	BC010645 Similar to sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)	Homo sapiens
979	AY040826	1715	97	alpha 2,3-sialyltransferase IV type B+18	Homo sapiens
979	L23767	1710	100	a2,3 sialyltransferse	Homo sapiens
980	AAH09329	887	82	BC009329 triosephosphate isomerase 1	Homo sapiens
980	AAH11611	887	82	BC011611 Similar to triosephosphate isomerase 1	Homo sapiens
980	AAH15100	887	82	BC015100 triosephosphate isomerase 1	Homo sapiens
981	AAH18986	1338	98	BC018986 Unknown (protein for MGC:20092)	Homo sapiens
981	J05594	1331	98	NAD+-dependent 15-hydroxyprostaglandin dehydrogenase	Homo sapiens
981	L76465	1331	98	NAD+-dependent 15-hydroxyprostaglandin dehydrogenase	Homo sapiens
982	AAH00690	794	100	BC000690 ribosomal protein L24	Homo sapiens
982	BC002110	794	100	ribosomal protein L24	Mus musculus
982	X78443	794	100	ribosomal protein L24	Rattus norvegicus
983	AAH11402	1122	100	BC011402 Similar to decidual protein induced by progesterone	Homo sapiens
983	AB022718	1122	100	DEPP	Homo sapiens
983	AL136653	1116	99	hypothetical protein	Homo sapiens
984	AF108841	406	74	pol protein	Homo sapiens
984	AF108843	420	75	pol protein	Homo sapiens
984	U88902	319	73	integrase	Homo sapiens
985	A07358	1657	99	VAC beta	Mus musculus
985	AAH04376	1666	100	BC004376 annexin A8	Homo sapiens
985	X16662	1657	99	vascular anticoagulant-beta (AA 1 - 327)	Homo sapiens
986	AF068227	2236	100	putative transmembrane protein	Homo sapiens
986	AK032293	1426	76	unnamed protein product	Mus musculus
986	BC025487	1447	77	Similar to ceroid-lipofuscinosis, neuronal 5	Mus musculus
987	AAH10652	1355	100	BC010652 Unknown (protein for MGC:9753)	Homo sapiens
987	AF217980_1	1338	98	AF217980 unknown	Homo sapiens
988	AK000496	378	68	unnamed protein product	Homo sapiens
988	AK025116	403	72	unnamed protein product	Homo sapiens

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988	AK090511	363	68	unnamed protein product	Homo sapiens
989	AF001900	1702	100	secreted frizzled-related protein	Homo sapiens
989	AF056087	1702	100	secreted frizzled related protein	Homo sapiens
989	BC036503	1690	99	Unknown (protein for MGC:43294)	Homo sapiens
990	AAH14052	2127	100	BC014052 transcriptional co-activator with PDZ-binding motif (TAZ)	Homo sapiens
990	AJ299431	2127	100	transcriptional coactivator	Homo sapiens
990	AK022036	2127	100	unnamed protein product	Homo sapiens
991	AAH07493	552	99	BC007493 galactosidase, beta 1	Homo sapiens
991	M22590	552	99	beta-galactosidase precursor (EC 3.2.1.23)	Homo sapiens
991	M34423	552	99	beta-galactosidase precursor (EC 3.2.1.23)	Homo sapiens
992	AAH15928	2186	100	BC015928 Unknown (protein for MGC:8773)	Homo sapiens
992	AB037797	2313	100	KIAA1376 protein	Homo sapiens
992	AK088288	2153	98	unnamed protein product	Mus musculus
993	AF087873_1	383	100	AF087873 protein kinase inhibitor	Homo sapiens
993	AF225513_1	383	100	AF225513 cAMP-dependent protein kinase inhibitor beta	Homo sapiens
993	BC036011	383	100	protein kinase (cAMP-dependent, catalytic) inhibitor beta	Homo sapiens
994	X53305	736	100	stathmin	Homo sapiens
994	X94912	736	100	Pr22	Homo sapiens
994	Z11566	736	100	Pr22 protein	Homo sapiens
995	AF148856_2	150	79	AF148856 unknown	Homo sapiens
995	AL096744	153	82	hypothetical protein	Homo sapiens
995	M80341	150	79	ORF2	Homo sapiens
996	AK002154	798	94	unnamed protein product	Homo sapiens
996	AK023417	819	100	unnamed protein product	Homo sapiens
996	AX399949	230	64	unnamed protein product	Homo sapiens
997	AF151807_1	2196	99	AF151807 CGI-49 protein	Homo sapiens
997	AK075178	2149	97	unnamed protein product	Homo sapiens
997	BC026185	2136	97	Similar to CGI-49 protein	Homo sapiens
998	AAH10123	2134	100	BC010123 SH3-domain binding protein 5 (BTK-associated)	Homo sapiens
998	AB005047	2134	100	SH3 binding protein	Homo sapiens
998	AB027562	2008	94	vascular endothelial cell specific protein 18	Rattus norvegicus
999	AJ131023	5309	99	oxytocinase/insulin-responsive aminopeptidase, variant 1	Homo sapiens
999	U62768	5318	99	oxytocinase splice variant 1	Homo sapiens
999	U62769	5242	99	oxytocinase splice variant 2	Homo sapiens
1000	AF234263	2521	99	cathepsin C	Homo sapiens
1000	U79415	2527	100	prepro dipeptidyl peptidase I	Homo sapiens
1000	X87212	2527	100	cathepsin C	Homo sapiens
1001	BC003426	1438	94	Similar to eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kD)	Mus musculus
1001	U05821	1419	92	translation initiation factor eIF-2B alpha-subunit	Rattus norvegicus
1001	X95648	1526	100	alfa subunit	Homo sapiens
1002	AAH14093	4073	96	BC014093 Similar to amiloride binding protein 1 (amine oxidase (copper-containing))	Homo sapiens
1002	U11862	4060	96	diamine oxidase, copper/topa quinone-containing	Homo sapiens
1002	X78212	4066	96	amiloride binding protein	Homo sapiens
1003	AK003633	925	98	unnamed protein product	Mus musculus
1003	AK007989	925	98	unnamed protein product	Mus musculus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
1003	AK076212	925	98	unnamed protein product	Mus musculus
1004	AAH18340	1692	99	BC018340 Unknown (protein for MGC:9372)	Homo sapiens
1004	X79066	1692	99	ERF-1	Homo sapiens
1004	X99404	1684	99	Berg36	Homo sapiens
1005	AB055977	492	93	I3 protein	Homo sapiens
1005	AF041430	492	93	PRGR2	Homo sapiens
1005	AF106966	492	93	I3 protein	Homo sapiens
1006	AAH14438	1018	100	BC014438 Unknown (protein for MGC:22947)	Homo sapiens
1006	AE006639_3	1018	100	AE006639 HN1 like	Homo sapiens
1006	AK023154	1018	100	unnamed protein product	Homo sapiens
1007	J03779	3944	100	common acute lymphoblastic leukemia antigen precursor	Homo sapiens
1007	M26628	3919	99	enkephalinase	Homo sapiens
1007	Y00811	3919	99	CALLA protein (AA 1 - 750)	Homo sapiens
1008	AB035304	4092	100	cadherin-5	Homo sapiens
1008	U84722	4086	99	vascular endothelial cadherin	Homo sapiens
1008	X79981	4092	100	VE-cadherin	Homo sapiens
1009	AX019983	739	100	unnamed protein product	Homo sapiens
1009	BC026254	739	100	insulin-like 4 (placenta)	Homo sapiens
1009	L34838	739	100	EPIL	Homo sapiens
1010	AF139894_1	1813	100	AF139894 RNA-binding protein alpha-CPI	Mus musculus
1010	AF139895_1	1813	100	AF139895 RNA-binding protein alpha-CPI	Mus musculus
1010	BC004793	1813	100	poly(rC)-binding protein 1	Mus musculus
1011	U12390	366	88	beta-galactosidase alpha peptide	Cloning vector pSport1
1011	U12391	355	88	beta-galactosidase alpha peptide	Cloning vector pSport2
1011	Y14836	290	77	beta-galactosidase	Phagemid cloning vector pTZ19U
1012	AF218012_1	1751	100	AF218012 unknown	Homo sapiens
1012	AF218030_1	1751	100	AF218030 unknown	Homo sapiens
1012	AL121586	2000	88	dJ47704.1.1 (novel protein similar to otoferlin and dysferlin, isoform 1)	Homo sapiens
1013	AAH00352	1286	100	BC000352 proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	Homo sapiens
1013	AAH07503	1286	100	BC007503 proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	Homo sapiens
1013	AF078829_1	1286	100	AF078829 proteasome activator PA28 alpha	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
101 4	AAH16155	521	89	BC016155 Ras homolog enriched in brain 2	Homo sapiens
101 4	AF493921_1	521	89	AF493921 Ras family small GTP binding protein RHEB2	Homo sapiens
101 4	Z29677	521	89	Ras-related GTP-binding protein	Homo sapiens
101 5	AAH10423	2657	100	BC010423 Ig superfamily receptor LNIR	Homo sapiens
101 5	AF160477_1	2655	99	AF160477 Ig superfamily receptor LNIR precursor	Homo sapiens
101 5	AF426163_1	2657	100	AF426163 nectin 4	Homo sapiens
101 6	AJ295142	3578	99	Clq receptor protein	Homo sapiens
101 6	BC028075	3577	99	complement component 1, q subcomponent, receptor 1	Homo sapiens
101 6	U94333	3587	100	ClqR(p)	Homo sapiens
101 7	AAH14271	3392	100	BC014271 endoglin (Osler-Rendu-Weber syndrome 1)	Homo sapiens
101 7	J05481	3319	99	endoglin precursor	Homo sapiens
101 7	U37439	3385	99	endoglin	Homo sapiens
101 8	AAH07411	540	86	BC007411 Unknown (protein for MGC:2554)	Homo sapiens
101 8	AF051782	536	85	diaphanous 1	Homo sapiens
101 8	U96963	495	80	p140mDia	Mus musculus
101 9	AF151966_1	1875	66	AF151966 GTPase activating protein Rap1-GAP	Gallus gallus
101 9	BC030891	2109	95	Unknown (protein for IMAGE:4485689)	Mus musculus
101 9	M64788	3477	100	GTPase activating protein	Homo sapiens
102 0	AX206708	1968	100	unnamed protein product	Homo sapiens
102 0	M92934	1968	100	connective tissue growth factor	Homo sapiens
102 0	X78947	1968	100	connective tissue growth factor	Homo sapiens
102 1	AAH18823	849	100	BC018823 Unknown (protein for MGC:1236)	Homo sapiens
102 1	AK007729	809	97	unnamed protein product	Mus musculus
102 1	U30826	849	100	SRp40-1	Homo sapiens
102 2	AAH07333	2823	100	BC007333 ets variant gene 5 (ets-related molecule)	Homo sapiens
102 2	X76184	2823	100	ets-related protein	Homo sapiens
102 2	X96381	2823	100	erm	Homo sapiens
102 3	AAH02599	996	99	BC002599 corticotropin releasing hormone	Homo sapiens
102 3	AAH11031	996	99	BC011031 Similar to corticotropin releasing hormone	Homo sapiens
102 3	V00571	996	99	corticotropin releasing factor	Homo sapiens
102 4	AK007731	1164	94	unnamed protein product	Mus musculus
102 4	AL110239	1234	99	hypothetical protein	Homo sapiens
102 4	AX399865	1355	100	unnamed protein product	Homo sapiens
102 5	AAH00732	1553	100	BC000732 glioblastoma amplified sequence	Homo sapiens
102	AAH01837	1553	100	BC001837 glioblastoma amplified	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
5				sequence	
1025	BC030821	1553	100	glioblastoma amplified sequence	Homo sapiens
1026	AAH01483	2103	100	BC001483 Unknown (protein for MGC:1364)	Homo sapiens
1026	AAH09241	2103	100	BC009241 Unknown (protein for MGC:3556)	Homo sapiens
1026	BC023599	2103	100	TRK-fused gene	Homo sapiens
1027	AAH12806	3278	100	BC012806 solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Homo sapiens
1027	AAH15631	3278	100	BC015631 solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Homo sapiens
1027	AF116241	3272	99	sodium-dependent multivitamin transporter	Homo sapiens
1029	AAH04324	744	100	BC004324 ribosomal protein S16	Homo sapiens
1029	AAH07977	744	100	BC007977 ribosomal protein S16	Homo sapiens
1029	X17665	744	100	ribosomal protein S16 (AA 1-146)	Rattus rattus
1030	AB047555	624	90	IZP6	Mus musculus musculus
1030	AK007948	624	90	unnamed protein product	Mus musculus
1030	BC004729	624	90	RIKEN cDNA 1810063P04 gene	Mus musculus
1031	BC003337	1957	100	actin, gamma 1	Mus musculus
1031	BC021796	1957	100	actin, gamma 1	Mus musculus
1031	BC023248	1957	100	actin, gamma, cytoplasmic	Mus musculus
1032	AAH11700	2048	100	BC011700 glutamate-ammonia ligase (glutamine synthase)	Homo sapiens
1032	AAH11852	2048	100	BC011852 glutamate-ammonia ligase (glutamine synthase)	Homo sapiens
1032	AAH18992	2048	100	BC018992 Unknown (protein for MGC:20095)	Homo sapiens
1033	AF234654_1	1155	100	AF234654 PLAC1	Homo sapiens
1033	AK075086	1155	100	unnamed protein product	Homo sapiens
1033	BC022335	1155	100	placenta-specific 1	Homo sapiens
1034	AAB67977	4108	99	AF019413 complement factor B	Homo sapiens
1034	AAH04143	4121	100	BC004143 B-factor, properdin	Homo sapiens
1034	AAH07990	4121	100	BC007990 B-factor, properdin	Homo sapiens
1035	AAH17399	355	98	BC017399 Similar to RIKEN cDNA 1810037I17 gene	Homo sapiens
1035	AK007721	236	68	unnamed protein product	Mus musculus
1035	BC002135	236	68	Unknown (protein for MGC:7243)	Mus musculus
1036	AAH13383	1701	100	BC013383 calumenin	Homo sapiens
1036	AF013759	1701	100	calumein	Homo sapiens
1036	U67280	1695	99	calumenin	Homo sapiens
1037	AF069065	596	97	inducible cAMP early repressor type 1	Homo sapiens
1037	AJ311667	588	95	induced cAMP early repressor, ICER I	Mus musculus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1037	D14826	608	100	hCREM 2alpha-a protein	Homo sapiens
1038	AAH00452	1043	100	BC000452 Similar to thioredoxin peroxidase 1	Homo sapiens
1038	AAH03022	1043	100	BC003022 Similar to thioredoxin peroxidase 1	Homo sapiens
1038	BC039428	1043	100	Similar to peroxiredoxin 2	Homo sapiens
1039	AB056107	2995	100	zinc finger protein homologous to mouse Zfp91	Homo sapiens
1039	AB057443	2775	100	testis specific ZFP91	Homo sapiens
1039	AF310246_1	2586	99	AF310246 FKSG11	Homo sapiens
1040	AF023476	4954	100	meltrin-L precursor	Homo sapiens
1040	AF023477	3855	99	meltrin-S	Homo sapiens
1040	D50411	3939	80	meltrin alpha	Mus musculus
1041	AF154121_1	3126	100	AF154121 sodium-dependent high-affinity dicarboxylate transporter	Homo sapiens
1041	AY072810	3057	98	energy metabolism-related sodium-dependent high-affinity dicarboxylate transporter	Homo sapiens
1041	BC035966	3056	98	similar to solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Homo sapiens
1042	AF400594	687	64	endothelial nitric oxide synthase	Homo sapiens
1042	AF519768_1	687	64	AF519768 nitric oxide synthase 3 (endothelial cell)	Homo sapiens
1042	L26914	687	64	nitric oxide synthase	Homo sapiens
1043	AAH01462	1835	100	BC001462 protease, serine, 8 (prostasin)	Homo sapiens
1043	L41351	1835	100	prostasin	Homo sapiens
1043	U33446	1835	100	prostasin	Homo sapiens
1044	AB051442	304	71	KIAA1655 protein	Homo sapiens
1044	AK090913	358	64	unnamed protein product	Homo sapiens
1044	BC024651	276	76	similar to PRO2550	Homo sapiens
1045	AF346465	7291	91	latent transforming growth factor beta binding protein 1S	Mus musculus
1045	AF489528_1	7887	99	AF489528 transforming growth factor-beta binding protein-1S	Homo sapiens
1045	M34057	7903	100	transforming growth factor-beta 1 binding protein precursor	Homo sapiens
1046	AY004254	1199	90	endoplasmic reticulum protein 29 precursor	Rattus norvegicus
1046	X94910	1334	100	ERp28	Homo sapiens
1046	Y10264	1199	90	ERp29 precursor	Rattus norvegicus
1047	AF119917_58	250	100	AF119896 PRO2751	Homo sapiens
1048	AB020692	4158	100	KIAA0885 protein	Homo sapiens
1048	BC016898	4107	98	Unknown (protein for MGC:19174)	Mus musculus
1048	X52311	4102	98	unr protein (AA 1-798)	Rattus norvegicus
105	AL049698	7034	98	dJ470B24.1.3 (myeloid/lymphoid or	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
0				mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 3))	
1050	AL049698	7050	98	dJ470B24.1.5 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 5))	Homo sapiens
1050	AL161973	7363	100	hypothetical protein	Homo sapiens
1051	AAH21288	2134	100	BC021288 Unknown (protein for MGC:29494)	Homo sapiens
1051	J03263	1934	98	membrane glycoprotein	Homo sapiens
1051	J04182	2041	96	lysosomal membrane glycoprotein-1	Homo sapiens
1052	AC002400	817	100	Acyl carrier protein, Mitochondrial (ACP) (5'partial)	Homo sapiens
1052	AF087660_1	788	100	AF087660 NADH:ubiquinone oxidoreductase SDAP subunit	Homo sapiens
1052	AK018717	672	85	unnamed protein product	Mus musculus
1053	AB031550	1490	95	pctp-L	Mus musculus
1053	AF151810_1	1853	98	AF151810 CGI-52 protein	Homo sapiens
1053	Z81134	477	41	Hypothetical protein T28D6.7	Caenorhabditis elegans
1055	AAH09392	5306	99	BC009392 Unknown (protein for MGC:15329)	Homo sapiens
1055	AB011149	5318	100	KIAA0577 protein	Homo sapiens
1055	AP000512	5318	100	RNA helicase	Homo sapiens
1056	AAH08751	3757	99	BC008751 calpain 1, (mu/I) large subunit	Homo sapiens
1056	AAH17200	3762	100	BC017200 calpain 1, (mu/I) large subunit	Homo sapiens
1056	X04366	3762	100	CANP, large subunit (aa 1-714)	Homo sapiens
1057	AB093679	740	100	ribosomal protein L26	Macaca fascicularis
1057	X69392	740	100	ribosomal protein L26	Homo sapiens
1057	X80699	740	100	L26	Mus musculus
1058	AAH06391	1974	100	BC006391 inhibin, alpha	Homo sapiens
1058	M13981	1974	100	inhibin A-subunit precursor	Homo sapiens
1058	X04445	1974	100	preproinhibin	Homo sapiens
1059	AK000385	267	65	unnamed protein product	Homo sapiens
1059	AK092450	270	58	unnamed protein product	Homo sapiens
1059	AK097214	354	74	unnamed protein product	Homo sapiens
1060	AF130117_48	357	77	AF130089 PRO2550	Homo sapiens
1060	AK000385	363	75	unnamed protein product	Homo sapiens
1060	U22376	327	76	alternatively spliced product using exon 13A	Homo sapiens
1061	AF090930_1	172	51	AF090930 PRO0478	Homo sapiens
1061	AX399919	158	68	unnamed protein product	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
106 2	AF063591_1	1401	99	AF063591 brain my033 protein	Homo sapiens
106 2	BC022522	1411	100	antigen identified by monoclonal antibody MRC OX-2	Homo sapiens
106 2	BC031103	1411	100	antigen identified by monoclonal antibody MRC OX-2	Homo sapiens
106 3	AAH00692	2582	100	BC000692 Similar to hyaluronoglucosaminidase 2	Homo sapiens
106 3	AC002455	2579	99	human PH-20 homolog (LUCA-2)	Homo sapiens
106 3	U09577	2579	99	lysosomal hyaluronidase	Homo sapiens
106 4	AAH02700	2294	100	BC002700 Similar to keratin 7	Homo sapiens
106 4	AF509887	2294	100	keratin 7	Homo sapiens
106 4	AF509892	2294	100	keratin 7	Homo sapiens
106 5	AF523361_1	1951	99	AF523361 CD34 antigen	Homo sapiens
106 5	M81945	1955	100	hematopoietic stem cell antigen	Homo sapiens
106 5	S53910	1951	99	CD34	Homo sapiens
106 6	AB037891	493	100	Bcl10	Mus musculus
106 6	AF303656_1	493	100	AF303656 bladder cancer-related protein	Mus musculus
106 6	BC026935	493	100	bladder cancer associated protein	Mus musculus
106 7	AF322909	3026	100	transmembrane glycoprotein HGFIN	Homo sapiens
106 7	BC032783	3003	97	Similar to glycoprotein (transmembrane) nmb	Homo sapiens
106 7	X76534	3026	100	NMB	Homo sapiens
106 8	AAH17352	3091	100	BC017352 Unknown (protein for MGC:29525)	Homo sapiens
106 8	AF230388_1	3085	99	AF230388 tripartite motif protein TRIM29 alpha	Homo sapiens
106 8	L24203	3085	99	ataxia-telangiectasia group D-associated protein	Homo sapiens
106 9	AK003609	1032	99	unnamed protein product	Mus musculus
106 9	AL136635	1039	100	hypothetical protein	Homo sapiens
106 9	BC016408	1032	99	RIKEN cDNA 1110011F09 gene	Mus musculus
107 0	AF073310	7103	100	insulin receptor substrate-2	Homo sapiens
107 0	AF385932_1	7014	99	AF385932 insulin receptor substrate 2 insertion mutant	Homo sapiens
107 0	AF385933_1	7026	99	AF385933 insulin receptor substrate 2 insertion mutant	Homo sapiens
107 1	AAH09586	2198	91	BC009586 Unknown (protein for MGC:14649)	Homo sapiens
107 1	D26485	2198	91	core I protein	Homo sapiens
107 1	L16842	2193	90	ubiquinol-cytochrome c reductase core I protein	Homo sapiens
107 2	AF062534	1919	100	genethonin 1	Homo sapiens
107 2	AK050416	1083	62	unnamed protein product	Mus musculus
107 2	BC022301	1919	100	genethonin 1	Homo sapiens
107 3	AAH08950	956	100	BC008950 Unknown (protein for MGC:3593)	Homo sapiens
107	AF112202_1	956	100	AF112202 prenylated rab acceptor	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
3				1	
1073	AJ133534	951	99	prenylated Rab acceptor 1 (PRA1)	Homo sapiens
1074	AAH14257	888	100	BC014257 Similar to DKFZp564J157 protein	Homo sapiens
1074	AAH16064	888	100	BC016064 DKFZp564J157 protein	Homo sapiens
1074	AX405840	888	100	unnamed protein product	Homo sapiens
1075	AAH02394	2275	100	BC002394 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Homo sapiens
1075	AAH04433	2275	100	BC004433 ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Homo sapiens
1075	U32680	2275	100	CLN3 protein	Homo sapiens
1076	AF443072_1	20090	99	AF443072 laminin alpha5 chain precursor	Homo sapiens
1076	AL354836	20063	99	ba157P1.1.1 (laminin alpha 5)	Homo sapiens
1076	AX463738	20090	99	laminin 5	Homo sapiens
1077	BC024366	703	100	ribosomal protein L27	Mus musculus
1077	X07424	703	100	ribosomal protein L27 (AA 1 - 136)	Rattus norvegicus
1077	X56852	703	100	ribosomal protein L27	Gallus gallus
1078	AAH13131	969	100	BC013131 Similar to hypothetical protein FLJ10702	Homo sapiens
1078	AK001564	969	100	unnamed protein product	Homo sapiens
1078	BC013719	969	100	hypothetical protein FLJ10702	Mus musculus
1079	AF214737_1	5676	100	AF214737 C9orf10a	Homo sapiens
1079	BC010304	3765	93	Unknown (protein for IMAGE:3597827)	Mus musculus
1079	D80005	5676	100	KIAA0183	Homo sapiens
1080	AF113127_1	1186	99	AF113127 S1R protein	Homo sapiens
1080	AF151877_1	1242	99	AF151877 CGI-119 protein	Homo sapiens
1080	AF182041_1	1186	99	AF182041 z-protein	Homo sapiens
1081	AAH11616	1514	100	BC011616 Similar to cyclin D3	Homo sapiens
1081	AF517525_1	1511	99	AF517525 cyclin D3	Homo sapiens
1081	M92287	1514	100	cyclin D3	Homo sapiens
1082	AAH11581	4280	100	BC011581 Similar to oxysterol binding protein	Homo sapiens
1082	AF185696_1	4280	100	AF185696 oxysterol-binding protein 1	Homo sapiens
1082	AF185705	4280	100	oxysterol binding protein 1	Homo sapiens
1083	AJ133816	1566	36	viral polypeptide	Porcine endogenous retrovirus
1083	D10032	1645	37	gag-pol precursor polyprotein	Baboon endogenous virus strain M7
1083	M26927	1571	36	pol polyprotein	Gibbon ape leukemia virus

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1084	AF012920	625	100	GEC-1	Cavia porcellus
1084	AF312680	625	100	GEC-1	Cavia porcellus
1084	BC004602	625	100	RIKEN cDNA 9130422N19 gene	Mus musculus
1085	AAH14241	1733	100	BC014241 Similar to hypothetical protein, MGC:7035	Homo sapiens
1085	AB093636	1687	96	hypothetical protein	Macaca fascicularis
1085	AK046512	1274	74	unnamed protein product	Mus musculus
1086	AF140240_1	749	100	AF140240 transcription factor TBX3	Homo sapiens
1086	AK075457	749	100	unnamed protein product	Homo sapiens
1086	BC025258	749	100	T-box 3 (ulnar mammary syndrome)	Homo sapiens
1087	AK025047	331	68	unnamed protein product	Homo sapiens
1087	AK025116	330	67	unnamed protein product	Homo sapiens
1087	AK090511	365	72	unnamed protein product	Homo sapiens
1088	AAH01863	320	100	BC001863 hypoxia-inducible protein 2	Homo sapiens
1088	AF144755_1	320	100	AF144755 hypoxia-inducible protein 2	Homo sapiens
1088	AX105363	320	100	unnamed protein product	Homo sapiens
1089	AAH00718	1965	98	BC000718 Similar to dynactin (dynactin complex 50 kD subunit)	Homo sapiens
1089	AAH09468	1965	98	BC009468 dynactin 2 (p50)	Homo sapiens
1089	AAH14083	1965	98	BC014083 dynactin 2 (p50)	Homo sapiens
1090	AB037669	2790	100	L-type amino acid transporter 2	Homo sapiens
1090	AF171669_1	2790	100	AF171669 glycoprotein-associated amino acid transporter LAT2	Homo sapiens
1090	Y18483	2778	99	SLC7A8 protein	Homo sapiens
1091	AAH16905	228	62	BC016905 Similar to hypothetical protein PRO1722	Homo sapiens
1091	AF118094_21	261	65	AF118082 PRO1902	Homo sapiens
1091	AK090913	202	59	unnamed protein product	Homo sapiens
1092	AK075392	1588	99	unnamed protein product	Homo sapiens
1092	AX136157	1588	99	unnamed protein product	Homo sapiens
1092	AX179293	1591	99	21676 ADH	Homo sapiens
1093	AAH13985	2426	91	BC013985 PC2 (positive cofactor 2, multiprotein complex) glutamine/Q-rich-associated protein	Homo sapiens
1093	AK090465	2677	99	FLJ00386 protein	Homo sapiens
1093	BC017110	2677	99	Unknown (protein for MGC:16010)	Homo sapiens
1094	AAH10514	2363	100	BC010514 clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	Homo sapiens
1094	AAH19588	2363	100	BC019588 clusterin (complement lysis inhibitor, SP-40,40,	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	
1094	X14723	2363	100	SP-40,40 preproptide (AA -22 to 427)	Homo sapiens
1095	AAH06786	1161	100	BC006786 cellular repressor of E1A-stimulated genes	Homo sapiens
1095	AAH08628	1161	100	BC008628 cellular repressor of E1A-stimulated genes	Homo sapiens
1095	AF084523	1161	100	cellular repressor of E1A-stimulated genes CREG	Homo sapiens
1096	AX167114	8220	99	unnamed protein product	Homo sapiens
1096	BC036531	8206	99	Unknown (protein for MGC:33668)	Homo sapiens
1096	Z74615	8220	99	prepro-alpha1(I) collagen	Homo sapiens
1097	AB025412	5671	98	Ten-m3	Mus musculus
1097	AF195418_1	5676	99	AF195418 ODZ3	Mus musculus
1097	AK001336	5447	100	unnamed protein product	Homo sapiens
1098	AAH03550	1419	100	BC003550 Similar to CGI-20 protein	Homo sapiens
1098	AF132954_1	1577	99	AF132954 CGI-20 protein	Homo sapiens
1098	AK003551	1613	95	unnamed protein product	Mus musculus
1099	BC022512	244	96	platelet/endothelial cell adhesion molecule (CD31 antigen)	Homo sapiens
1099	L34657	244	96	platelet endothelial cell adhesion molecule-1	Homo sapiens
1099	M28526	244	96	PECAM-1 precursor	Homo sapiens
1100	AAH12138	1849	100	BC012138 Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Homo sapiens
1100	AF493906_1	1849	100	AF493906 guanine nucleotide binding protein alpha i2	Homo sapiens
1100	X04828	1849	100	G protein alpha-subunit (AA 1-355)	Homo sapiens
1101	AF081258_1	3091	100	AF081258 testis-specific chromodomain Y-like protein	Homo sapiens
1101	AF081259_1	3091	100	AF081259 testis-specific chromodomain Y-like protein	Homo sapiens
1101	AF081261_1	2614	88	AF081261 testis-specific chromodomain Y-like protein	Mus musculus
1102	AF162856_1	5147	65	AF162856 receptor-like protein tyrosine phosphatase rho-1	Mus musculus
1102	X58287	7569	97	protein-tyrosine phosphatase	Mus musculus
1102	X58288	7731	99	protein-tyrosine phosphatase	Homo sapiens
1103	AK097965	330	74	unnamed protein product	Homo sapiens
1103	AX400008	319	69	unnamed protein product	Homo sapiens
1103	BC033959	362	79	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
1104	AAH18991	1272	100	BC018991 hepatoma-derived growth factor (high-mobility group protein 1-like)	Homo sapiens
1104	AJ237996	1205	95	hepatoma derived growth factor	Bos taurus
1104	D16431	1272	100	hepatoma-derived GF	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
110 5	AAH17197	1785	99	BC017197 myeloid cell leukemia sequence 1 (BCL2-related)	Homo sapiens
110 5	AF147742_1	1785	99	AF147742 myeloid cell differentiation protein	Homo sapiens
110 5	AF162677	1785	99	myeloid cell leukemia protein 1	Homo sapiens
110 6	AF274892	2520	100	glucose transporter 3	Homo sapiens
110 6	BC039196	2520	100	solute carrier family 2 (facilitated glucose transporter), member 3	Homo sapiens
110 6	M20681	2520	100	glucose transporter-like protein	Homo sapiens
110 7	AAH00730	3448	100	BC000730 calpain 6	Homo sapiens
110 7	AJ000388	3439	99	calpain-like protease, CANPX	Homo sapiens
110 7	AL031117	3448	100	dJ914P14.1 (calpain-like protease CANPX)	Homo sapiens
110 8	AAH03143	1980	100	BC003143 dual specificity phosphatase 6	Homo sapiens
110 8	AAH03562	1980	100	BC003562 dual specificity phosphatase 6	Homo sapiens
110 8	X93920	1980	100	protein-tyrosine-phosphatase	Homo sapiens
110 9	AB023194	6006	100	KIAA0977 protein	Homo sapiens
110 9	AK052533	3549	61	unnamed protein product	Mus musculus
110 9	AL049939	1823	99	hypothetical protein	Homo sapiens
111 0	AAH15031	4447	100	BC015031 Unknown (protein for MGC:9105)	Homo sapiens
111 0	AB018266	4447	100	KIAA0723 protein	Homo sapiens
111 0	BC029070	4375	98	Similar to matrin 3	Mus musculus
111 1	AAH18726	1229	100	BC018726 CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Homo sapiens
111 1	M13560	1229	100	cell surface glycoprotein	Homo sapiens
111 1	X00497	1229	100	putative p33	Homo sapiens
111 2	AF114262_3	2305	88	AF114260 forkhead protein AFXH	Mus musculus
111 2	X93996	2624	100	AFX	Homo sapiens
111 2	Y11284	2489	97	AFX1	Homo sapiens
111 3	AAH09409	1688	100	BC009409 Unknown (protein for MGC:10655)	Homo sapiens
111 3	X13425	1688	100	GA733-1 protein (AA 1-323)	Homo sapiens
111 3	X77754	1688	100	gp50/TROP-2	Homo sapiens
111 4	AAH02532	795	100	BC002532 epididymal secretory protein (19.5kD)	Homo sapiens
111 4	X67698	795	100	orf	Homo sapiens
111 4	X78134	795	100	epididymal secretory protein 14.6	Macaca fascicularis
111 5	AK075092	233	100	unnamed protein product	Homo sapiens
111 6	AAH16692	1163	100	BC016692 progesterone receptor membrane component 2	Homo sapiens
111 6	AJ002030	1163	100	progesterone binding protein	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
111 6	AY069921	525	60	membrane progesterone receptor-like protein	Oncorhynchus mykiss
111 7	AAH16041	1441	100	BC016041 insulin-like growth factor-binding protein 4	Homo sapiens
111 7	M62403	1441	100	IGF-BP 4	Homo sapiens
111 7	Y12508	1441	100	insulin-like growth factor binding protein 4	Homo sapiens
111 8	AK000575	734	100	unnamed protein product	Homo sapiens
111 8	AK013438	484	72	unnamed protein product	Mus musculus
111 8	AY116892	734	100	HCF-1 beta-propeller interacting protein	Homo sapiens
111 9	AAH14410	2710	100	BC014410 Similar to EGF-containing fibulin-like extracellular matrix protein 1	Homo sapiens
111 9	AK077302	2581	94	unnamed protein product	Mus musculus
111 9	AY004330	2710	100	EGF-containing fibulin-like extracellular matrix protein 1	Homo sapiens
112 0	AF102552	11066	84	270 kDa ankyrin G isoform	Rattus norvegicus
112 0	L40632	7184	95	ankyrin 3	Mus musculus
112 0	U13616	20107	99	ankyrin G	Homo sapiens
112 1	AC002073	3406	100	Lim Kinase	Homo sapiens
112 1	AL117466	3183	100	hypothetical protein	Homo sapiens
112 1	D45906	3406	100	LIMK-2	Homo sapiens
112 2	AAH00836	633	100	BC000836 CGI-127 protein	Homo sapiens
112 2	AF135161_1	633	100	AF135161 unknown	Homo sapiens
112 2	AF151885_1	633	100	AF151885 CGI-127 protein	Homo sapiens
112 3	A16768	356	79	kunitz type protease inhibitor	synthetic construct
112 3	BC033174	501	98	Similar to collagen, type VI, alpha 3	Homo sapiens
112 3	X52022	501	98	collagen type VI, alpha 3 chain	Homo sapiens
112 4	AAH04440	776	100	BC004440 Unknown (protein for MGC:4033)	Homo sapiens
112 4	AAH19336	821	100	BC019336 Unknown (protein for IMAGE:3617778)	Homo sapiens
112 4	U91512	770	99	ninjurin	Homo sapiens
112 5	AAH18127	1250	93	BC018127 Similar to Peptidylglycine alpha-amidating monooxygenase	Homo sapiens
112 5	AB095007	1250	93	peptidylglycine alpha-amidating monooxygenase	Homo sapiens
112 5	AF035320	1279	100	peptidylglycine alpha-amidating monooxygenase	Homo sapiens
112 6	AAH13398	6167	100	BC013398 pumilio (Drosophila) homolog 1	Homo sapiens
112 6	AF315592_1	6167	100	AF315592 Pumilio 1	Homo sapiens
112 6	D43951	6233	100	KIAA0099 protein	Homo sapiens
112 7	AAH00465	826	100	BC000465 growth arrest and DNA-damage-inducible, gamma	Homo sapiens
112 7	AAH19325	826	100	BC019325 growth arrest and DNA-damage-inducible, gamma	Homo sapiens
112	AF494037_1	826	100	AF494037 growth arrest and DNA-	Homo sapiens

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7				damage-inducible, gamma	
1128	AAH01955	883	100	BC001955 ribosomal protein S10	Homo sapiens
1128	AAH04334	883	100	BC004334 ribosomal protein S10	Homo sapiens
1128	AAH05012	883	100	BC005012 ribosomal protein S10	Homo sapiens
1129	AAH12740	4687	99	BC012740 Similar to dystroglycan 1 (dystrophin-associated glycoprotein 1)	Homo sapiens
1129	AAH14616	4687	99	BC014616 Unknown (protein for MGC:3618)	Homo sapiens
1129	L19711	4703	100	dystroglycan	Homo sapiens
1130	AAH20983	978	100	BC020983 pituitary tumor-transforming 1 interacting protein	Homo sapiens
1130	BC031097	978	100	pituitary tumor-transforming 1 interacting protein	Homo sapiens
1130	BC034250	978	100	pituitary tumor-transforming 1 interacting protein	Homo sapiens
1131	AAH07082	185	100	BC007082 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Homo sapiens
1131	AAH11017	185	100	BC011017 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	Homo sapiens
1131	AF035262	185	100	BAF57	Homo sapiens
1133	AF099154	13656	86	von Willebrand factor	Canis familiaris
1133	M25865	15510	99	von Willebrand factor	Homo sapiens
1133	X04385	15515	100	VWF pre-pro-polypeptide (-22 to 2791)	Homo sapiens
1134	AAH17692	3143	99	BC017692 Similar to quiescin Q6	Homo sapiens
1134	AF361868	3135	98	sulfhydryl oxidase	Homo sapiens
1134	U97276	3911	99	quiescin	Homo sapiens
1136	AAH12123	1528	100	BC012123 golgi phosphoprotein 3	Homo sapiens
1136	AJ296152	1528	100	Golgi protein	Homo sapiens
1136	BC033725	1528	100	golgi phosphoprotein 3 (coat-protein)	Homo sapiens
1137	AAH08726	2687	100	BC008726 oxidative-stress responsive 1	Homo sapiens
1137	AB017642	2687	100	oxidative-stress responsive 1	Homo sapiens
1137	AB029024	2355	100	KIAA1101 protein	Homo sapiens
1138	AAH00478	3403	99	BC000478 heat shock 70kD protein 9B (mortalin-2)	Homo sapiens
1138	BC024034	3403	99	heat shock 70kD protein 9B (mortalin-2)	Homo sapiens
1138	BC030634	3399	99	heat shock 70kD protein 9B (mortalin-2)	Homo sapiens
1139	BC006834	892	100	B-cell translocation gene 1, anti-proliferative	Mus musculus
1139	BC018309	892	100	B-cell translocation gene 1, anti-proliferative	Mus musculus
1139	Z16410	892	100	btgl	Mus musculus
1140	AK075720	517	92	unnamed protein product	Mus musculus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1140	BC003862	517	92	Similar to transmembrane 9 superfamily member 2	Mus musculus
1140	U81006	518	93	p76	Homo sapiens
1141	A03736	3879	100	factor XIIIa	Homo sapiens
1141	M14354	3879	100	clotting factor XIIIa precursor (EC 2.3.2.13)	Homo sapiens
1141	M14539	4016	99	factor XIII precursor	Homo sapiens
1142	AAH06541	969	99	BC006541 integrin, beta 5	Homo sapiens
1142	J05633	962	98	integrin beta-5 subunit precursor	Homo sapiens
1142	X53002	969	99	precursor polypeptide (AA -23 to 776)	Homo sapiens
1143	D50929	7262	100	The KIAA0139 gene product is related to mouse centrosomin B.	Homo sapiens
1143	U58046	7262	100	p167	Homo sapiens
1143	U78311	7262	100	translation initiation factor 3 large subunit	Homo sapiens
1144	AAH01571	4708	99	BC001571 eukaryotic translation initiation factor 3, subunit 8 (110kD)	Homo sapiens
1144	AC002544	4708	99	Translation initiation factor eIF-p110	Homo sapiens
1144	U46025	4708	99	translation initiation factor eIF-3 p110 subunit	Homo sapiens
1145	AB019987	6513	99	chromosome-associated polypeptide-C	Homo sapiens
1145	AF092564	6041	99	chromosome-associated protein-C	Homo sapiens
1145	AL136877	6517	100	hypothetical protein	Homo sapiens
1146	AAH01756	2880	99	BC001756 phosphoglucomutase 1	Homo sapiens
1146	AAH19920	2873	99	BC019920 Unknown (protein for MGC:29909)	Homo sapiens
1146	M83088	2880	99	PGM1	Homo sapiens
1147	AB020664	3759	100	KIAA0857 protein	Homo sapiens
1147	AF334812_1	3333	100	AF334812 Rab11 interacting protein Ripla	Homo sapiens
1147	BC035013	3303	99	Similar to Rab coupling protein	Homo sapiens
1148	AF356518_1	1637	100	AF356518 junctional adhesion molecule 3 precursor	Homo sapiens
1148	AF448478_1	1637	100	AF448478 junctional adhesional molecule-3	Homo sapiens
1148	AJ416101	1870	100	junction adhesion molecule 3	Homo sapiens
1149	AF130117_48	355	77	AF130089 PRO2550	Homo sapiens
1149	AK000385	353	74	unnamed protein product	Homo sapiens
1149	AK097266	324	79	unnamed protein product	Homo sapiens
1150	AAH01562	3284	100	BC001562 nuclear receptor coactivator 4	Homo sapiens
1150	AL162047	3284	100	hypothetical protein	Homo sapiens
1150	L49399	3284	100	ORF	Homo sapiens
1151	AAH02356	2379	100	BC002356 nucleobindin 1	Homo sapiens
1151	M96824	2326	98	nucleobindin	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
115 1	U31342	2357	99	nucleobindin	Homo sapiens
115 2	AAH17180	4694	100	BC017180 Unknown (protein for MGC:790)	Homo sapiens
115 2	AK088028	4597	97	unnamed protein product	Mus musculus
115 2	BC007126	4597	97	Unknown (protein for MGC:5677)	Mus musculus
115 3	AAH08099	378	100	BC008099 Unknown (protein for IMAGE:4183312)	Homo sapiens
115 4	AF137053_1	2310	99	AF137053 mutant desmin	Homo sapiens
115 4	BC032116	2313	99	desmin	Homo sapiens
115 4	U59167	2325	100	desmin	Homo sapiens
115 5	AL445795	23376	99	heparan sulfate proteoglycan perlecan	Homo sapiens
115 5	M85289	23477	99	heparan sulfate proteoglycan	Homo sapiens
115 5	X62515	23627	99	Human basement membrane heparan sulfate proteoglycan core protein	Homo sapiens
115 6	AK057830	270	51	unnamed protein product	Homo sapiens
115 6	BC024651	210	58	similar to PR02550	Homo sapiens
115 6	BC032019	230	55	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
115 7	AAH00429	309	100	BC000429 chromosome 14 open reading frame 2	Homo sapiens
115 7	AAH01944	309	100	BC001944 chromosome 14 open reading frame 2	Homo sapiens
115 7	AF054175	309	100	mitochondrial proteolipid 68MP homolog	Homo sapiens
115 8	AAH01263	2152	100	BC001263 serum/glucocorticoid regulated kinase	Homo sapiens
115 8	AF153609_1	2152	100	AF153609 serine/threonine protein kinase sgk	Homo sapiens
115 8	AX553549	2152	100	unnamed protein product	Homo sapiens
115 9	AAH07103	710	100	BC007103 small acidic protein	Homo sapiens
115 9	AAH16352	710	100	BC016352 small acidic protein	Homo sapiens
115 9	AAH20937	710	100	BC020937 small acidic protein	Homo sapiens
116 1	AY043487	412	100	selenoprotein SelM	Homo sapiens
116 1	AY043488	367	85	selenoprotein SelM	Mus musculus
116 1	BC019742	345	85	Unknown (protein for MGC:30803)	Mus musculus
116 2	AF124719_1	1018	100	AF124719 GM2 activator protein	Homo sapiens
116 2	X61095	1039	97	GM2-activator protein	Homo sapiens
116 2	X62078	1018	100	GM2 activator protein	Homo sapiens
116 3	AB028974	1802	100	KIAA1051 protein	Homo sapiens
116 3	AB049150	1703	100	MEF3 like 1	Homo sapiens
116 3	AX082622	2129	100	unnamed protein product	Homo sapiens
116 4	BC026690	3964	100	CD97 antigen	Homo sapiens
116 4	U76764	3796	87	CD97	Homo sapiens

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116 4	X84700	3951	99	leucocyte antigen CD97	Homo sapiens
116 5	K03195	2485	99	glucose transporter glycoprotein	Homo sapiens
116 5	M13979	2430	97	glucose-transporter protein	Rattus norvegicus
116 5	M22063	2430	97	glucose transporter protein	Rattus norvegicus
116 6	AAH19297	1801	100	BC019297 Unknown (protein for MGC:4111)	Homo sapiens
116 6	AK021655	1801	100	unnamed protein product	Homo sapiens
116 6	AK022757	1801	100	unnamed protein product	Homo sapiens
116 7	AC005943	1522	100	methyl-CpG binding protein MBD3	Homo sapiens
116 7	AF072247	1522	100	methyl-CpG binding domain-containing protein MBD3	Homo sapiens
116 7	AF072248	1427	95	methyl-CpG binding domain-containing protein MBD3	Mus musculus
116 8	AB018009	2602	100	L-type amino acid transporter 1	Homo sapiens
116 8	AB018542	2602	100	CD98 light chain	Homo sapiens
116 8	AF104032	2602	100	L-type amino acid transporter subunit LAT1	Homo sapiens
117 0	AAH10737	1911	100	BC010737 Similar to reticulon 4	Homo sapiens
117 0	AAH12619	1911	100	BC012619 Unknown (protein for MGC:13655)	Homo sapiens
117 0	BC026788	1911	100	reticulon 4	Homo sapiens
117 1	AAH02412	3766	99	BC002412 inner membrane protein, mitochondrial (mitofilin)	Homo sapiens
117 1	D21094	3766	99	motor protein	Homo sapiens
117 1	L42572	3771	100	transmembrane protein	Homo sapiens
117 2	AAH01925	573	100	BC001925 FK506-binding protein 1A (12kD)	Homo sapiens
117 2	AAH05147	573	100	BC005147 FK506-binding protein 1A (12kD)	Homo sapiens
117 2	M93060	573	100	FK506-binding protein 12	Homo sapiens
117 3	AF116721_20	391	100	AF116620 PRO1068	Homo sapiens
117 4	AK075023	1335	99	unnamed protein product	Homo sapiens
117 4	AL117442	1344	100	hypothetical protein	Homo sapiens
117 4	BC002138	1302	96	Unknown (protein for IMAGE:3484538)	Mus musculus
117 5	AAH07674	382	100	BC007674 CD24 antigen (small cell lung carcinoma cluster 4 antigen)	Homo sapiens
117 5	L33930	382	100	signal transducer CD24	Homo sapiens
117 5	M58664	382	100	signal transducer CD24	Homo sapiens
117 6	AAH12181	4260	100	BC012181 Similar to paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein)	Homo sapiens
117 6	U20436	4060	95	furin endoprotease	Cricetulus griseus
117 6	X17094	4260	100	furin (AA 1-794)	Homo sapiens
117 7	AAH15236	1189	100	BC015236 hypothetical protein	Homo sapiens
117	AF335324_1	1189	100	AF335324 RTP801	Homo sapiens

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7					
1177	AY090097	1189	100	REDD-1	Homo sapiens
1178	AK026800	289	72	unnamed protein product	Homo sapiens
1178	AK057830	364	69	unnamed protein product	Homo sapiens
1178	BC032019	330	70	similar to Alu subfamily SQ sequence contamination warning entry	Homo sapiens
1179	AAH10058	3813	100	BC010058 exostoses (multiple) 2	Homo sapiens
1179	U62740	3813	100	EXT2	Homo sapiens
1179	U67368	3813	100	multiple exostosis 2	Homo sapiens
1180	AAH08301	1967	100	BC008301 tuftelin 1	Homo sapiens
1180	AF254260_1	1967	100	AF254260 tuftelin 1	Homo sapiens
1180	AF254860	1967	100	tuftelin 1	Homo sapiens
1182	AF272662_1	9764	94	AF272662 alpha 1 type V collagen	Rattus norvegicus
1182	D90279	10311	99	collagen alpha 1(V) chain precursor	Homo sapiens
1182	M76729	10277	99	pro-alpha-1 type V collagen	Homo sapiens
1183	AAH03155	1475	90	BC003155 coatomer protein complex, subunit epsilon	Homo sapiens
1183	AAH07250	1475	90	BC007250 coatomer protein complex, subunit epsilon	Homo sapiens
1183	AAH17285	1475	90	BC017285 Unknown (protein for MGC:29652)	Homo sapiens
1184	AX354381	347	100	unnamed protein product	Homo sapiens
1185	AF202636_1	2164	100	AF202636 angiopoietin-like protein PP1158	Homo sapiens
1185	AX079971	2164	100	unnamed protein product	Homo sapiens
1185	BC023647	2164	100	angiopoietin-like 4	Homo sapiens
1186	AK056767	1189	100	unnamed protein product	Homo sapiens
1186	AL831913	713	85	hypothetical protein	Homo sapiens
1187	AAH01270	1896	100	BC001270 SH3-domain GRB2-like 1	Homo sapiens
1187	U65999	1896	100	SH3-containing protein EEN	Homo sapiens
1187	X99656	1896	100	SH3-containing Grb-2-like 1	Homo sapiens
1188	AAH00385	4505	100	BC000385 Unknown (protein for MGC:8429)	Homo sapiens
1188	AF102803	4505	100	alphaE-catenin	Homo sapiens
1188	D13866	4505	100	alpha-catenin	Homo sapiens
1189	AAH07564	607	90	BC007564 annexin A11	Homo sapiens
1189	AJ278464	607	90	annexin A11	Homo sapiens
1189	AJ278465	607	90	annexin A11	Homo sapiens
1190	AAH01491	1470	99	BC001491 heme oxygenase (decycling) 1	Homo sapiens
1190	X06985	1475	100	heme oxygenase (AA 1 - 288)	Homo sapiens
119	Z82244	1475	100	bK286B10.2 (Heme Oxygenase	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
0				(decycling) 1 (HO-1 EC 1.14.99.3))	
119 2	AAH13910	1671	100	BC013910 Similar to death effector domain-containing	Homo sapiens
119 2	AAH16724	1671	100	BC016724 death effector domain-containing	Homo sapiens
119 2	AJ010973	1671	100	DEDD protein	Homo sapiens
119 3	AAH17882	1276	100	BC017882 proteasome (prosome, macropain) subunit, alpha type 6	Homo sapiens
119 3	BC022354	1276	100	proteasome (prosome, macropain) subunit, alpha type 6	Homo sapiens
119 3	D10755	1276	100	proteasome subunit R-IOTA	Rattus sp.
119 4	AAH09581	2041	100	BC009581 hydroxysteroid (17-beta) dehydrogenase 2	Homo sapiens
119 4	L11708	2041	100	17 beta hydroxysteroid dehydrogenase type 2	Homo sapiens
119 4	L40802	2041	100	17-hydroxysteroid dehydrogenase	Homo sapiens
119 5	AAH08452	586	100	BC008452 ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), member J	Homo sapiens
119 5	AF038954	586	100	vacuolar H(+)-ATPase subunit	Homo sapiens
119 5	S82464	573	96	vacuolar H(+)-ATPase subunit; V-ATPase subunit; M16	Bos taurus
119 6	AE003452	193	35	CG9350-PB	Drosophila melanogaster
119 6	AJ510148	571	72	mitochondrial NADH:ubiquinone oxidoreductase B14.7 subunit	Bos taurus
119 6	AK008201	532	65	unnamed protein product	Mus musculus
119 7	AB020685	3216	100	KIAA0878 protein	Homo sapiens
119 7	AK006650	2065	93	unnamed protein product	Mus musculus
119 7	BC041337	3212	99	Rho-related BTB domain containing 3	Homo sapiens
119 8	AB058749	1868	100	KIAA1846 protein	Homo sapiens
119 8	AK092295	1868	100	unnamed protein product	Homo sapiens
119 8	AL035661	1868	100	dJ568C11.3 (novel AMP-binding enzyme similar to acetyl-coenzyme A synthetase (acetate-coA ligase))	Homo sapiens
119 9	AF009242	1163	100	proline-rich Gla protein 1	Homo sapiens
119 9	AF419154	572	52	mitotic phosphoprotein 77	Xenopus laevis
119 9	BC030786	1246	100	proline-rich Gla (G-carboxyglutamic acid) polypeptide 1	Homo sapiens
120 0	AF000652	1503	99	syntenin	Homo sapiens
120 0	AF006636	1508	100	melanoma differentiation associated protein-9	Homo sapiens
120 0	U83463	1503	99	scaffold protein Pbp1	Homo sapiens
120 1	AF312032	5200	99	ephrin type-B receptor 4 precursor	Homo sapiens
120 1	AY056047	5200	99	receptor protein tyrosine kinase EphB4	Homo sapiens
120 1	U07695	5196	99	tyrosine kinase	Homo sapiens
120 2	AF015553	4955	99	TFII-I protein	Homo sapiens
120	AF038969	4949	99	general transcription factor 2-I	Homo sapiens

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2					
120 2	Y14946	4949	99	SPIN protein	Homo sapiens
120 3	AAH07452	1442	100	BC007452 Similar to WW domain binding protein 2	Homo sapiens
120 3	AAH10616	1442	100	BC010616 Unknown (protein for MGC:18269)	Homo sapiens
120 3	U79458	1458	100	WW domain binding protein-2	Homo sapiens
120 4	AB097511	3996	93	hypothetical protein	Macaca fascicularis
120 4	AL359292	7373	99	dJ448K1.1.1 (absent in melanoma 1, isoform 1)	Homo sapiens
120 4	U83115	8577	100	non-lens beta gamma-crystallin like protein	Homo sapiens
120 5	AAH05921	589	87	BC005921 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
120 5	AAH20756	589	87	BC020756 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
120 5	AAH22044	589	87	BC022044 chorionic somatomammotropin hormone 2	Homo sapiens
120 6	AY158924	650	100	histone protein Hist2h2aa2	Mus musculus
120 6	AY158925	650	100	histone protein Hist2h2aa1	Mus musculus
120 6	AY158953	650	100	histone protein Hist2h3c2	Mus musculus
120 7	AF226614_1	2929	100	AF226614 ferroportin1	Homo sapiens
120 7	AF231121_1	2929	100	AF231121 iron-regulated transporter IREG1	Homo sapiens
120 7	BC037733	2929	100	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3	Homo sapiens
120 8	AAH01693	709	100	BC001693 lectin, galactoside-binding, soluble, 1 (galectin 1)	Homo sapiens
120 8	AAH20675	709	100	BC020675 lectin, galactoside-binding, soluble, 1 (galectin 1)	Homo sapiens
120 8	X14829	709	100	beta-galactoside-binding lectin (AA 1-135)	Homo sapiens
120 9	AF151794	1678	38	pol protein	Phascolarctos cinereus
120 9	AY099324	1671	38	gag-pol polyprotein	porcine endogenous retrovirus B
120 9	M26927	1717	38	pol polyprotein	Gibbon ape leukemia virus
121 0	AAD18076	689	99	AF129756 G6c	Homo sapiens
121 0	AJ012008	689	99	Ly6-C protein	Homo sapiens
121 0	AJ315533	689	99	LY6G6C protein	Homo sapiens
121 1	AAH11682	2559	100	BC011682 Similar to cathepsin F	Homo sapiens
121 1	AF132894_1	2559	100	AF132894 cathepsin F	Homo sapiens
121 1	AJ007331	2559	100	cysteine proteinase	Homo sapiens
121 2	AF247565_1	513	97	AF247565 anaphase promoting complex subunit 11	Homo sapiens
121 2	AF247789_1	513	97	AF247789 putative anaphase-promoting complex subunit APC11	Homo sapiens
121 2	AX061622	513	97	unnamed protein product	Homo sapiens
121	AAH11811	559	92	BC011811 Unknown (protein for	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
3				MGC:20260)	
121 3	AF218016_1	432	76	AF218016 unknown	Homo sapiens
121 4	AAH17201	680	92	BC017201 insulin-like growth factor binding protein 7	Homo sapiens
121 4	L19182	680	92	MAC25	Homo sapiens
121 4	S75725	680	92	prostacyclin-stimulating factor; PGI2-stimulating factor; PSF	Homo sapiens
121 5	AAH00590	250	71	BC000590 actin related protein 2/3 complex, subunit 2 (34 kD)	Homo sapiens
121 5	AF006085	250	71	p34-Arc	Homo sapiens
121 5	U50523	250	71	unknown	Homo sapiens
121 6	AF126110_1	718	96	AF126110 fibulin-1 isoform D precursor	Homo sapiens
121 6	AF217999_1	718	96	AF217999 unknown	Homo sapiens
121 6	BC022497	718	96	fibulin 1	Homo sapiens
121 7	AAH05839	502	97	BC005839 follistatin-like 3 (secreted glycoprotein)	Homo sapiens
121 7	BC033119	502	97	follistatin-like 3 (secreted glycoprotein)	Homo sapiens
121 7	U76702	502	97	follistatin-related protein FLRG	Homo sapiens
121 8	AAH00163	601	99	BC000163 vimentin	Homo sapiens
121 8	BC030573	601	99	Unknown (protein for MGC:16183)	Homo sapiens
121 8	X56134	601	99	vimentin	Homo sapiens
121 9	AB018265	5555	100	KIAA0722 protein	Homo sapiens
121 9	AF045458	5460	100	serine/threonine kinase ULK1	Homo sapiens
121 9	AF072370_1	4865	89	AF072370 UNC51.1 serine/threonine kinase	Mus musculus
122 0	AAH00865	227	100	BC000865 Unknown (protein for IMAGE:3460093)	Homo sapiens
122 1	AAH02978	279	91	BC002978 CD81 antigen (target of antiproliferative antibody 1)	Homo sapiens
122 1	AF116600	279	91	CD81	Pan troglodytes
122 1	M33680	279	91	26-kDa cell surface protein TAPA-1	Homo sapiens
122 2	AAH15156	678	100	BC015156 ferritin, heavy polypeptide 1	Homo sapiens
122 2	AAH16009	678	100	BC016009 ferritin, heavy polypeptide 1	Homo sapiens
122 2	AAH16857	678	100	BC016857 ferritin, heavy polypeptide 1	Homo sapiens
122 3	AAH08012	518	100	BC008012 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
122 3	AAH09907	518	100	BC009907 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
122 3	AAH12819	518	100	BC012819 eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Homo sapiens
122 4	AAH05921	556	83	BC005921 chorionic somatomammotropin hormone 1 (placental lactogen)	Homo sapiens
122	AAH20756	556	83	BC020756 chorionic	Homo sapiens

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4				somatomammotropin hormone 1 (placental lactogen)	
122 4	AAH22044	556	83	BC022044 chorionic somatomammotropin hormone 2	Homo sapiens
122 5	A65264	705	100	unnamed protein product	unidentified
122 5	AAH01288	574	93	BC001288 Similar to decay accelerating factor for complement (CD55, Cromer blood group system)	Homo sapiens
122 5	AF149760_1	574	93	AF149760 decay-accelerating factor	Pan troglodytes
122 6	AK022217	191	76	unnamed protein product	Homo sapiens
122 6	AK056734	191	72	unnamed protein product	Homo sapiens
122 6	AK097342	209	78	unnamed protein product	Homo sapiens
122 7	AAH05326	499	98	BC005326 ribosomal protein L27a	Homo sapiens
122 7	AAH20169	499	98	BC020169 Unknown (protein for IMAGE:3543815)	Homo sapiens
122 7	U14968	499	98	ribosomal protein L27a	Homo sapiens
122 9	AAH21297	569	94	BC021297 Similar to Dynein heavy chain 64C	Homo sapiens
122 9	AB002323	569	94	KIAA0325	Homo sapiens
122 9	AY004877	539	89	cytoplasmic dynein heavy chain	Mus musculus
123 0	BC026018	643	100	Similar to laminin, beta 1	Homo sapiens
123 0	M20206	643	100	laminin B1	Homo sapiens
123 0	M55370	643	100	laminin B1	Homo sapiens
123 1	AF061658	591	91	cytidine deaminase	Homo sapiens
123 1	AJ000474	591	91	cytidine deaminase	Homo sapiens
123 1	L27943	591	91	cytidine deaminase	Homo sapiens
123 2	AAH18986	486	83	BC018986 Unknown (protein for MGC:20092)	Homo sapiens
123 2	AF229830	486	83	prostaglandin dehydrogenase	Papio hamadryas
123 2	U63296	486	83	15-hydroxyprostaglandin dehydrogenase	Homo sapiens
123 3	AAH00749	507	100	BC000749 lactate dehydrogenase A	Homo sapiens
123 3	AAH01829	507	100	BC001829 lactate dehydrogenase A	Homo sapiens
123 3	X03077	507	100	lactate dehydrogenase-A	Homo sapiens
123 4	AAH00903	791	88	BC000903 high-mobility group (nonhistone chromosomal) protein 2	Homo sapiens
123 4	AAH01063	791	88	BC001063 high-mobility group (nonhistone chromosomal) protein 2	Homo sapiens
123 4	X62534	791	88	HMG-2	Homo sapiens
123 5	AF193055_1	594	88	AF193055 unknown	Homo sapiens
123 5	AK075214	594	88	unnamed protein product	Homo sapiens
123 5	BC038587	594	88	Similar to EGF-like-domain, multiple 6	Homo sapiens
123	AF135060	632	96	fibrillin-2	Rattus

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6					norvegicus
123 6	U03272	637	99	fibrillin-2	Homo sapiens
123 6	X62009	637	98	fibrillin 5	Homo sapiens
123 7	AAH13083	522	100	BC013083 Similar to cystatin C (amyloid angiopathy and cerebral hemorrhage)	Homo sapiens
123 7	X12763	522	100	ompA - cystatin C fusion preprotein (AA -21 to 120)	synthetic construct
123 7	X61681	522	100	cystatin C	Homo sapiens
123 9	AF135060	523	89	fibrillin-2	Rattus norvegicus
123 9	L39790	532	90	fibrillin 2	Mus musculus
123 9	U03272	597	100	fibrillin-2	Homo sapiens
124 0	M65149	1200	85	CELF	Rattus norvegicus
124 0	M83667	1430	100	NF-IL6-beta protein	Homo sapiens
124 0	S63168	1418	99	CCAAT/enhancer-binding protein delta; C/EBP delta	Homo sapiens
124 1	AF186111_1	230	52	AF186111 NOTCH4-like protein	Homo sapiens
124 1	AL512735	230	52	hypothetical protein	Homo sapiens
124 1	AX133831	230	52	unnamed protein product	Homo sapiens
124 2	BC015302	664	87	lamin A	Mus musculus
124 2	M13452	715	95	lamin A protein	Homo sapiens
124 2	X76297	670	88	lamin A	Rattus norvegicus
124 4	AB049946	666	100	mitochondrial ribosomal protein S15	Homo sapiens
124 4	BC029193	433	69	mitochondrial ribosomal protein S15	Mus musculus
124 4	BC031336	666	100	mitochondrial ribosomal protein S15	Homo sapiens
124 5	AAH13733	392	93	BC013733 px19-like protein	Homo sapiens
124 5	AAH13748	392	93	BC013748 px19-like protein	Homo sapiens
124 5	AF201925_1	392	93	AF201925 PRELI	Homo sapiens
124 6	AAH02362	694	100	BC002362 lactate dehydrogenase B	Homo sapiens
124 6	AAH15122	694	100	BC015122 lactate dehydrogenase B	Homo sapiens
124 6	Y00711	694	100	lactate dehydrogenase B (AA 1 - 334)	Homo sapiens
124 7	AAH03070	504	86	BC003070 GATA-binding protein 3	Homo sapiens
124 7	AAH06793	504	86	BC006793 GATA-binding protein 3	Homo sapiens
124 7	X55037	504	86	GATA-3	Homo sapiens
124 8	AF269289_1	357	100	AF269289 unknown	Homo sapiens
124 9	AAH07728	546	86	BC007728 Unknown (protein for MGC:12671)	Homo sapiens
124 9	AL080102	546	86	hypothetical protein	Homo sapiens
124 9	U49436	546	86	translation initiation factor 5	Homo sapiens
125	AAH03190	472	94	BC003190 p75NTR-associated cell	Homo sapiens

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0				death executor; ovarian granulosa cell protein (13kD)	
1250	AF187064_1	472	94	AF187064 p75NTR-associated cell death executor; NADE	Homo sapiens
1250	M38188	472	94	unknown	Homo sapiens
1251	AB037767	5427	99	KIAA1346 protein	Homo sapiens
1251	AF207664_1	5274	100	AF207664 matrix metalloprotease	Homo sapiens
1251	AP001697	5274	100	metalloprotease with thrombospondin type 1 motifs	Homo sapiens
1252	U90938	222	76	Fc gamma receptor IIc1	Homo sapiens
1252	X17652	222	76	IgG Fc receptor	Homo sapiens
1252	X17652	222	76	IgG Fc receptor	Homo sapiens
1253	AAH01768	390	93	BC001768 neuronatin	Homo sapiens
1253	AL109614	390	93	bA425M5.3.1 (neuronatin (isoform 1))	Homo sapiens
1253	U31767	390	93	neuronatin alpha	Homo sapiens
1254	AF151373_1	542	75	AF151373 nucleolin-related protein NRP	Rattus norvegicus
1254	AK091742	670	96	unnamed protein product	Homo sapiens
1254	M60858	670	96	nucleolin	Homo sapiens
1255	AAH13428	616	93	BC013428 PP1201 protein	Homo sapiens
1255	AF193045_1	616	93	AF193045 unknown	Homo sapiens
1255	BC026348	616	93	PP1201 protein	Homo sapiens
1256	AF393832_1	765	99	AF393832 beta-actin	Morulus calbasu
1256	AY039657	765	99	beta-actin	Chrysophrys auratus
1256	AY148350	765	99	actin	Dicentrarchus labrax
1257	AK055593	379	100	unnamed protein product	Homo sapiens
1258	AAH21233	1036	100	BC021233 ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	Homo sapiens
1258	BC022865	1036	100	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	Homo sapiens
1258	X83218	1036	100	ATP synthase, oligomycin sensitivity conferring protein	Homo sapiens
1259	AAH04368	1221	99	BC004368 proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	Homo sapiens
1259	AAH19885	1221	99	BC019885 proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	Homo sapiens
1259	D45248	1226	100	proteasome activator hPA28 suunit beta	Homo sapiens
1260	AF090306	2306	100	retinoblastoma binding protein	Rattus norvegicus
1260	U35143	2306	100	retinoblastoma-binding protein RbAp46	Homo sapiens
1260	X72841	2306	100	IEF 7442	Homo sapiens
126	AAH00413	1748	100	BC000413 eukaryotic translation	Homo sapiens

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1				initiation factor 3, subunit 2 (beta, 36kD)	
126 1	AAH03140	1748	100	BC003140 eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)	Homo sapiens
126 1	U39067	1748	100	translation initiation factor eIF3 p36 subunit	Homo sapiens
126 2	AF042166	13721	100	beta-filamin	Homo sapiens
126 2	AF043045	13709	99	actin-binding protein homolog ABP-278	Homo sapiens
126 2	AF191633	13721	100	filamin	Homo sapiens
126 3	AF165515_1	1862	100	AF165515 ancient ubiquitous protein 1 precursor	Homo sapiens
126 3	AK023983	1935	100	unnamed protein product	Homo sapiens
126 3	BC033646	1862	100	ancient ubiquitous protein 1	Homo sapiens
126 4	AB009865	1347	100	Angiopoietin-2	Homo sapiens
126 4	AF187858_1	1335	99	AF187858 angiopoietin-2 isoform-1	Homo sapiens
126 4	AF218015_1	1347	100	AF218015 unknown	Homo sapiens
126 5	AF035718	914	99	mesoderm-specific basic-helix-loop-helix protein; Pod-1	Homo sapiens
126 5	AL356109	917	100	bA373A10.1 (transcription factor 21)	Homo sapiens
126 5	BC025697	917	100	transcription factor 21	Homo sapiens
126 6	M38690	1200	100	CD9 antigen	Homo sapiens
126 6	S60489	1200	100	CD9 antigen	Homo sapiens
126 6	X60111	1200	100	MRP-1 (motility related protein)	Homo sapiens
126 7	AAH02368	4629	99	BC002368 proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Homo sapiens
126 7	AAH02997	4629	99	BC002997 proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	Homo sapiens
126 7	D78151	4637	100	human 26S proteasome subunit p97	Homo sapiens
126 8	AAH00182	1622	100	BC000182 annexin A4	Homo sapiens
126 8	AAH11659	1622	100	BC011659 Similar to annexin A4	Homo sapiens
126 8	D78152	1622	100	annexin IV (carbohydrate-binding protein p33/41)	Homo sapiens
126 9	AAH03064	4016	99	BC003064 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)	Homo sapiens
126 9	AF205890	4028	100	disabled-2	Homo sapiens
126 9	U39050	4028	100	DOC-2	Homo sapiens
127 0	AAH07075	780	100	BC007075 hemoglobin, beta	Homo sapiens
127 0	U01317	780	100	beta-globin	Homo sapiens
127 0	V00499	780	100	beta globin	Homo sapiens
127 1	AAH21557	4093	99	BC021557 transmembrane protein 8 (five membrane-spanning domains)	Homo sapiens
127 1	AB045292	4100	100	M83 protein	Homo sapiens
127	AE006463_7	4088	99	AE006463 M83	Homo sapiens

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1					
127 2	AF193048_1	946	100	AF193048 unknown	Homo sapiens
127 3	AF151980_1	2009	100	AF151980 connexin 43	Homo sapiens
127 3	BC026329	2009	100	gap junction protein, alpha 1, 43kD (connexin 43)	Homo sapiens
127 3	X52947	2009	100	gap junction protein (AA 1-382)	Homo sapiens
127 4	AJ313463	1258	100	adipsin/complement factor D precursor	Homo sapiens
127 4	BC034529	1249	100	Unknown (protein for IMAGE:4780594)	Homo sapiens
127 4	M84526	1198	98	adipsin/complement factor D	Homo sapiens
127 5	AF258549_1	533	100	AF258549 PP1292	Homo sapiens
127 6	AF217963_1	4215	99	AF217963 NRAGE	Homo sapiens
127 6	AF258554_1	4223	100	AF258554 PP2250	Homo sapiens
127 6	BC032473	4223	100	melanoma antigen, family D, 1	Homo sapiens
127 7	AAH14635	635	100	BC014635 Similar to SH3-domain, GRB2-like, endophilin B2	Homo sapiens
127 7	AF257319_1	635	100	AF257319 SH3-containing protein SH3GLB2	Homo sapiens
127 7	AF258589_1	635	100	AF258589 PP578	Homo sapiens
127 8	AAH03390	707	100	BC003390 hypothetical protein	Homo sapiens
127 8	AAH14334	707	100	BC014334 Unknown (protein for MGC:22874)	Homo sapiens
127 8	AF275807_1	822	100	AF275807 PNAS-110	Homo sapiens
127 9	AAH05238	469	100	BC005238 FXYD domain-containing ion transport regulator 3	Homo sapiens
127 9	U28249	411	75	11kD protein	Homo sapiens
127 9	X93036	469	100	MAT8 protein	Homo sapiens
128 0	AF014402	1500	100	type-2 phosphatidic acid phosphatase alpha-1	Homo sapiens
128 0	BC039847	1500	100	Similar to phosphatidic acid phosphatase type 2A	Homo sapiens
128 0	Y14436	1500	100	phosphatidic acid phosphatase type 2	Homo sapiens
128 1	AL163249	2729	99	T-complex protein 1 theta subunit	Homo sapiens
128 1	D13627	2730	99	KIAA0002	Homo sapiens
128 1	D42052	2734	100	predicted protein of 548 amino acids	Homo sapiens
128 2	AAH01312	2306	100	BC001312 protein disulfide isomerase-related protein	Homo sapiens
128 2	BC006865	2220	95	Similar to protein disulfide isomerase-related protein	Mus musculus
128 2	D49489	2306	100	human P5	Homo sapiens
128 3	AF439513_1	7917	91	AF439513 pregnancy-associated plasma protein-A	Mus musculus
128 3	U28727	8980	100	pregnancy-associated plasma protein-A preproform	Homo sapiens
128 3	X68280	8574	100	unnamed protein product	Homo sapiens
128 4	AAH01936	1357	100	BC001936 Similar to BCL2-associated athanogene	Homo sapiens
128 4	AAH14774	1357	100	BC014774 Unknown (protein for MGC:17086)	Homo sapiens

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128 4	Z35491	1357	100	glucocortoid receptor-associated protein RAP46	Homo sapiens
128 5	AAH04490	1953	100	BC004490 v-fos FBJ murine osteosarcoma viral oncogene homolog	Homo sapiens
128 5	AF111167	1953	100	cfos	Homo sapiens
128 5	V01512	1953	100	c-fos	Homo sapiens
128 6	AAH20235	3282	99	BC020235 Unknown (protein for MGC:31939)	Homo sapiens
128 6	M19645	3314	100	GRP78 precursor	Homo sapiens
128 6	X87949	3314	100	BiP	Homo sapiens
128 7	AAH14433	2640	100	BC014433 Unknown (protein for MGC:2159)	Homo sapiens
128 7	BC036000	2640	100	Unknown (protein for IMAGE:4712175)	Homo sapiens
128 7	U42068	2640	100	P58	Homo sapiens
128 8	BC032722	1478	100	tumor necrosis factor (ligand) superfamily, member 10	Homo sapiens
128 8	U37518	1478	100	TNF-related apoptosis inducing ligand TRAIL	Homo sapiens
128 8	U57059	1478	100	Apo-2 ligand	Homo sapiens
128 9	AAH01022	1591	100	BC001022 pyrophosphatase (inorganic)	Homo sapiens
128 9	AF119665_1	1591	100	AF119665 inorganic pyrophosphatase	Homo sapiens
128 9	AF217186_1	1591	100	AF217186 inorganic pyrophosphatase 1	Homo sapiens
129 0	AAH08743	3145	100	BC008743 zyxin	Homo sapiens
129 0	AAH09360	3145	100	BC009360 zyxin	Homo sapiens
129 0	AAH10031	3145	100	BC010031 zyxin	Homo sapiens
129 1	AAH05901	919	100	BC005901 Microfibril-associated glycoprotein-2	Homo sapiens
129 1	AF084927	919	100	microfibril-associated glycoprotein 2	Homo sapiens
129 1	U37283	919	100	microfibril-associated glycoprotein-2 MAGP-2	Homo sapiens
129 2	AAH00933	2015	100	BC000933 isocitrate dehydrogenase 3 (NAD+) gamma	Homo sapiens
129 2	Z68129	2015	100	NAD(H)-specific isocitrate dehydrogenase gamma-subunit precursor	Homo sapiens
129 2	Z68907	2015	100	NAD (H)-specific isocitrate dehydrogenase gamma subunit precursor	Homo sapiens
129 3	AAH12265	846	100	BC012265 Similar to cofilin 1, non-muscle	Homo sapiens
129 3	AAH12318	846	100	BC012318 Similar to cofilin 1, non-muscle	Homo sapiens
129 3	AAH18256	846	100	BC018256 Similar to cofilin 1, non-muscle	Homo sapiens
129 4	AB069964	861	100	ubiquitin-conjugating enzyme 9	Gallus gallus
129 4	AF461016_1	861	100	AF461016 ubiquitin-conjugating enzyme	Gallus gallus
129 4	U88561	861	100	E2 ubiquitin conjugating enzyme	Xenopus laevis
129 5	AAH06249	989	100	BC006249 guanylate kinase 1	Homo sapiens
129 5	AAH09914	989	100	BC009914 guanylate kinase 1	Homo sapiens

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129 5	U66895	989	100	guanylate kinase	Homo sapiens
129 6	AF095770_1	224	94	AF095770 PTH-responsive osteosarcoma D1 protein	Homo sapiens
129 7	AAH01120	1369	99	BC001120 lectin, galactoside-binding, soluble, 3 (galectin 3)	Homo sapiens
129 7	AF031425	1369	99	galectin 3	Homo sapiens
129 7	M35368	1377	100	galactose-specific lectin	Homo sapiens
129 8	AF241786_1	1125	100	AF241786 NPD013	Homo sapiens
129 9	AAH02503	547	70	BC002503 spermidine/spermine N1-acetyltransferase	Homo sapiens
129 9	AAH08424	547	70	BC008424 spermidine/spermine N1-acetyltransferase	Homo sapiens
129 9	AF251292_1	1059	100	AF251292 DC21	Homo sapiens
130 0	AF135157_1	190	63	AF135157 complement C1q A chain precursor	Homo sapiens
130 0	AF260332_1	1550	100	AF260332 DC33	Homo sapiens
130 0	BC030153	190	63	complement component 1, q subcomponent, alpha polypeptide	Homo sapiens
130 1	AAH00589	770	100	BC000589 CGI-39 protein; cell death-regulatory protein GRIM19	Homo sapiens
130 1	AAH09189	770	100	BC009189 CGI-39 protein; cell death-regulatory protein GRIM19	Homo sapiens
130 1	AF261134_1	1196	100	AF261134 CDA016	Homo sapiens
130 2	AAH12296	1135	99	BC012296 hypothetical protein FLJ21174	Homo sapiens
130 2	AF271783_1	1141	100	AF271783 NPD017	Homo sapiens
130 2	AF314542_1	1141	100	AF314542 B lymphocyte activation-related protein	Homo sapiens
130 3	AK090427	13940	99	FLJ00343 protein	Homo sapiens
130 3	L44140	14011	100	filamin	Homo sapiens
130 3	X53416	14004	99	actin-binding protein	Homo sapiens
130 4	AAH12341	1492	100	BC012341 Similar to M5-14 protein	Homo sapiens
130 4	AL136622	1492	100	hypothetical protein	Homo sapiens
130 4	AL390090	1492	100	c3orf1 hypothetical protein, M5-14 similar to (AE003703)140up gene product Drosophila melanogaster	Homo sapiens
130 5	AC005624	824	100	MY18_HUMAN	Homo sapiens
130 5	AF078077	824	100	growth arrest and DNA-damage-inducible protein GADD45beta	Homo sapiens
130 5	AF087853_1	824	100	AF087853 growth arrest and DNA damage inducible protein beta	Homo sapiens
130 6	AF020185	478	100	protein inhibitor of nitric oxide synthase	Mus musculus
130 6	BC008106	478	100	dynein, cytoplasmic, light polypeptide	Mus musculus
130 6	BC034258	478	100	dynein, cytoplasmic, light polypeptide	Mus musculus
130 7	AAH01539	1466	100	BC001539 dickkopf (Xenopus laevis) homolog 1	Homo sapiens
130 7	AF177394_1	1466	100	AF177394 dickkopf-1	Homo sapiens
130 7	AF261158	1466	100	dickkopf homolog 1	Homo sapiens
130	AAC33279	1396	100	AC005559 basigin	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
8					
1308	AAH09040	1396	100	BC009040 basigin (OK blood group)	Homo sapiens
1308	AF042855	1396	100	EMMPRIN	Homo sapiens
1309	L47125	3057	100	glypican	Homo sapiens
1309	L47176	3057	100	GTR2-2 gene product	Homo sapiens
1309	Z37987	3057	100	MXR7	Homo sapiens
1310	D83476	4306	77	Xtld protein	Xenopus laevis
1310	L24755	4948	92	bone morphogenetic protein	Mus musculus
1310	U50330	5416	100	procollagen C-proteinase	Homo sapiens
1311	AAH01287	669	100	BC001287 histidine triad nucleotide-binding protein	Homo sapiens
1311	AAH07090	669	100	BC007090 histidine triad nucleotide-binding protein	Homo sapiens
1311	U51004	669	100	protein kinase C inhibitor	Homo sapiens
1312	AB003306	1280	94	PSMB5	Mus musculus
1312	AF060091_1	1280	94	AF060091 proteasome subunit X	Mus musculus
1312	X95586	1370	100	proteasome	Homo sapiens
1313	AF102848_1	2178	100	AF102848 keratin 23	Homo sapiens
1313	AK002047	2151	98	unnamed protein product	Homo sapiens
1313	BC028356	2155	99	type I intermediate filament cytokeratin	Homo sapiens
1314	AAH00097	3483	100	BC000097 transforming growth factor, beta-induced, 68kD	Homo sapiens
1314	AAH04972	3483	100	BC004972 transforming growth factor, beta-induced, 68kD	Homo sapiens
1314	AY149344	3483	100	transforming growth factor, beta-induced, 68kDa	Homo sapiens
1315	AF414110_1	635	100	AF414110 histone variant H2A.F/Z	Danio rerio
1315	AF414111_1	635	100	AF414111 histone variant H2A.F/Z	Danio rerio
1315	V00414	635	100	histone H2A	Gallus gallus
1316	BC011457	957	100	Unknown (protein for MGC:7976)	Mus musculus
1316	BC019761	957	100	putative membrane protein	Mus musculus
1316	BC020098	957	100	putative membrane protein	Mus musculus
1317	AAH00140	3579	100	BC000140 propionyl Coenzyme A carboxylase, alpha polypeptide	Homo sapiens
1317	AF385926_1	3579	100	AF385926 propionyl-CoA carboxylase alpha subunit	Homo sapiens
1317	AY035808	3579	100	propionyl-CoA carboxylase alpha polypeptide precursor	Homo sapiens
1318	AF372216_1	562	99	AF372216 tropomyosin alpha isoform	Rattus norvegicus
1318	M19267	565	100	tropomyosin	Homo sapiens
1318	M19715	565	100	skeletal muscle tropomyosin	Homo sapiens
1319	AAH00191	704	100	BC000191 hypothetical protein	Homo sapiens
1319	AAH14329	704	100	BC014329 Unknown (protein for MGC:22862)	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1319	AF212248_1	704	100	AF212248 CDA09	Homo sapiens
1320	AAH00255	783	100	BC000255 Unknown (protein for MGC:2495)	Homo sapiens
1320	AF320778_1	783	100	AF320778 cervical cancer oncogene 3	Homo sapiens
1320	AY032594	783	100	hepatitis C virus core-binding protein 6	Homo sapiens
1321	AAH00271	799	100	BC000271 Unknown (protein for MGC:3204)	Homo sapiens
1321	AAH01434	799	100	BC001434 Unknown (protein for MGC:2477)	Homo sapiens
1321	AK007390	449	82	unnamed protein product	Mus musculus
1322	AAH00421	1243	100	BC000421 lysosomal-associated protein transmembrane 4 alpha	Homo sapiens
1322	AAH03158	1240	99	BC003158 lysosomal-associated protein transmembrane 4 alpha	Homo sapiens
1322	D14696	1243	100	KIAA0108	Homo sapiens
1323	AAH00461	1738	100	BC000461 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	Homo sapiens
1323	AAH00934	1735	99	BC000934 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	Homo sapiens
1323	AL031668	1738	100	dJ64K7.2 (eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD))	Homo sapiens
1324	AAH00466	1059	100	BC000466 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI)	Homo sapiens
1324	AAH19276	1059	100	BC019276 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI)	Homo sapiens
1324	AF044958	1059	100	NADH:ubiquinone oxidoreductase ASHI subunit	Homo sapiens
1325	AAH00490	1821	100	BC000490 eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD)	Homo sapiens
1325	AK095574	1774	98	unnamed protein product	Homo sapiens
1325	U94855	1821	100	translation initiation factor 3 47 kDa subunit	Homo sapiens
1326	AAH00502	970	100	BC000502 ribosomal protein L17	Homo sapiens
1326	AAH17831	970	100	BC017831 ribosomal protein L17	Homo sapiens
1326	X53777	970	100	putative ribosomal protein (AA 1-184)	Homo sapiens
1327	AAH00505	808	100	BC000505 microsomal glutathione S-transferase 3	Homo sapiens
1327	AAH03034	808	100	BC003034 microsomal glutathione S-transferase 3	Homo sapiens
1327	AAH05964	808	100	BC005964 microsomal glutathione S-transferase 3	Homo sapiens
1328	AAH00509	1425	100	BC000509 proteasome (prosome, macropain) subunit, beta type, 7	Homo sapiens
1328	AAH17116	1393	100	BC017116 proteasome (prosome, macropain) subunit, beta type, 7	Homo sapiens
1328	D38048	1421	99	proteasome subunit z	Homo sapiens
1329	BC033015	4539	100	RAS p21 protein activator (GTPase activating protein) 1	Homo sapiens
1329	M23379	4539	100	GTPase-activating protein	Homo sapiens
1329	M23612	4555	100	GTPase-activating protein	Homo sapiens
133	BC003860	2254	100	protease (prosome, macropain) 26S	Mus musculus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
0				subunit, ATPase 1	
1330	D50696	2254	100	proteasomal ATPase (S4)	Rattus norvegicus
1330	U39302	2254	100	P26s4	Mus musculus
1331	AAH00522	2131	100	BC000522 Similar to serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor). member 1	Homo sapiens
1331	AF400442_1	2125	99	AF400442 pigment epithelium-derived factor	Homo sapiens
1331	M76979	2119	99	pigment epithelial-differentiating factor	Homo sapiens
1332	AAH00529	1616	100	BC000529 prostate differentiation factor	Homo sapiens
1332	AAH08962	1616	100	BC008962 Unknown (protein for MGC:4145)	Homo sapiens
1332	AF003934	1613	99	prostate differentiation factor	Homo sapiens
1333	AAH00548	806	100	BC000548 receptor (calcitonin) activity modifying protein 1	Homo sapiens
1333	AF181550_1	596	71	AF181550 receptor activity modifying protein 1	Rattus norvegicus
1333	AJ001014	806	100	RAMP1	Homo sapiens
1334	AAH00554	1409	100	BC000554 Similar to integral membrane protein 2B	Homo sapiens
1334	AF136973_1	1409	100	AF136973 putative transmembrane protein E3-16	Homo sapiens
1334	AF152462_1	1409	100	AF152462 transmembrane protein BRI	Homo sapiens
1335	AAH00601	479	100	BC000601 DKFZP564K247 protein	Homo sapiens
1335	AAH09583	479	100	BC009583 DKFZP564K247 protein	Homo sapiens
1335	AAH09594	479	100	BC009594 DKFZP564K247 protein	Homo sapiens
1336	AAH00691	906	100	BC000691 brain specific protein	Homo sapiens
1336	AF132972_1	902	99	AF132972 CGI-38 protein	Homo sapiens
1336	BC010788	888	96	RIKEN cDNA 2700055K07 gene	Mus musculus
1337	AAH00720	798	100	BC000720 ubiquitously-expressed transcript	Homo sapiens
1337	AAH08890	798	100	BC008890 ubiquitously-expressed transcript	Homo sapiens
1337	AF092737_1	798	100	AF092737 ubiquitously expressed transcript	Homo sapiens
1338	AAH01016	958	100	BC001016 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (19kD, PGIV)	Homo sapiens
1338	AF044953_1	958	100	AF044953 NADH:ubiquinone oxidoreductase PGIV subunit	Homo sapiens
1338	X59697	866	88	19 kDa subunit of NADH:ubiquinone oxidoreductase complex (complex I)	Bos taurus
1339	AAH01066	763	100	BC001066 hypothetical protein	Homo sapiens
1339	AAH21986	763	100	BC021986 mitochondrial ribosomal protein L27	Homo sapiens
1339	AB049647	763	100	mitochondrial ribosomal protein L27 (L27mt)	Homo sapiens
1340	AAH01101	2975	100	BC001101 HSPC025	Homo sapiens
1340	AAH07510	2975	100	BC007510 HSPC025	Homo sapiens
134	BC029265	2975	100	eukaryotic translation initiation	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
0				factor 3, subunit 6 interacting protein	
134 1	AAH01150	2803	100	BC001150 metalloprotease 1 (pitrilysin family)	Homo sapiens
134 1	AAH05025	2802	99	BC005025 Similar to metalloprotease 1 (pitrilysin family)	Homo sapiens
134 1	AB029027	2803	100	KIAA1104 protein	Homo sapiens
134 2	AAH01288	2064	100	BC001288 Similar to decay accelerating factor for complement (CD55, Cromer blood group system)	Homo sapiens
134 2	M30142	2064	100	decay-accelerating factor A	Homo sapiens
134 2	M31516	2064	100	decay-accelerating factor	Homo sapiens
134 3	AAH01387	833	100	BC001387 similar to rat HREV107	Homo sapiens
134 3	AB030814	833	100	H-REV107 protein homolog	Homo sapiens
134 3	AF317086	833	100	HREV107-3	Homo sapiens
134 4	AAH01420	800	100	BC001420 HN1 protein	Homo sapiens
134 4	AF177862_1	800	100	AF177862 HN1 protein	Homo sapiens
134 4	AF348672	800	100	hematological and neurological expressed 1 protein	Homo sapiens
134 5	AAH01426	482	100	BC001426 Similar to ubiquinol-cytochrome c reductase hinge protein	Homo sapiens
134 5	AAH01934	482	100	BC001934 Similar to ubiquinol-cytochrome c reductase hinge protein	Homo sapiens
134 5	AAH15177	482	100	BC015177 Unknown (protein for MGC:10149)	Homo sapiens
134 6	AAH21173	429	100	BC021173 normal mucosa of esophagus specific 1	Homo sapiens
134 6	AB026707	429	100	FOAP-11 protein	Homo sapiens
134 6	AF228422_1	429	100	AF228422 normal mucosa of esophagus specific 1	Homo sapiens
134 7	AF274958_1	737	100	AF274958 PNAS-101	Homo sapiens
134 8	AAH14908	1453	100	BC014908 stem-loop (histone) binding protein	Homo sapiens
134 8	AAH15703	1453	100	BC015703 stem-loop (histone) binding protein	Homo sapiens
134 8	Z71188	1453	100	histone RNA hairpin-binding protein	Homo sapiens
134 9	AB000491	2046	100	proteasome p45/SUG	Rattus norvegicus
134 9	D83521	2046	100	proteasomal ATPase (rat SUG1)	Rattus norvegicus
134 9	Z54219	2046	100	mSUG1 protein	Mus musculus
135 0	AK075215	831	100	unnamed protein product	Homo sapiens
135 1	AAH02481	480	100	BC002481 HSPC162 protein	Homo sapiens
135 1	AF132750_1	480	100	AF132750 bithoraxoid-like protein	Homo sapiens
135 1	AF178431_1	480	100	AF178431 BITH	Homo sapiens
135 2	AAH02559	3087	100	BC002559 high-glucose-regulated protein 8	Homo sapiens
135 2	AK083882	3077	99	unnamed protein product	Mus musculus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
135 2	BC014797	3077	99	Unknown (protein for MGC:11691)	Mus musculus
135 3	AAH02589	2230	100	BC002589 proteasome (prosome, macropain) 26S subunit, ATPase, 2	Homo sapiens
135 3	BC005462	2226	99	proteasome (prosome, macropain) 26S subunit, ATPase 2	Mus musculus
135 3	D11094	2230	100	MSS1 protein	Homo sapiens
135 4	AAH02634	1769	100	BC002634 Unknown (protein for MGC:4272)	Homo sapiens
135 4	AK003354	1732	96	unnamed protein product	Mus musculus
135 4	BC002128	1725	96	Unknown (protein for MGC:6737)	Mus musculus
135 5	AAH02803	843	100	BC002803 hypothetical protein	Homo sapiens
135 5	AF151072_1	843	100	AF151072 HSPC238	Homo sapiens
135 5	BC005559	711	78	RIKEN cDNA 2500002L14 gene	Mus musculus
135 6	AAH02911	856	100	BC002911 Unknown (protein for MGC:11276)	Homo sapiens
135 6	AK003237	722	84	unnamed protein product	Mus musculus
135 6	BC031732	722	84	DNA segment, Chr 7, Wayne State University 86, expressed	Mus musculus
135 7	AAH02945	2197	100	BC002945 Similar to hypothetical protein FLJ10101	Homo sapiens
135 7	AAH21095	1290	100	BC021095 Unknown (protein for MGC:31800)	Homo sapiens
135 7	AK027586	1290	100	unnamed protein product	Homo sapiens
135 8	AAH02954	2552	100	BC002954 UDP-glucose pyrophosphorylase 2	Homo sapiens
135 8	BC023810	2524	98	UDP-glucose pyrophosphorylase 2	Mus musculus
135 8	U27460	2542	99	uridine diphosphoglucose pyrophosphorylase	Homo sapiens
135 9	AAH03005	886	100	BC003005 inactive progesterone receptor, 23 kD	Homo sapiens
135 9	BC003708	876	98	telomerase binding protein, p23	Mus musculus
135 9	L24804	886	100	p23	Homo sapiens
136 0	AAH03056	2132	100	BC003056 HSPC028 protein	Homo sapiens
136 0	AAH08453	2132	100	BC008453 HSPC028 protein	Homo sapiens
136 0	AAH09597	2132	100	BC009597 HSPC028 protein	Homo sapiens
136 1	L29075	151	24	G-box binding factor	Dictyostelium discoideum
136 2	AAH01773	591	100	BC001773 Similar to ribosomal protein L34	Homo sapiens
136 2	AB061832	591	100	ribosomal protein L34	Homo sapiens
136 2	BC028517	587	99	Unknown (protein for MGC:41239)	Mus musculus
136 3	AAH01882	533	100	BC001882 Similar to ribosomal protein L5	Homo sapiens
136 3	D10737	512	100	ribosomal protein L5	Gallus gallus
136 3	X57016	512	100	ribosomal protein L5	Gallus gallus
136 4	AAH01884	589	100	BC001884 NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)	Homo sapiens
136	AF020352	589	100	NADH:ubiquinone oxidoreductase 15	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
4				kDa IP subunit	
136 4	AF047434	589	100	NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein	Homo sapiens
136 5	AAH01926	2197	100	BC001926 creatine kinase, mitochondrial 1 (ubiquitous)	Homo sapiens
136 5	AAH06467	2197	100	BC006467 creatine kinase, mitochondrial 1 (ubiquitous)	Homo sapiens
136 5	J04469	2197	100	creatine kinase	Homo sapiens
136 6	AAH03373	763	100	BC003373 prefoldin 5	Homo sapiens
136 6	AB055803	763	100	MM-1 alpha	Homo sapiens
136 6	D89667	763	100	c-myc binding protein	Homo sapiens
136 7	AAH05939	998	100	BC005939 prostaglandin D2 synthase (21kD, brain)	Homo sapiens
136 7	AY026356	998	100	prostaglandin D synthase	Homo sapiens
136 7	M98539	998	100	prostaglandin D2 synthase	Homo sapiens
136 8	AAH00045	1388	100	BC000045 TONDU	Homo sapiens
136 8	AAH03362	1388	100	BC003362 TONDU	Homo sapiens
136 8	Z97632	1388	100	dJ196E23.1.1 (novel protein) (isoform 1)	Homo sapiens
136 9	AAH03366	796	100	BC003366 calcium-regulated heat-stable protein (24kD)	Homo sapiens
136 9	AF115345_1	787	99	AF115345 calcium-regulated heat stable protein CRHSP-24	Homo sapiens
136 9	AF115346_1	785	97	AF115346 calcium-regulated heat stable protein CRHSP-24	Rattus sp.
137 0	AAH03369	581	100	BC003369 ribosomal protein, large, P1	Homo sapiens
137 0	AAH07590	581	100	BC007590 ribosomal protein, large, P1	Homo sapiens
137 0	AB061836	581	100	ribosomal protein P1	Homo sapiens
137 1	AAH03377	550	100	BC003377 Similar to thioredoxin	Homo sapiens
137 1	AF313911_1	550	100	AF313911 thioredoxin	Homo sapiens
137 1	AY004872	550	100	thioredoxin	Homo sapiens
137 2	BC032493	1086	100	cysteine and glycine-rich protein 1	Homo sapiens
137 2	M33146	1086	100	cysteine-rich protein	Homo sapiens
137 2	M76378	1086	100	cysteine-rich protein	Homo sapiens
137 3	AAH03382	2620	100	BC003382 sorting nexin 2	Homo sapiens
137 3	AF065482	2612	99	sorting nexin 2	Homo sapiens
137 3	AK075929	2564	98	unnamed protein product	Mus musculus
137 4	AAH03394	1485	100	BC003394 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
137 4	AAH08364	1478	99	BC008364 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
137 4	AAH08423	1461	95	BC008423 heterogeneous nuclear ribonucleoprotein C (C1/C2)	Homo sapiens
137 5	AAH03501	2155	100	BC003501 Similar to RIKEN cDNA 2310001A20 gene	Homo sapiens
137 5	AB033767	2155	100	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	Homo sapiens
137	AL035661	2155	100	dJ568C11.2 (chromosome 20 open	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
5				reading frame 3)	
137 6	AAH03512	3204	100	BC003512 mesothelin	Homo sapiens
137 6	AE006464_21	3189	99	AE006464 pre-pro-megakaryocyte potentiating factor precursor	Homo sapiens
137 6	D49441	3192	99	pre-pro-megakaryocyte potentiating factor	Homo sapiens
137 7	AAH03077	5288	100	BC003077 Similar to ATPase, Na+K+ transporting, alpha 1 polypeptide	Homo sapiens
137 7	D00099	5288	100	Na,K-ATPase alpha-subunit	Homo sapiens
137 7	X04297	5288	100	ATPase alpha subunit (aa 1-1023)	Homo sapiens
137 8	AAH03079	786	100	BC003079 16.7Kd protein	Homo sapiens
137 8	AAH15639	786	100	BC015639 16.7Kd protein	Homo sapiens
137 8	AF078845	786	100	16.7Kd protein	Homo sapiens
137 9	AAH00161	1827	100	BC000161 secretory carrier membrane protein 3	Homo sapiens
137 9	AAH05135	1827	100	BC005135 secretory carrier membrane protein 3	Homo sapiens
137 9	AF005039	1817	99	secretory carrier membrane protein	Homo sapiens
138 0	AAH08704	887	100	BC008704 cytochrome c oxidase subunit IV	Homo sapiens
138 0	AAH21236	887	100	BC021236 cytochrome c oxidase subunit IV isoform 1	Homo sapiens
138 0	X54802	887	100	cytochrome-c oxidase subunit IV	Homo sapiens
138 1	AAH00915	1731	100	BC000915 PDZ and LIM domain 1 (elfin)	Homo sapiens
138 1	AAH18755	1731	100	BC018755 PDZ and LIM domain 1 (elfin)	Homo sapiens
138 1	AJ310549	1731	100	CLP-36 protein	Homo sapiens
138 2	AF236636	1302	98	uridine-cytidine kinase 2	Mus musculus
138 2	AF236637	1333	100	uridine-cytidine kinase 2	Homo sapiens
138 2	BC023789	1302	98	uridine-cytidine kinase 2	Mus musculus
138 3	AAH00176	940	100	BC000176 RAP1B, member of RAS oncogene family	Homo sapiens
138 3	AF493913_1	940	100	AF493913 Ras family small GTP binding protein RAP1B	Homo sapiens
138 3	BC033382	1016	91	RAP1B, member of RAS oncogene family	Mus musculus
138 4	D63519	870	100	leptin	Homo sapiens
138 4	D63710	870	100	ob protein	Homo sapiens
138 4	U43653	870	100	obese protein	Homo sapiens
138 5	BC002088	637	100	ribosomal protein S25	Mus musculus
138 5	BC027208	637	100	ribosomal protein S25	Mus musculus
138 5	X62482	637	100	ribosomal protein S25	Rattus rattus
138 6	AAH03662	2092	100	BC003662 KIAA0111 gene product	Homo sapiens
138 6	AAH04386	2092	100	BC004386 KIAA0111 gene product	Homo sapiens
138 6	AAH11151	2092	100	BC011151 Similar to KIAA0111 gene product	Homo sapiens
138 7	AF349038_1	1780	100	AF349038 TFIID subunit TAFII55	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1387	BC032737	1780	100	similar to TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55 kD	Homo sapiens
1387	X97999	1780	100	transcription factor IID	Homo sapiens
1388	AAH02601	1673	100	BC002601 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Homo sapiens
1388	AAH04983	1673	100	BC004983 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Homo sapiens
1388	AY033600	1673	100	NFKBIA	Homo sapiens
1389	AF211480_1	2102	100	AF211480 CD001	Homo sapiens
1389	AK002102	2086	100	unnamed protein product	Homo sapiens
1389	AX191505	2086	100	unnamed protein product	Homo sapiens
1390	AAH05110	4609	100	BC005110 Unknown (protein for MGC:13217)	Homo sapiens
1390	AK049371	4473	93	unnamed protein product	Mus musculus
1390	AY044865	4609	100	sorting nexin 14	Homo sapiens
1391	AAH05118	592	100	BC005118 Similar to putative translation initiation factor	Homo sapiens
1391	AAH08710	592	100	BC008710 putative translation initiation factor	Homo sapiens
1391	AF083441_1	592	100	AF083441 SUI1 isolog	Homo sapiens
1392	AAH05127	2190	100	BC005127 adipose differentiation-related protein	Homo sapiens
1392	AF443203_1	2190	100	AF443203 adipose differentiation-related protein	Homo sapiens
1392	AX025098	2181	99	unnamed protein product	Homo sapiens
1393	AAH05143	964	100	BC005143 vitamin A responsive; cytoskeleton related	Homo sapiens
1393	AAH20797	964	100	BC020797 vitamin A responsive; cytoskeleton related	Homo sapiens
1393	AY102608	964	100	JWA protein	Homo sapiens
1394	AAH05228	360	100	BC005228 Unknown (protein for MGC:12250)	Homo sapiens
1395	AF072506	2871	100	envelope protein precursor	Homo sapiens
1395	AF208161	2868	99	syncytin precursor	Homo sapiens
1395	AF513360_1	2868	99	AF513360 enverin	Homo sapiens
1396	AAH05322	1866	100	BC005322 decorin	Homo sapiens
1396	AF138300	1866	100	decorin variant A	Homo sapiens
1396	AF491944_1	1866	100	AF491944 decorin	Homo sapiens
1397	AAH01392	827	100	BC001392 ribosomal protein S27a	Homo sapiens
1397	D83209	827	100	ubiquitin extention protein	Cavia porcellus
1397	M24507	827	100	ubiquitin	synthetic construct
1398	AAH05330	1306	100	BC005330 tissue factor pathway inhibitor 2	Homo sapiens
1398	AF217542	1306	100	tissue factor pathway inhibitor 2	Homo sapiens
1398	D29992	1306	100	placental protein 5 (PP5)	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
1399	AAH05361	1334	100	BC005361 proteasome (prosome, macropain) subunit, alpha type, 4	Homo sapiens
1399	BC022445	1334	100	proteasome (prosome, macropain) subunit, alpha type, 4	Homo sapiens
1399	D00763	1334	100	proteasome subunit C9	Homo sapiens
1400	AAH05366	1298	100	BC005366 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Homo sapiens
1400	AAH16350	1298	100	BC016350 Unknown (protein for MGC:24431)	Homo sapiens
1400	AL390195	1298	100	bA552M11.3 (ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1)	Homo sapiens
1401	AAH05390	1993	100	BC005390 Unknown (protein for MGC:12520)	Homo sapiens
1401	AF006305	1993	100	26S proteasome regulatory subunit	Homo sapiens
1401	U36395	1993	100	conserved ATPase domain protein 44	Spermophilus tridecemlineatus
1402	AAH10370	1800	99	BC010370 Putative prostate cancer tumor suppressor	Homo sapiens
1402	U42349	1826	100	39 kDa encoded by N33	Homo sapiens
1402	U42360	1808	99	N33 protein form 1	Homo sapiens
1403	AAH05839	1492	100	BC005839 follistatin-like 3 (secreted glycoprotein)	Homo sapiens
1403	BC033119	1492	100	follistatin-like 3 (secreted glycoprotein)	Homo sapiens
1403	U76702	1492	100	follistatin-related protein FLRG	Homo sapiens
1404	AAH05354	564	100	BC005354 ribosomal protein, large P2	Homo sapiens
1404	AAH05920	564	100	BC005920 ribosomal protein, large P2	Homo sapiens
1404	AAH07573	564	100	BC007573 ribosomal protein, large P2	Homo sapiens
1405	AAH17660	414	100	BC017660 Unknown (protein for MGC:14608)	Homo sapiens
1405	AJ249731	414	100	putative G8.2 protein	Homo sapiens
1405	AP000503	414	100	unknown function	Homo sapiens
1406	AAH05966	647	100	BC005966 ring finger protein 7	Homo sapiens
1406	AAH08627	647	100	BC008627 ring finger protein 7	Homo sapiens
1406	AF092878_1	647	100	AF092878 zinc RING finger protein SAG	Homo sapiens
1407	AAH05975	1163	100	BC005975 calcyclin binding protein	Homo sapiens
1407	AF314752_1	1163	100	AF314752 calcyclin binding protein	Homo sapiens
1407	BC022352	1163	100	Siah-interacting protein	Homo sapiens
1408	AAH06337	739	100	BC006337 Unknown (protein for MGC:12798)	Homo sapiens
1408	M37194	739	100	clathrin-associated protein 17	Rattus norvegicus
1408	X97074	729	98	clathrin-associated protein	Homo sapiens
1409	AAH01928	3365	100	BC001928 protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Homo sapiens
1409	AAH06344	3365	100	BC006344 protein disulfide isomerase related protein	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
				(calcium-binding protein, intestinal-related)	
1409	AAH11754	3365	100	BC011754 Similar to protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Homo sapiens
1410	AF453478_1	1155	100	AF453478 phosphopantetheine adenylyltransferase / dephosphocoenzyme A kinase	Homo sapiens
1410	AY094602	1155	100	bifunctional phosphopantetheine adenylyl transferase / dephospho CoA kinase	Homo sapiens
1410	BC020985	1155	100	Unknown (protein for MGC:9724)	Homo sapiens
1411	AAH06393	2797	100	BC006393 Similar to carboxypeptidase Z	Homo sapiens
1411	AF017638	2419	86	carboxypeptidase Z	Rattus norvegicus
1411	U83411	2787	99	carboxypeptidase Z precursor	Homo sapiens
1412	AF126110_1	3913	100	AF126110 fibulin-1 isoform D precursor	Homo sapiens
1412	U01244	3913	100	fibulin-1D	Homo sapiens
1412	X70854	3392	84	BM-90/fibulin	Mus musculus
1413	AAH02343	2494	100	BC002343 Similar to nucleolin	Homo sapiens
1413	AAH06494	2494	100	BC006494 Unknown (protein for MGC:1440)	Homo sapiens
1413	AAH06516	2494	100	BC006516 Unknown (protein for MGC:3588)	Homo sapiens
1414	AAH20515	772	100	BC020515 ribosomal protein S14	Homo sapiens
1414	M11241	772	100	ribosomal protein S14	Cricetulus griseus
1414	M35008	772	100	ribosomal protein S14	Cricetulus griseus
1415	AAH08926	796	98	BC008926 ribosomal protein L29	Homo sapiens
1415	U10248	796	98	ribosomal protein L29	Homo sapiens
1415	U49083	796	98	HIP	Homo sapiens
1416	AAH06791	1105	100	BC006791 ribosomal protein L10a	Homo sapiens
1416	AAH11366	1105	100	BC011366 Similar to ribosomal protein L10a	Homo sapiens
1416	X93352	1105	100	ribosomal protein L10a	Rattus norvegicus
1417	AAH01418	1132	100	BC001418 Similar to RIKEN cDNA 1810017F10 gene	Homo sapiens
1417	AAH13953	1132	100	BC013953 Unknown (protein for MGC:2853)	Homo sapiens
1417	AY027543	1132	100	beta-casein-like protein	Homo sapiens
1418	AAH07038	1762	100	BC007038 lumican	Homo sapiens
1418	BC035997	1762	100	lumican	Homo sapiens
1418	U21128	1762	100	lumican	Homo sapiens
1419	AAH03609	1441	100	BC003609 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
1419	AAH07107	1441	100	BC007107 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
1419	AAH16770	1441	100	BC016770 thioredoxin peroxidase (antioxidant enzyme)	Homo sapiens
142	AAH07282	952	100	BC007282 Unknown (protein for	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
0				MGC:15626)	
1420	AK014338	909	97	unnamed protein product	Mus musculus
1420	M83751	937	98	arginine-rich protein	Homo sapiens
1421	AAH07402	1005	100	BC007402 apolipoprotein D	Homo sapiens
1421	J02611	1005	100	apolipoprotein D precursor	Homo sapiens
1421	M16696	1005	100	apolipoprotein D precursor	Homo sapiens
1422	AAH01603	849	100	BC001603 Similar to ribosomal protein L21	Homo sapiens
1422	AAH07505	849	100	BC007505 Unknown (protein for MGC:4136)	Homo sapiens
1422	X89401	849	100	ribosomal protein L21	Homo sapiens
1423	AAH07507	605	100	BC007507 ribosomal protein S20	Homo sapiens
1423	BC011323	605	100	Similar to ribosomal protein S20	Mus musculus
1423	X51537	605	100	ribosomal protein S20 (AA 1-119)	Rattus rattus
1424	AAH14459	791	100	BC014459 Similar to ribosomal protein L23a	Homo sapiens
1424	BC029892	791	100	ribosomal protein L23a	Mus musculus
1424	X65228	791	100	ribosomal protein L23a	Rattus rattus
1425	AJ420896	2114	99	SPPL2a protein	Homo sapiens
1425	AK027446	2126	100	unnamed protein product	Homo sapiens
1425	BC025740	2114	99	Similar to hypothetical protein FLJ14540	Homo sapiens
1426	AF036548	573	83	RGC-32	Rattus norvegicus
1426	AF036549_1	569	100	AF036549 RGC32	Homo sapiens
1426	AL354833	629	92	ba157L14.2 (RGC32, a novel gene induced by complement activation in oligodendrocytes)	Homo sapiens
1427	AAH01024	2749	99	BC001024 putative nucleotide binding protein, estradiol-induced	Homo sapiens
1427	AK027514	2756	100	unnamed protein product	Homo sapiens
1427	AK027516	2753	99	unnamed protein product	Homo sapiens
1428	AAH07834	563	100	BC007834 Unknown (protein for MGC:14141)	Homo sapiens
1429	AAH03061	2338	99	BC003061 protease, cysteine, 1 (legumain)	Homo sapiens
1429	D55696	2335	99	cysteine protease	Homo sapiens
1429	Y09862	2339	100	legumain	Homo sapiens
1430	AAH08081	1095	100	BC008081 Similar to KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Homo sapiens
1430	AAH14568	1095	100	BC014568 Similar to KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	Homo sapiens
1430	X63745	1095	100	KDEL receptor	Homo sapiens
1431	AF004877	7574	99	pro-alpha 2(I) collagen	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
143 1	J03464	7554	99	pre-pro-alpha-2 type I collagen	Homo sapiens
143 1	Z74616	7596	100	prepro-alpha2(I) collagen	Homo sapiens
143 2	AAH08188	946	100	BC008188 Unknown (protein for MGC:5243)	Homo sapiens
143 2	AF021819	946	100	RNA-binding protein regulatory subunit	Homo sapiens
143 2	AL034417	946	100	bK215D11.1 (RNA-binding protein regulatory subunit)	Homo sapiens
143 3	AAH08283	594	100	BC008283 cholecystokinin	Homo sapiens
143 3	L00354	594	100	cholecystokinin	Homo sapiens
143 3	M60458	569	95	cholecystokinin	Macaca fascicularis
143 4	AAH06794	693	99	BC006794 Similar to interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
143 4	AAH08417	698	100	BC008417 Similar to interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
143 4	BC022439	698	100	interferon induced transmembrane protein 3 (1-8U)	Homo sapiens
143 5	AAH05993	1421	100	BC005993 Unknown (protein for MGC:14796)	Homo sapiens
143 5	AAH08691	1421	100	BC008691 Unknown (protein for MGC:8886)	Homo sapiens
143 5	AAH15644	1421	100	BC015644 Ras suppressor protein 1	Homo sapiens
143 6	AAH08938	1942	100	BC008938 Similar to histocompatibility 13	Homo sapiens
143 6	AAH08959	1942	100	BC008959 Similar to histocompatibility 13	Homo sapiens
143 6	AF483215_1	1934	99	AF483215 minor histocompatibility antigen H13 isoform 1	Homo sapiens
143 7	AAH16320	2150	100	BC016320 cathepsin D (lysosomal aspartyl protease)	Homo sapiens
143 7	M11233	2150	100	preprocathepsin D	Homo sapiens
143 7	X05344	2150	100	precursor polypeptide (AA -20 to 392)	Homo sapiens
143 8	AAH08983	1364	100	BC008983 complement component 1, q subcomponent, beta polypeptide	Homo sapiens
143 8	X03084	1240	100	Clq B-chain precursor	Homo sapiens
143 8	X16874	1075	79	precursor polypeptide (AA -25 to 228)	Mus musculus
143 9	AAH09177	1014	100	BC009177 ras homolog gene family, member C	Homo sapiens
143 9	AF498972_1	1014	100	AF498972 small GTP binding protein RhoC	Homo sapiens
143 9	BC004627	1014	100	ras homolog gene family, member C	Mus musculus
144 0	AAH09200	1068	100	BC009200 Rho GDP dissociation inhibitor (GDI) beta	Homo sapiens
144 0	AF498927_1	1068	100	AF498927 Rho GDP dissociation inhibitor beta	Homo sapiens
144 0	X69549	1068	100	Human rho GDP-dissociation Inhibitor 2(IEF 8120)	Homo sapiens
144 1	AAH09201	1137	100	BC009201 clathrin, light polypeptide (Lca)	Homo sapiens
144 1	AAH19287	1137	100	BC019287 clathrin, light polypeptide (Lca)	Homo sapiens
144 1	AL158830	1137	100	bA421H8.4.2 (clathrin, light polypeptide (LCA))	Homo sapiens
144 2	AAH09232	596	100	BC009232 Similar to G antigen 8	Homo sapiens
144	AJ318880	596	100	XAGE-2 protein	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
2					
144 2	AJ318891	596	100	XAGE-2 protein	Homo sapiens
144 3	AAH03378	1149	100	BC003378 high-mobility group (nonhistone chromosomal) protein 1	Homo sapiens
144 3	BC030981	1149	100	high-mobility group (nonhistone chromosomal) protein 1	Homo sapiens
144 3	X12597	1149	100	HMG-1 protein (AA 1-215)	Homo sapiens
144 4	AB002368	5586	100	KIAA0370	Homo sapiens
144 4	AY026388	5765	100	ran binding protein RanBP20	Homo sapiens
144 4	AY029528	5663	97	RANBP20	Mus musculus
144 5	AAH09799	1308	100	BC009799 amphiregulin (schwannoma-derived growth factor)	Homo sapiens
144 5	M30703	1308	100	amphiregulin	Homo sapiens
144 5	M30704	1308	100	amphiregulin	Homo sapiens
144 6	AAH09869	511	100	BC009869 Unknown (protein for MGC:16406)	Homo sapiens
144 6	AAH15491	511	100	BC015491 Unknown (protein for MGC:8965)	Homo sapiens
144 6	BC022326	511	100	Unknown (protein for MGC:22741)	Homo sapiens
144 7	AAH09898	1921	100	BC009898 spermine synthase	Homo sapiens
144 7	AD001528	1921	100	spermidine aminopropyltransferase	Homo sapiens
144 7	Z49099	1916	100	spermine synthase	Homo sapiens
144 8	AL365410	1055	100	hypothetical protein	Homo sapiens
144 9	AAH10016	1542	100	BC010016 Similar to CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	Homo sapiens
144 9	AAH12884	1542	100	BC012884 Unknown (protein for MGC:9240)	Homo sapiens
144 9	Z25521	1542	100	integrin associated protein	Homo sapiens
145 0	AAH10055	784	100	BC010055 hypothetical protein PRO2605	Homo sapiens
145 0	AF116721_109	642	100	AF116709 PRO2605	Homo sapiens
145 1	AAH04976	634	100	BC004976 Unknown (protein for IMAGE:2958115)	Homo sapiens
145 1	AAH10076	634	100	BC010076 Unknown (protein for MGC:19576)	Homo sapiens
145 1	AY061855	634	100	mitochondrial ribosomal protein S6	Homo sapiens
145 2	AAH10129	907	100	BC010129 Similar to hypothetical protein R33729 1	Homo sapiens
145 2	AAH14655	907	100	BC014655 Unknown (protein for MGC:20383)	Homo sapiens
145 2	AL365374	894	100	R33729_1 hypothetical protein	Homo sapiens
145 3	AB028894	824	100	ribosomal protein S11	Mus musculus
145 3	BC012641	824	100	ribosomal protein S11	Mus musculus
145 3	U93864	824	100	ribosomal protein S11	Mus musculus
145 4	BC002077	1058	100	RAB1, member RAS oncogene family	Mus musculus
145	X15744	1058	100	GTP-binding protein	Mus musculus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
4					
145 4	Y00094	1058	100	Ypt1 protein (AA 1-205)	Mus musculus
145 5	AAH02947	1482	100	BC002947 folate receptor 1 (adult)	Homo sapiens
145 5	U20391	1482	100	folate receptor	Homo sapiens
145 5	X62753	1482	100	adult folate binding protein	Homo sapiens
145 6	U65932	3016	100	extracellular matrix protein 1	Homo sapiens
145 6	U65938	3016	100	extracellular matrix protein 1	Homo sapiens
145 6	U68186	3016	100	extracellular matrix protein 1	Homo sapiens
145 7	AAH10897	541	100	BC010897 Similar to JM27 protein	Homo sapiens
145 7	AF275258_1	541	100	AF275258 PAGE-4	Homo sapiens
145 7	AJ005894	541	100	JM27	Homo sapiens
145 8	AAH11171	2528	100	BC011171 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1	Homo sapiens
145 8	AF435921_1	2524	99	AF435921 C1 esterase inhibitor	Homo sapiens
145 8	X07427	2524	99	C1 inhibitor	Homo sapiens
145 9	D38112	1803	93	cytochrome b	Homo sapiens
145 9	U09500	1802	93	cytochrome b	Homo sapiens
145 9	V00662	1807	93	cytochrome B	Homo sapiens
146 0	AAH11514	696	100	BC011514 Similar to ribosomal protein L32	Homo sapiens
146 0	K02060	696	100	ribosomal protein L32-3A	Mus musculus
146 0	X06483	696	100	ribosomal protein L32	Rattus norvegicus
146 1	AAH11786	645	100	BC011786 Unknown (protein for MGC:19839)	Homo sapiens
146 1	AF318382_1	645	100	AF318382 unknown	Homo sapiens
146 1	X07868	456	100	1.8 kb mRNA (AA 1-84)	Homo sapiens
146 2	AAH11792	1649	100	BC011792 Unknown (protein for MGC:19561)	Homo sapiens
146 2	AAH17408	1643	99	BC017408 Unknown (protein for MGC:27221)	Homo sapiens
146 2	U16660	1603	97	peroxisomal enoyl-CoA hydratase-like protein	Homo sapiens
146 3	AAH00159	2163	100	BC000159 keratin 17	Homo sapiens
146 3	AAH11901	2163	100	BC011901 Similar to keratin 17	Homo sapiens
146 3	X62571	2163	100	keratin related product	Homo sapiens
146 4	AAH12132	3933	100	BC012132 Similar to DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	Homo sapiens
146 4	BC010624	3872	97	Unknown (protein for MGC:11570)	Mus musculus
146 4	X70649	3933	100	member of DEAD box protein family	Homo sapiens
146 5	AF157623_1	2466	100	AF157623 HTRA serine protease	Homo sapiens
146 5	D87258	2466	100	serin protease with IGF-binding motif	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1465	Y07921	2466	100	novel serine protease, PRSS11	Homo sapiens
1466	AF242550_1	1030	100	AF242550 cellular nucleic acid binding protein	Rattus norvegicus
1466	AF389887	1030	100	zinc finger protein 9	Homo sapiens
1466	D45254	1030	100	Cellular Nucleic Acid Binding Protein	Rattus norvegicus
1467	AAH14277	1191	100	BC014277 Similar to tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	Homo sapiens
1467	U33114	1191	100	tissue inhibitor of metalloproteinases-3	Homo sapiens
1467	X76227	1191	100	tissue inhibitor of metalloproteinases-3	Homo sapiens
1468	AAH12384	1017	100	BC012384 Similar to programmed cell death 6	Homo sapiens
1468	AF035606	1017	100	calcium binding protein	Homo sapiens
1468	U58773_1	1017	100	U58773 calcium binding protein	Homo sapiens
1469	AAH12464	755	100	BC012464 prefoldin 2	Homo sapiens
1469	AF117237_1	755	100	AF117237 prefoldin subunit 2	Homo sapiens
1469	BC026839	729	96	Similar to prefoldin 2	Mus musculus
1470	AAH08230	849	100	BC008230 ribosomal protein L12	Homo sapiens
1470	BC018321	848	99	ribosomal protein L12	Mus musculus
1470	L06505	849	100	ribosomal protein L12	Homo sapiens
1471	AAH12606	1665	100	BC012606 Similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	Homo sapiens
1471	D50063	1637	98	proteasome subunit p40 / Mov34 protein	Homo sapiens
1471	M64640	1597	96	36 kD protein	Mus musculus
1472	AAH11835	1485	100	BC011835 Similar to ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide	Homo sapiens
1472	AF005896	1485	100	Na K-ATPase beta-3 subunit	Homo sapiens
1472	U51478	1485	100	sodium/potassium-transporting ATPase beta-3 subunit	Homo sapiens
1473	AAH13041	5526	100	BC013041 Unknown (protein for MGC:4781)	Homo sapiens
1473	M58028	5526	100	ubiquitin-activating enzyme E1	Homo sapiens
1473	X56976	5516	99	ubiquitin activating enzyme E1	Homo sapiens
1474	AAH13162	491	100	BC013162 Similar to heat shock protein, 30 kDa	Homo sapiens
1474	AF085359	491	100	HSPC030	Homo sapiens
1474	AF537132	491	100	selenoprotein K	Homo sapiens
1475	AAH13175	992	100	BC013175 Similar to novel RGD-containing protein	Homo sapiens
1475	BC029249	958	96	dynactin 6	Mus musculus
1475	D84145	992	100	WS-3	Homo sapiens
1476	BC003825	2344	100	tubulin, beta 5	Mus musculus
147	X04663	2344	100	beta-tubulin AA 1-444 (79 is 1st	Mus musculus

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
6				base in codon)	
147 6	X07011	2344	100	c(beta)7 tubulin (AA 1 - 444)	Gallus gallus
147 7	A47413	3336	96	CALPASTATINE HUMAINE	Homo sapiens
147 7	AAH13579	3420	100	BC013579 Similar to calpastatin	Homo sapiens
147 7	D16217	3340	93	calpastatin	Homo sapiens
147 8	BC024378	567	100	defender against cell death 1	Mus musculus
147 8	Y13335	567	100	DAD-1	Mus musculus
147 8	Y13336	567	100	DAD-1	Rattus norvegicus
147 9	AAH13975	3963	100	BC013975 Similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	Homo sapiens
147 9	BC024220	3963	100	Unknown (protein for MGC:1483)	Homo sapiens
147 9	U28369	3951	99	semaphorin V	Homo sapiens
148 0	AAH14142	3503	100	BC014142 Similar to glucuronidase, beta	Homo sapiens
148 0	AX147652	3496	99	unnamed protein product	Homo sapiens
148 0	M15182	3496	99	beta-glucuronidase precursor (EC 3.2.1.31)	Homo sapiens
148 1	AB022163	2024	92	mouse ortholog of the zebrafish hagoromo gene	Mus musculus
148 1	AF281859	2217	100	dactylin	Homo sapiens
148 1	BC027031	2024	92	f-box and WD-40 domain protein 4	Mus musculus
148 2	AAH01377	1114	100	BC001377 DKFZP586G1722 protein	Homo sapiens
148 2	AAH06514	1114	100	BC006514 DKFZP586G1722 protein	Homo sapiens
148 2	AAH14391	1114	100	BC014391 DKFZP586G1722 protein	Homo sapiens
148 3	AF159256_1	1147	100	AF159256 Lps/Ran GTPase	Mus musculus
148 3	AF306457_1	1147	100	AF306457 GTPase	Rattus norvegicus
148 3	BC014829	1147	100	RAN, member RAS oncogene family	Mus musculus
148 4	AAH15000	1347	100	BC015000 Similar to major histocompatibility complex, class II, DP beta 1	Homo sapiens
148 4	M57466	1306	96	light chain	Homo sapiens
148 4	X01426	1301	96	SB-2-beta precursor polypeptide (aa -29 to 229)	Homo sapiens
148 5	AAH15039	1006	100	BC015039 microfibrillar-associated protein 2	Homo sapiens
148 5	AL049569	1006	100	dJ37C10.4 (microfibrillar-associated protein 2 (microfibril-associated glycoprotein precursor, MGAP1))	Homo sapiens
148 5	U19718	1006	100	microfibril-associated glycoprotein	Homo sapiens
148 6	AF117383_1	746	100	AF117383 placental protein 13; PPI3	Homo sapiens
148 6	AY055826	746	100	placenta protein 13	Homo sapiens
148 6	BC022257	510	69	Similar to placental protein 13-like protein	Homo sapiens
148	AAH02387	2063	100	BC002387 nucleosome assembly	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
7				protein 1-like 1	
148 7	AAH15599	2063	100	BC015599 nucleosome assembly protein 1-like 1	Homo sapiens
148 7	AL162068	2063	100	hypothetical protein	Homo sapiens
148 8	A03911	2017	99	glia-derived neurite-promoting factor (GdNPF)	Homo sapiens
148 8	AAH15663	2040	100	BC015663 Similar to serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	Homo sapiens
148 8	M17783	2016	99	glia-derived nexin precursor	Homo sapiens
148 9	AAH02403	3107	100	BC002403 lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	Homo sapiens
148 9	AAH02998	3107	100	BC002998 lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	Homo sapiens
148 9	AAH15761	3107	100	BC015761 lectin, galactoside-binding, soluble, 3 binding protein	Homo sapiens
149 0	AAH15032	2122	100	BC015032 ribosomal protein L3	Homo sapiens
149 0	AAH15767	2122	100	BC015767 ribosomal protein L3	Homo sapiens
149 0	BC008003	2122	100	ribosomal protein L3	Homo sapiens
149 1	AF052694	2391	100	alpha-tubulin	Meriones unguiculatus
149 1	BC002219	2391	100	Similar to tubulin alpha 1	Mus musculus
149 1	BC008117	2391	100	tubulin alpha 1	Mus musculus
149 2	AAH21822	264	71	BC021822 Unknown (protein for MGC:24986)	Homo sapiens
149 2	AK025116	265	71	unnamed protein product	Homo sapiens
149 2	AK090511	279	71	unnamed protein product	Homo sapiens
149 3	AAH02449	1196	99	BC002449 Similar to CG10641 gene product	Homo sapiens
149 3	AAH04128	1331	99	BC004128 Unknown (protein for IMAGE:3940060)	Homo sapiens
149 3	AK023674	1199	100	unnamed protein product	Homo sapiens
149 4	AAH01537	2971	100	BC001537 Unknown (protein for MGC:786)	Homo sapiens
149 4	AB021743	2968	99	PR65	Mus musculus
149 4	BC006606	2968	99	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Mus musculus
149 5	AAH09642	939	100	BC009642 FXD domain-containing ion transport regulator 5	Homo sapiens
149 5	AB072911	939	100	dysadherin	Homo sapiens
149 5	AF161462_1	923	98	AF161462 HSPC113	Homo sapiens
149 6	AAH09687	869	100	BC009687 epithelial membrane protein 2	Homo sapiens
149 6	AY057060	869	100	epithelial membrane protein 2	Homo sapiens
149 6	U52100	869	100	XMP	Homo sapiens
149	AB012214	6727	78	DNA cytosine 5 methyltransferase	Rattus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
7					rattus
1497	AF180682	6869	100	DNA (cytosine-5)-methyltransferase	Homo sapiens
1497	X63692	8587	100	DNA (cytosine-5)-methyltransferase	Homo sapiens
1498	AAH15961	961	100	BC015961 adrenomedullin	Homo sapiens
1498	D14874	961	100	adrenomedullin precursor	Homo sapiens
1498	S73906	961	100	adrenomedullin; AM	Homo sapiens
1499	AAH15973	514	100	BC015973 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))	Homo sapiens
1499	M38591	514	100	cellular ligand of annexin II	Homo sapiens
1499	M81457	514	100	calpactin I light chain	Homo sapiens
1500	AAH16056	1137	100	BC016056 claudin 3	Homo sapiens
1500	AB000714	1137	100	RVP1	Homo sapiens
1500	AF007189	1137	100	claudin 3	Homo sapiens
1501	AAH16142	1432	100	BC016142 Similar to RIKEN cDNA 2310032N20 gene	Homo sapiens
1501	AAH20773	1432	100	BC020773 Unknown (protein for MGC:22685)	Homo sapiens
1501	AX405824	1432	100	unnamed protein product	Homo sapiens
1502	AF315378_1	1955	98	AF315378 suppressor of profilin/p41 of actin-related complex 2/3	Rattus norvegicus
1502	BC039594	1964	99	actin related protein 2/3 complex, subunit 1A, 41kDa	Homo sapiens
1502	Y08999	1980	100	Sop2p-like protein	Homo sapiens
1503	AF492677_1	383	100	AF492677 odd homeobox 1 protein isoform A	Homo sapiens
1503	AF492680_1	383	100	AF492680 odd homeobox 1 protein isoform A	Homo sapiens
1503	AF492681_1	383	100	AF492681 odd homeobox 1 protein isoform A	Homo sapiens
1504	AK056992	2163	100	unnamed protein product	Homo sapiens
1504	AX392121	2155	99	unnamed protein product	Homo sapiens
1504	AY033237	2155	99	alcohol dehydrogenase 8	Homo sapiens
1505	AAH16748	485	100	BC016748 ribosomal protein L37a	Homo sapiens
1505	X14069	485	100	ribosomal protein L37a (AA 1 - 92)	Rattus rattus
1505	X73331	485	100	ribosomal protein L37a	Mus musculus
1506	AAH12807	3702	100	BC012807 Unknown (protein for MGC:3483)	Homo sapiens
1506	AAH14485	3702	100	BC014485 Unknown (protein for MGC:23206)	Homo sapiens
1506	AAH16753	3702	100	BC016753 Unknown (protein for MGC:1138)	Homo sapiens
1507	AAH15834	1724	100	BC015834 annexin A2	Homo sapiens
1507	AAH16774	1724	100	BC016774 annexin A2	Homo sapiens
1507	AAH21114	1724	100	BC021114 annexin A2	Homo sapiens
150	AAH17343	644	100	BC017343 ribosomal protein L31	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
8					
1508	BC008223	644	100	ribosomal protein L31	Mus musculus
1508	X04809	644	100	ribosomal protein L31 (AA 1-125)	Rattus norvegicus
1509	AAH17378	2955	100	BC017378 hexosaminidase B (beta polypeptide)	Homo sapiens
1509	AF378118_1	2955	100	AF378118 cervical cancer proto-oncogene 7	Homo sapiens
1509	M23294	2955	100	beta-hexosaminidase beta-subunit	Homo sapiens
1510	AAH12168	1373	100	BC012168 Similar to proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
1510	AAH17451	1373	100	BC017451 proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
1510	AAH17486	1373	100	BC017486 proteasome (prosome, macropain) subunit, beta type, 4	Homo sapiens
1511	AAH06124	2618	100	BC006124 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
1511	AAH12840	2618	100	BC012840 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
1511	AAH15567	2618	100	BC015567 IMP (inosine monophosphate) dehydrogenase 2	Homo sapiens
1512	AAH07457	1103	100	BC007457 hypothetical protein	Homo sapiens
1512	AAH20796	1103	100	BC020796 hypothetical protein HSPC177	Homo sapiens
1512	AAH21168	1103	100	BC021168 hypothetical protein HSPC177	Homo sapiens
1513	AAH04904	2894	99	BC004904 nuclear RNA export factor 1	Homo sapiens
1513	BC028041	2894	99	nuclear RNA export factor 1	Homo sapiens
1513	U80073	2905	100	tip associating protein	Homo sapiens
1514	AF064238_1	4503	97	AF064238 smoothelin large isoform L2	Homo sapiens
1514	AY061971	4653	100	smoothelin-B2	Homo sapiens
1514	AY061972	4533	96	smoothelin-B3	Homo sapiens
1515	AAH17773	1214	100	BC017773 triggering receptor expressed on myeloid cells 1	Homo sapiens
1515	AF196329_1	1214	100	AF196329 triggering receptor expressed on monocytes 1	Homo sapiens
1515	AF287008_1	1214	100	AF287008 triggering receptor expressed on monocytes 1	Homo sapiens
1516	AAH17891	579	100	BC017891 vesicle-associated membrane protein 5 (myobrevin)	Homo sapiens
1516	AF054825	579	100	VAMP5	Homo sapiens
1516	AF077197	579	100	VAMP5-like protein	Homo sapiens
1517	AAH17931	819	100	BC017931 Similar to RIKEN cDNA 1110055A02 gene	Homo sapiens
1517	AF400652_1	819	100	AF400652 thyroid hormone receptor interacting protein 3	Homo sapiens
1517	L40410	806	100	thyroid receptor interactor	Homo sapiens
1518	AAH18732	1606	100	BC018732 Unknown (protein for MGC:31847)	Homo sapiens
1518	AF125533_1	1606	100	AF125533 NADH-cytochrome b5 reductase isoform	Homo sapiens
1518	AX083421	1606	100	unnamed protein product	Homo sapiens
1519	AAH02453	3263	100	BC002453 heat shock 70kD protein 1A	Homo sapiens
1519	AAH09322	3263	100	BC009322 heat shock 70kD protein	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
9				1A	
151 9	AAH18740	3263	100	BC018740 heat shock 70kD protein 1A	Homo sapiens
152 0	1680052_1	2856	100	S62076 lysosomal enzyme beta-N-acetylhexosaminidase A	Homo sapiens
152 0	AAH18927	2856	100	BC018927 hexosaminidase A (alpha polypeptide)	Homo sapiens
152 0	M16424	2856	100	beta-hexosaminidase alpha chain	Homo sapiens
152 1	AAH12992	2115	99	BC012992 Similar to RNA binding motif, single stranded interacting protein 1	Homo sapiens
152 1	AAH12993	2115	99	BC012993 Similar to RNA binding motif, single stranded interacting protein 1	Homo sapiens
152 1	AAH18951	2142	100	BC018951 RNA binding motif, single stranded interacting protein 1	Homo sapiens
152 2	AAH16346	908	100	BC016346 Unknown (protein for MGC:24392)	Homo sapiens
152 2	AAH16354	908	100	BC016354 Unknown (protein for MGC:24480)	Homo sapiens
152 2	AAH18990	908	100	BC018990 Unknown (protein for MGC:20176)	Homo sapiens
152 3	AAH01206	2235	99	BC001206 Unknown (protein for MGC:3208)	Homo sapiens
152 3	AK025822	3505	99	unnamed protein product	Homo sapiens
152 3	AL833865	3414	100	hypothetical protein	Homo sapiens
152 4	AAH06772	769	100	BC006772 ribosomal protein S13	Homo sapiens
152 4	BC029732	769	100	ribosomal protein S13	Homo sapiens
152 4	X53378	769	100	ribosomal protein S13	Rattus rattus
152 5	J05192	1982	100	alpha-actin	Homo sapiens
152 5	X06801	1968	99	alpha-actin (AA 1-377)	Rattus rattus
152 5	X13297	1968	99	alpha-actin (AA 1-377)	Mus musculus
152 6	AAH00260	1675	99	BC000260 aldo-keto reductase family 1, member B1 (aldose reductase)	Homo sapiens
152 6	AAH10391	1675	99	BC010391 aldo-keto reductase family 1, member B1 (aldose reductase)	Homo sapiens
152 6	J05017	1677	100	aldose reductase	Homo sapiens
152 7	M22246	2623	100	aromatase precursor (EC 1.14.14.1)	Homo sapiens
152 7	X13589	2623	100	aromatase (AA 1-503)	Homo sapiens
152 7	Y07508	2620	99	aromatase (AA 1-503)	Homo sapiens
152 8	M59916	3466	100	acid sphingomyelinase	Homo sapiens
152 8	M81780	3450	99	acid sphingomyelinase	Homo sapiens
152 8	X63600	3461	99	acid sphingomyelinase	Homo sapiens
152 9	AAH21993	1707	100	BC021993 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	Homo sapiens
152 9	M24193	1707	100	MHC B complex protein 12.3	Gallus gallus
152 9	X75313	1707	100	B complex protein mRNA 12-3	Mus musculus

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1530	AAH05358	642	100	BC005358 non-histone chromosome protein 2 (S. cerevisiae)-like 1	Homo sapiens
1530	AAH19282	642	100	BC019282 non-histone chromosome protein 2 (S. cerevisiae)-like 1	Homo sapiens
1530	BC026755	642	100	Similar to sperm specific antigen 1	Mus musculus
1531	AAH19296	2747	100	BC019296 chaperonin containing TCP1, subunit 7 (eta)	Homo sapiens
1531	AF026292	2747	100	chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta	Homo sapiens
1531	BC008255	2628	95	chaperonin subunit 7 (eta)	Mus musculus
1532	BC035220	3879	99	similar to complement component	Homo sapiens
1532	M14058	3885	100	human complement C1r	Homo sapiens
1532	X04701	3879	99	precursor of C1r (AA -17 to 688)	Homo sapiens
1533	J04080	3789	100	complement component C1s	Homo sapiens
1533	M18767	3789	100	complement subcomponent C1s precursor	Homo sapiens
1533	X06596	3789	100	complement protein C1s precursor	Homo sapiens
1534	AAH03175	2072	100	BC003175 N-myc downstream regulated	Homo sapiens
1534	AF004162	2072	100	nickel-specific induction protein	Homo sapiens
1534	D87953	2072	100	RTP	Homo sapiens
1535	AF085250	759	100	calmodulin	Perca flavescens
1535	D83350	759	100	calmodulin	Anas platyrhynchos
1535	K01945	759	100	calmodulin (cDNA clone 71)	Xenopus laevis
1536	AAH07911	2282	100	BC007911 calreticulin	Homo sapiens
1536	AAH20493	2282	100	BC020493 calreticulin	Homo sapiens
1536	AY047586	2282	100	calreticulin	Homo sapiens
1537	AAH16300	533	100	BC016300 S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	Homo sapiens
1537	Z18950	533	100	CAPL	Homo sapiens
1537	Z33457	533	100	mts1	Homo sapiens
1538	AAH01506	710	100	BC001506 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)	Homo sapiens
1538	X16447	710	100	precursor polypeptide (AA -25 to 103)	Homo sapiens
1538	X17198	710	100	CD59 antigen precursor	Homo sapiens
1539	AAH06290	898	100	BC006290 chorionic gonadotropin, beta polypeptide	Homo sapiens
1539	BC022796	898	100	Unknown (protein for MGC:39080)	Homo sapiens
1539	BC030994	898	100	chorionic gonadotropin, beta polypeptide	Homo sapiens
1540	J03225	1674	100	lipoprotein-associated coagulation inhibitor precursor	Homo sapiens
154	M58650	1674	100	lipoprotein associated	Homo sapiens

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0				coagulation inhibitor	
154 0	M59499	1674	100	lipoprotein-associated coagulation inhibitor	Homo sapiens
154 1	AAH14167	1072	100	BC014167 Unknown (protein for MGC:20892)	Homo sapiens
154 1	AAH20804	1072	100	BC020804 ribosomal protein L13	Homo sapiens
154 1	BC027463	1072	100	ribosomal protein L13	Homo sapiens
154 2	AAH21136	1333	100	BC021136 Unknown (protein for MGC:32056)	Homo sapiens
154 2	AF097362_1	1333	100	AF097362 gamma-interferon inducible lysosomal thiol reductase	Homo sapiens
154 2	BC031020	1329	99	interferon, gamma-inducible protein 30	Homo sapiens
154 3	AAH07008	929	100	BC007008 crystallin, alpha B	Homo sapiens
154 3	M28638	929	100	alpha-B2-crystallin	Homo sapiens
154 3	S45630	929	100	alpha B-crystallin	Homo sapiens
154 4	BC003775	1169	99	casein kinase II, beta subunit	Mus musculus
154 4	M30448	1174	100	casein kinase II beta subunit	Homo sapiens
154 4	M59458	1169	99	casein kinase II beta subunit	Gallus gallus
154 5	M77820	6209	50	fibronectin	Xenopus laevis
154 5	X02761	12570	99	fibronectin precursor	Homo sapiens
154 5	X15906	7305	65	precursor polypeptide (AA -32 to 2445)	Rattus norvegicus
154 6	BC032329	2740	99	cytochrome P450, subfamily XIA (cholesterol side chain cleavage)	Homo sapiens
154 6	M14565	2753	100	cholesterol side-chain cleavage enzyme P450scc (EC 1.14.15.67)	Homo sapiens
154 6	X05367	2734	99	desmolase	Homo sapiens
154 7	AF318372_1	592	99	AF318372 unknown	Homo sapiens
154 7	AJ318881	601	100	XAGE-3 protein	Homo sapiens
154 7	AJ318893	601	100	XAGE-3 protein	Homo sapiens
154 8	AAH18641	2406	100	BC018641 eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
154 8	AAH21686	2406	100	BC021686 eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
154 8	BC028674	2406	100	eukaryotic translation elongation factor 1 alpha 1	Homo sapiens
154 9	AAH07044	2377	100	BC007044 fibrinogen, gamma polypeptide	Homo sapiens
154 9	AAH21674	2377	100	BC021674 fibrinogen, gamma polypeptide	Homo sapiens
154 9	AF350254_1	2377	100	AF350254 fibrinogen gamma chain, isoform gamma-A precursor	Homo sapiens
155 0	AAH07785	2357	100	BC007785 Unknown (protein for IMAGE:2819608)	Homo sapiens
155 0	AAH21565	2387	100	BC021565 Unknown (protein for MGC:31904)	Homo sapiens
155 0	AF121858_1	2387	100	AF121858 sorting nexin 8	Homo sapiens
155 1	AAH05929	1222	100	BC005929 proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	Homo sapiens
155	X14088	1222	100	major basic protein precursor (AA	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
1				1-222)	
155 1	Y00809	1222	100	major basic preproprotein (AA -15 to 207)	Homo sapiens
155 2	AL050169	951	100	hypothetical protein	Homo sapiens
155 2	M34046	951	100	placental protein 14 precursor (PP14)	Homo sapiens
155 2	M61886	951	100	pregnancy-associated endometrial alpha2-globulin	Homo sapiens
155 3	AAH15641	2224	100	BC015641 enolase 1, (alpha)	Homo sapiens
155 3	BC022545	2224	100	enolase 1, (alpha)	Homo sapiens
155 3	BC027725	2224	100	enolase 1, (alpha)	Homo sapiens
155 4	AF272142	2649	100	cytochrome P450	Homo sapiens
155 4	BC032594	2649	100	cytochrome P450, subfamily IIJ (arachidonic acid epoxigenase) polypeptide 2	Homo sapiens
155 4	U37143	2649	100	cytochrome P450 monooxygenase CYP2J2	Homo sapiens
155 5	AAH17123	1367	100	BC017123 ribosomal protein S3A	Homo sapiens
155 5	AAH19072	1367	100	BC019072 ribosomal protein S3A	Homo sapiens
155 5	BC030161	1367	100	ribosomal protein S3A	Homo sapiens
155 6	AB042200	2004	88	low-density lipoprotein receptor-related protein 9	Mus musculus
155 6	AL834518	2154	99	hypothetical protein	Homo sapiens
155 6	AX359701	2268	99	unnamed protein product	Homo sapiens
155 7	BC040431	5104	99	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	Homo sapiens
155 7	M34424	5105	100	acid alpha-glucosidase	Homo sapiens
155 7	X55080	5105	100	acid alpha-glucosidase	Homo sapiens
155 8	AAH10914	768	100	BC010914 Similar to hemoglobin, gamma G	Homo sapiens
155 8	BC029387	768	100	hemoglobin, gamma G	Homo sapiens
155 8	M91037	768	100	G-gamma globin	Homo sapiens
155 9	AY148100	4568	100	colony stimulating factor 3 receptor (granulocyte)	Homo sapiens
155 9	M59818	4568	100	granulocyte colony-stimulating factor receptor	Homo sapiens
155 9	X55721	4568	100	granulocyte colony stimulating factor receptor 25-1	Homo sapiens
156 0	AAH00013	1579	100	BC000013 insulin-like growth factor binding protein 3	Homo sapiens
156 0	AAH18962	1579	100	BC018962 insulin-like growth factor binding protein 3	Homo sapiens
156 0	M35878	1579	100	growth factor-binding protein-3 precursor	Homo sapiens
156 1	M23595	1413	100	insulin-like growth factor binding protein 1	Homo sapiens
156 1	M59316	1413	100	insulin-like growth factor binding protein-1	Homo sapiens
156 1	X12385	1413	100	PP12 precursor (AA -25 to 234)	Homo sapiens
156 2	BC041218	676	100	H3 histone, family 3B	Xenopus laevis
156 2	M11393	676	100	histone 3.3	Gallus gallus

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156 2	Y00392	676	100	histone H3.3B (AA 1 - 136)	Gallus gallus
156 3	AF523281	1916	99	MHC class Ib antigen	Homo sapiens
156 3	AF523283	1916	99	MHC class Ib antigen	Homo sapiens
156 3	M20022	1922	100	HLA-E class I protein precursor	Homo sapiens
156 4	AAH03569	1980	100	BC003569 E74-like factor 3 (ets domain transcription factor, epithelial-specific)	Homo sapiens
156 4	AF017307	1980	100	Ets-related transcription factor	Homo sapiens
156 4	AF110184_1	1980	100	AF110184 epithelium-restricted Ets protein ESX	Homo sapiens
156 5	AF523305	1810	100	MHC class Ib antigen	Homo sapiens
156 5	AF523306	1810	100	MHC class Ib antigen	Homo sapiens
156 5	AF523309	1810	100	MHC class Ib antigen	Homo sapiens
156 6	AAH09507	836	99	BC009507 Unknown (protein for MGC:3945)	Homo sapiens
156 6	AY168648	836	99	ubiquitin-like protein ISG15	Homo sapiens
156 6	M13755	839	100	17-kDa protein	Homo sapiens
156 7	AB033054	2567	94	KIAA1228 protein	Homo sapiens
156 7	AF099138	1352	50	GLUT4 vesicle protein	Rattus norvegicus
156 7	BC011482	1348	50	Similar to membrane bound C2 domain containing protein	Mus musculus
156 8	AAH10853	1129	100	BC010853 Similar to integral type I protein	Homo sapiens
156 8	AAH17495	1129	100	BC017495 integral type I protein	Homo sapiens
156 8	BC022232	1129	100	integral type I protein	Homo sapiens
156 9	AF357203_1	1832	97	AF357203 MAP kinase phosphatase-1	Rattus norvegicus
156 9	BC022463	1886	100	dual specificity phosphatase 1	Homo sapiens
156 9	X68277	1886	100	protein-tyrosine phosphatase	Homo sapiens
157 0	AAH09407	687	100	BC009407 ribosomal protein S17	Homo sapiens
157 0	AAH19899	687	100	BC019899 ribosomal protein S17	Homo sapiens
157 0	BC022370	687	100	ribosomal protein S17	Homo sapiens
157 1	AAH15105	1370	100	BC015105 proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
157 1	AAH15356	1370	100	BC015356 proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
157 1	BC022372	1370	100	proteasome (prosome, macropain) subunit, alpha type, 1	Homo sapiens
157 2	AAH03352	723	100	BC003352 tumor protein, translationally-controlled 1	Homo sapiens
157 2	BC022436	723	100	Similar to tumor protein, translationally-controlled 1	Homo sapiens
157 2	X16064	723	100	tumor protein (AA 1 - 172)	Homo sapiens
157 3	BC023006	3271	100	Unknown (protein for MGC:30059)	Homo sapiens
157 3	M27024	3271	100	heat shock protein	Homo sapiens
157 3	X15183	3271	100	90 kDa heat-shock protein (AA 1-732)	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
157 4	AAH08064	2806	100	BC008064 monoamine oxidase A	Homo sapiens
157 4	M68857	2806	100	monoamine oxidase A	Homo sapiens
157 4	M69226	2806	100	monoamine oxidase A	Homo sapiens
157 5	M84378	1952	100	lymphocyte antigen	Homo sapiens
157 5	M84379	1945	99	MHC class I lymphocyte antigen	Homo sapiens
157 5	Z27120	1946	99	HLA-A2 SLU	Homo sapiens
157 6	BC032350	1338	100	major histocompatibility complex, class II, DR alpha	Homo sapiens
157 6	M60334	1338	100	cell surface glycoprotein	Homo sapiens
157 6	Z84814	1338	100	dJ172K2.4.1 (major histocompatibility complex, class II, DR alpha, isoform 1)	Homo sapiens
157 7	AAH02476	803	100	BC002476 non-metastatic cells 2, protein (NM23B) expressed in	Homo sapiens
157 7	L16785	803	100	c-myc transcription factor	Homo sapiens
157 7	X58965	803	100	NM23-H2 protein	Homo sapiens
157 8	AAH11645	1585	100	BC011645 Similar to Ras-related associated with diabetes	Homo sapiens
157 8	L24564	1585	100	Rad	Homo sapiens
157 8	U46165	1565	99	Rad GTPase	Homo sapiens
157 9	AAH03358	1151	100	BC003358 ribosomal protein L10	Homo sapiens
157 9	BC026276	1151	100	ribosomal protein L10	Homo sapiens
157 9	L44140	1151	100	QM	Homo sapiens
158 0	A84527	2912	100	unnamed protein product	unidentified
158 0	AX024042	2912	100	fusion between Aequorea victoria and human	synthetic construct
158 0	M62399	2912	100	NF-kappa-B transcription factor	Homo sapiens
158 1	AAH10860	2071	100	BC010860 serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	Homo sapiens
158 1	AF386492_1	2071	100	AF386492 serine-cysteine proteinase inhibitor clade E member 1	Homo sapiens
158 1	X04429	2071	100	precursor polypeptide	Homo sapiens
158 2	AAH00491	1316	100	BC000491 proliferating cell nuclear antigen	Homo sapiens
158 2	AF347680_1	1316	100	AF347680 proliferating cell nuclear antigen	Macaca fascicularis
158 2	AL121924	1316	100	dJ746J20.2 (proliferating cell nuclear antigen)	Homo sapiens
158 3	AC007165	2130	100	interleukin-1 receptor type II	Homo sapiens
158 3	AY124010	2130	100	interleukin 1 receptor, type II	Homo sapiens
158 3	X59770	2130	100	type II interleukin-1 receptor	Homo sapiens
158 4	BC041071	2366	100	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Homo sapiens
158 4	M64929	2366	100	protein phosphatase-2A subunit-alpha	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
158 4	U09356	2366	100	protein phosphatase 2A1 B alpha subunit	Oryctolagus cuniculus
158 5	M34421	2279	99	pregnancy-specific beta-1 glycoprotein precursor	Homo sapiens
158 5	M34481	2279	99	pregnancy-specific beta-1-glycoprotein 11	Homo sapiens
158 5	M58591	2291	100	PSG11	Homo sapiens
158 6	BC018254	703	97	retinol binding protein 1, cellular	Mus musculus
158 6	M11433	724	100	retinol-binding protein	Homo sapiens
158 6	X07437	724	100	cellular retinol binding protein	Homo sapiens
158 7	J03149	4237	83	M-CSF receptor	Felis catus
158 7	U63963	5158	100	CSF-1 receptor	Homo sapiens
158 7	X03663	5150	99	put. c-fms precursor	Homo sapiens
158 8	BC005580	902	100	polymerase (RNA) II (DNA directed) polypeptide G	Mus musculus
158 8	U52427	902	100	RNA polymerase II seventh subunit	Homo sapiens
158 8	Z71925	902	100	RNA polymerase II RPB7 subunit-like protein	Rattus norvegicus
158 9	AAH11601	658	100	BC011601 interferon, alpha-inducible protein (clone IFI-6-16)	Homo sapiens
158 9	AAH15603	658	100	BC015603 interferon, alpha-inducible protein (clone IFI-6-16)	Homo sapiens
158 9	D11384	652	98	ORF	Pan troglodytes
159 0	AF147083	1683	100	gamma-glutamyl hydrolase	Homo sapiens
159 0	BC025025	1683	100	gamma-glutamyl hydrolase (conjugase, folylpolyglutamyl hydrolase)	Homo sapiens
159 0	U55206	1683	100	human gamma-glutamyl hydrolase	Homo sapiens
159 1	AAH10418	1552	100	BC010418 laminin receptor 1 (67kD, ribosomal protein SA)	Homo sapiens
159 1	AAH13827	1552	100	BC013827 laminin receptor 1 (67kD, ribosomal protein SA)	Homo sapiens
159 1	U43901	1552	100	37 kD laminin receptor precursor/p40 ribosome associated protein	Homo sapiens
159 2	BC026033	4101	100	gelsolin (amyloidosis, Finnish type)	Homo sapiens
159 2	X04412	4101	100	plasma gelsolin	Homo sapiens
159 2	X13871	3849	94	gelsolin	Sus scrofa
159 3	AF304463_1	2813	100	AF304463 calcium transport protein CaT1	Homo sapiens
159 3	AF365927_1	2813	100	AF365927 calcium transport protein CaT1	Homo sapiens
159 3	AF365928_1	2946	100	AF365928 calcium transport protein CaT1	Homo sapiens
159 4	AY040542	2353	100	sialic acid binding immunoglobulin-like lectin 6	Homo sapiens
159 4	D86358	2353	100	CD33L1	Homo sapiens
159 4	U71382	2246	97	OB binding protein-1	Homo sapiens
159 5	AF286534_1	1115	100	AF286534 GTP-binding protein RAB11B	Rattus norvegicus
159	AF498947_1	1115	100	AF498947 small GTP binding	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
5				protein RAB11B	
159 5	X79780	1110	99	YPT3	Homo sapiens
159 6	BC010604	1253	99	ribosomal protein S6	Mus musculus
159 6	BC027620	1256	100	ribosomal protein S6	Homo sapiens
159 6	Z54209	1253	99	rpS6	Mus musculus
159 7	AJ005654	703	100	secondary lymphoid tissue chemokine	Homo sapiens
159 7	BC027918	703	100	small inducible cytokine subfamily A (Cys-Cys), member 21	Homo sapiens
159 7	U88320	703	100	beta chemokine Exodus-2	Homo sapiens
159 8	AF148856_2	6613	98	AF148856 unknown	Homo sapiens
159 8	AF149422_2	6615	98	AF149422 unknown	Homo sapiens
159 8	U93564	6714	100	putative p150	Homo sapiens
159 9	AK012013	1608	100	unnamed protein product	Mus musculus
159 9	BC003742	1608	100	26S proteasome-associated pad1 homolog	Mus musculus
159 9	U86782	1608	100	26S proteasome-associated pad1 homolog	Homo sapiens
160 0	BC041218	676	100	H3 histone, family 3B	Xenopus laevis
160 0	M11393	676	100	histone 3.3	Gallus gallus
160 0	Y00392	676	100	histone H3.3B (AA 1 - 136)	Gallus gallus
160 1	AAH11262	2716	99	BC011262 Unknown (protein for MGC:18226)	Homo sapiens
160 1	AF006043	2719	100	3-phosphoglycerate dehydrogenase	Homo sapiens
160 1	AF171237_1	2719	100	AF171237 3-phosphoglycerate dehydrogenase	Homo sapiens
160 2	AF109197_1	1254	100	AF109197 nuclear chloride channel	Homo sapiens
160 2	AJ012008	1251	99	RNCC protein	Homo sapiens
160 2	U93205	1254	100	nuclear chloride ion channel protein	Homo sapiens
160 3	BC029402	1311	100	proteasome (prosome, macropain) subunit, alpha type, 3	Homo sapiens
160 3	BC038990	1307	99	Similar to proteasome (prosome, macropain) subunit, alpha type, 3	Homo sapiens
160 3	D00762	1307	99	proteasome subunit C8	Homo sapiens
160 4	AB062400	671	100	Similar to ribosomal protein S15a	Homo sapiens
160 4	BC030569	671	100	ribosomal protein S15a	Homo sapiens
160 4	X77953	671	100	ribosomal protein S15a	Rattus norvegicus
160 5	AB062438	1926	100	OK/SW-CL.30	Homo sapiens
160 5	BC025832	1581	90	Unknown (protein for MGC:37936)	Mus musculus
160 5	BC036872	1912	99	Unknown (protein for IMAGE:5225889)	Homo sapiens
160 6	AAH16706	2319	100	BC016706 eukaryotic translation initiation factor 3, subunit 6 (48kD)	Homo sapiens
160 6	AAH21679	2319	100	BC021679 eukaryotic translation initiation factor 3, subunit 6 (48kD)	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
1606	BC029177	2319	100	eukaryotic translation initiation factor 3, subunit 6 (48kD)	Mus musculus
1607	AAH04138	1465	99	BC004138 ribosomal protein L6	Homo sapiens
1607	BC031009	1475	100	ribosomal protein L6	Homo sapiens
1607	BC032299	1465	99	ribosomal protein L6	Homo sapiens
1608	AAH15813	2331	100	BC015813 eukaryotic translation elongation factor 1 gamma	Homo sapiens
1608	BC028179	2331	100	eukaryotic translation elongation factor 1 gamma	Homo sapiens
1608	BC031012	2331	100	eukaryotic translation elongation factor 1 gamma	Homo sapiens
1609	AAH04927	1051	100	BC004927 Unknown (protein for MGC:10432)	Homo sapiens
1609	AF013711	1051	100	22 kDa actin-binding protein	Homo sapiens
1609	D84342	1051	100	SM22 alpha	Homo sapiens
1610	AB007510	12543	100	PRP8 protein	Homo sapiens
1610	AB047391	12461	99	pre-mRNA processing 8 protein	Mus musculus
1610	AF092565	12477	99	splicing factor Prp8	Homo sapiens
1611	AAH10034	3127	100	BC010034 thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
1611	AAH12154	3127	100	BC012154 Similar to thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
1611	AAH18259	3127	100	BC018259 thyroid autoantigen 70kD (Ku antigen)	Homo sapiens
1612	AL050369	2492	99	hypothetical protein	Homo sapiens
1612	AY040822	2500	100	U4/U6 snRNP-associated 61 kDa protein	Homo sapiens
1612	BC018376	2479	98	Unknown (protein for MGC:19247)	Mus musculus
1613	AF343440_1	454	98	AF343440 lysosomal H+ transporting-ATPase subunit M9.2	Canis familiaris
1613	AX400012	459	100	unnamed protein product	Homo sapiens
1613	Y15286	459	100	vacuolar proton-ATPase subunit M9.2	Homo sapiens
1614	AAH01273	1831	99	BC001273 galactose-4-epimerase, UDP-	Homo sapiens
1614	AF022382	1835	100	UDP-galactose 4' epimerase	Homo sapiens
1614	L41668	1835	100	UDP-galactose-4-epimerase	Homo sapiens
1615	AAH05270	900	99	BC005270 NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase)	Homo sapiens
1615	AF020351	904	100	NADH:ubiquinone oxidoreductase 18 kDa IP subunit	Homo sapiens
1615	X63215	839	90	NADH dehydrogenase	Bos taurus
1616	AAH04963	674	100	BC004963 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Homo sapiens
1616	AL080089	674	100	hypothetical protein	Homo sapiens
1616	X69907	674	100	P1 gene for c subunit of human mitochondrial ATP synthase	Homo sapiens
1617	AF100620_1	1492	100	AF100620 transcription factor-like protein MRGX	Homo sapiens
161	AF167174_1	1492	100	AF167174 MSL3-2 protein	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
7					
1617	AL049610	1492	100	dJ1055C14.2 (KIAA0026 (transcription factor-like protein MRGX))	Homo sapiens
1618	AAH15557	1854	99	BC015557 Unknown (protein for MGC:1567)	Homo sapiens
1618	BC021637	1140	66	CD68 antigen	Mus musculus
1618	S57235	1858	100	CD68	Homo sapiens
1619	L27631	4010	100	amyloid precursor-like protein 2	Homo sapiens
1619	S60099	4010	100	APPH	Homo sapiens
1619	Z22572	4010	100	CDEI binding protein	Homo sapiens
1620	AAH08850	1273	99	BC008850 Unknown (protein for MGC:14308)	Homo sapiens
1620	AAH09599	1273	99	BC009599 Unknown (protein for MGC:14690)	Homo sapiens
1620	L16558	1276	100	ribosomal protein L7	Homo sapiens
1621	AF062482	845	99	SDP3	Mus musculus
1621	AF062483	852	100	SDP3	Homo sapiens
1621	AF520420	838	98	sorting nexin 3	Mus musculus
1622	AF063657	6995	100	vascular endothelial growth factor receptor	Homo sapiens
1622	D28498	5882	82	Fit-1 tyrosine kinase receptor	Rattus norvegicus
1622	X51602	6989	99	flt gene product (AA 1-1338)	Homo sapiens
1623	AF149422_2	703	49	AF149422 unknown	Homo sapiens
1623	U93572	710	50	putative p150	Homo sapiens
1623	U93574	709	49	putative p150	Homo sapiens
1624	AF029729	3066	100	neuralized	Homo sapiens
1624	BC026336	3041	99	neuralized-like (Drosophila)	Homo sapiens
1624	U87864	3066	100	neuralized homolog	Homo sapiens
1625	AAH20782	643	100	BC020782 glycoprotein hormones, alpha polypeptide	Homo sapiens
1625	J00152	643	100	glycoprotein alpha subunit	Homo sapiens
1625	V00518	643	100	chorionic gonadotropin	Homo sapiens
1626	AAH02722	2070	100	BC002722 guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1	Homo sapiens
1626	AF493897_1	2070	100	AF493897 guanine nucleotide binding protein alpha s long	Homo sapiens
1626	X04408	2070	100	alpha-S2 (aa 1-394)	Homo sapiens
1627	BC033714	1724	100	heterogeneous nuclear ribonucleoprotein A1	Homo sapiens
1627	D86729	1724	100	TIS	Mus musculus
1627	M99167	1724	100	RNA binding protein	Mus musculus
1628	AF072836	1827	100	Sox-like transcriptional factor	Homo sapiens
162	AF146223_1	620	100	AF146223 HMG domain protein HMGX2	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
8					
1628	AF288679	620	100	smarcel-related protein	Homo sapiens
1629	AAH21979	1360	100	BC021979 ribosomal protein L7a	Homo sapiens
1629	BC032533	1360	100	ribosomal protein L7a	Homo sapiens
1629	X15013	1360	100	ribosomal protein L7a (AA 1-266)	Rattus rattus
1630	X51538	693	100	ribosomal protein S24 (AA 1-133)	Rattus rattus
1630	X52445	693	100	ribosomal protein S24	Rattus norvegicus
1630	X52658	693	100	ribosomal protein S19 (AA 1 - 133)	Mesocricetus auratus
1631	AAH01503	2789	100	BC001503 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
1631	AAH04275	2789	100	BC004275 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
1631	AAH07612	2789	100	BC007612 prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	Homo sapiens
1632	AAH11776	1369	100	BC011776 Similar to tropomyosin 2 (beta)	Homo sapiens
1632	M74817	1369	100	tropomyosin-1	Homo sapiens
1632	M75165	1369	100	tropomyosin	Homo sapiens
1633	AL023883	1173	99	dJ404K8.1 (prolactin)	Homo sapiens
1633	BC015850	1185	100	similar to prolactin precursor	Homo sapiens
1633	V00566	1185	100	reading frame prolactin	Homo sapiens
1634	AK012601	247	64	unnamed protein product	Mus musculus
1634	AK021409	286	69	unnamed protein product	Mus musculus
1634	AK075801	246	64	unnamed protein product	Mus musculus
1635	AF300943_1	9468	94	AF300943 tyrosine phosphatase LAR	Mus musculus
1635	L11586	9484	95	leukocyte common antigen-related phosphatase	Rattus norvegicus
1635	Y00815	9953	100	put. LAR preprotein (AA -16 to 1881)	Homo sapiens
1636	AAH16046	2739	100	BC016046 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Homo sapiens
1636	AAH19310	2739	100	BC019310 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	Homo sapiens
1636	X65460	2739	100	ATP synthase alpha subunit	Homo sapiens
1637	AF237581_1	613	100	AF237581 migration inhibitory factor-related protein 14 variant P	Homo sapiens
1637	M26311	613	100	cystic fibrosis antigen	Homo sapiens
1637	X06233	613	100	MRP-14 (AA 1-114)	Homo sapiens
1638	AAH15492	523	96	BC015492 Unknown (protein for MGC:8967)	Homo sapiens
1638	BC032626	280	64	TLH29 protein precursor	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
1638	X67325	556	100	ISG12	Homo sapiens
1639	L00160	2135	100	phosphoglycerate kinase	Homo sapiens
1639	M11968	2135	100	phosphoglycerate kinase	Homo sapiens
1639	V00572	2135	100	coding sequence	Homo sapiens
1640	AF075575	11112	100	dysferlin	Homo sapiens
1640	AF188290_1	10355	93	AF188290 dysferlin	Mus musculus
1640	AK074104	7939	98	FLJ00175 protein	Homo sapiens
1641	AB052229	10414	100	RNA polymerase II largest subunit	Cricetulus griseus
1641	D87294	10414	100	RNA polymerase II largest subunit	Cricetulus griseus
1641	X63564	10414	100	RNA polymerase II largest subunit	Homo sapiens
1642	AF070650	844	100	F1FO-type ATP synthase subunit d	Homo sapiens
1642	AF087135	844	100	F1FO-type ATPase subunit d	Homo sapiens
1642	BC038092	844	100	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	Homo sapiens
1643	U01153	4046	97	GRP94	Canis familiaris
1643	X15187	4112	100	precursor polypeptide (AA -21 to 782)	Homo sapiens
1643	Y09136	4038	97	gp96/GRP94	Sus scrofa
1644	AF297036_1	670	100	AF297036 ubiquitin fusion protein	Ophiophagus hannah
1644	BC014772	670	100	ubiquitin A-52 residue ribosomal protein fusion product 1	Mus musculus
1644	M24508	670	100	ubiquitin	synthetic construct
1645	AK000385	211	44	unnamed protein product	Homo sapiens
1645	AK097085	245	51	unnamed protein product	Homo sapiens
1645	AK097214	201	59	unnamed protein product	Homo sapiens
1646	AF100956	782	100	ribosomal protein subunit S18	Mus musculus
1646	AF110520	782	100	RPS18	Mus musculus
1646	M76763	782	100	ribosomal protein	Mus musculus
1647	BC025077	930	100	RIKEN cDNA 2010203J19 gene	Mus musculus
1647	L05092	930	100	ribosomal protein L11	Homo sapiens
1647	X62146	930	100	ribosomal protein L11	Rattus rattus
1648	AB037890	6795	99	pre-mRNA splicing factor SF3b 155 kDa subunit	Mus musculus
1648	AF054284	6808	100	spliceosomal protein SAP 155	Homo sapiens
1648	Y08997	6566	96	146kDa nuclear protein	Xenopus laevis
1649	AF072097	624	100	beta-2 microglobulin	Homo sapiens
1649	AY007153	624	100	similar to Homo sapiens mRNA for beta 2-microglobulin with GenBank Accession Number AB021288	
164	BC032589	624	100	beta-2-microglobulin	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
9					
1650	AAH17839	1602	100	BC017839 caspase 4, apoptosis-related cysteine protease	Homo sapiens
1650	U28977	1769	100	Mihl/TX isoform beta	Homo sapiens
1650	U28978	1602	100	Mihl/TX isoform gamma	Homo sapiens
1651	AAH07967	974	100	BC007967 Unknown (protein for MGC:14460)	Homo sapiens
1651	AAH12149	974	100	BC012149 Unknown (protein for MGC:20365)	Homo sapiens
1651	BC031906	974	100	similar to ribosomal protein L9; 60S ribosomal protein L9	Homo sapiens
1652	BC002145	745	100	ribosomal protein S23	Mus musculus
1652	D14530	745	100	ribosomal protein	Homo sapiens
1652	X77398	745	100	ribosomal protein S23	Rattus norvegicus
1653	AF227256_1	405	100	AF227256 NEDD8	Bos taurus
1653	BC004625	398	98	neural precursor cell expressed, developmentally down-regulated gene 8	Mus musculus
1653	D23662	405	100	ubiquitin-like protein	Homo sapiens
1654	U46034	2076	83	stromelysin 3	Rattus norvegicus
1654	X57766	2679	100	stromelysin-3 precursor	Homo sapiens
1654	Z12604	2164	81	stromelysin-3	Mus musculus
1655	AAH01734	499	100	BC001734 protein translocation complex beta	Homo sapiens
1655	AL137067	499	100	bA13B9.2 (novel protein similar to the beta subunit of transport protein SEC61)	Homo sapiens
1655	L25085	499	100	Sec61-complex beta-subunit	Homo sapiens
1656	AF165522_1	360	100	AF165522 ras-related GTP-binding protein 4b	Homo sapiens
1656	AF217985_1	360	100	AF217985 unknown	Homo sapiens
1656	AF498935_1	360	100	AF498935 small GTP binding protein RAB4B	Homo sapiens
1657	AF006602	5436	94	histone deacetylase mHDA1	Mus musculus
1657	AF132608_1	5784	100	AF132608 histone deacetylase 5	Homo sapiens
1657	AF207748_1	5431	94	AF207748 histone deacetylase 5	Mus musculus
1658	AL050259	4009	100	hypothetical protein	Homo sapiens
1658	BC032681	4009	100	RAB2, member RAS oncogene family-like	Homo sapiens
1658	Z97184	4009	100	cICF0811.4.1 (RAB2, member RAS oncogene family-like, isoform 1)	Homo sapiens
1659	AF151855_1	1278	100	AF151855 CGI-97 protein	Homo sapiens
1659	AK001779	1214	96	unnamed protein product	Homo sapiens
1659	BC003849	1200	94	RIKEN cDNA 4733401P19 gene	Mus musculus
1660	AAH00234	1377	100	BC000234 nicotinamide N-methyltransferase	Homo sapiens
1660	U08021	1377	100	nicotinamide N-methyltransferase	Homo sapiens
1660	U20971	1377	100	nicotinamide N-methyltransferase	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
166 1	AAH03137	1240	100	BC003137 ribosomal protein S3	Homo sapiens
166 1	BC034149	1240	100	ribosomal protein S3	Homo sapiens
166 1	U14992	1240	100	ribosomal protein S3	Homo sapiens
166 2	AF090891_1	3913	99	AF090891 PRO0105	Homo sapiens
166 2	AF268075_1	3913	99	AF268075 TRAF6-binding protein T6BP	Homo sapiens
166 2	U33821	3924	100	tax1-binding protein TXBP151	Homo sapiens
166 3	AF186112_1	619	100	AF186112 neurokinin B-like protein ZNEUROK1	Homo sapiens
166 3	AF216586_1	619	100	AF216586 neurokinin B	Homo sapiens
166 3	BC032145	619	100	tachykinin 3 (neuromedin K, neurokinin beta)	Homo sapiens
166 4	AAH08405	2044	90	BC008405 Unknown (protein for MGC:14528)	Homo sapiens
166 4	M94891	2042	90	pregnancy-specific beta-1 glycoprotein	Homo sapiens
166 4	U18467	2252	100	pregnancy-specific beta 1-glycoprotein 7 precursor	Homo sapiens
166 5	AK002989	980	93	unnamed protein product	Mus musculus
166 5	D38076	1041	99	Ran-BP1(Ran-binding protein 1)	Homo sapiens
166 5	X83617	1057	100	RanBP1	Homo sapiens
166 6	AF152604	3398	100	bromodomain-containing protein	Homo sapiens
166 6	AF213969	3369	99	bromodomain protein CELTIX1	Homo sapiens
166 6	AJ271881	3398	100	bromodomain containing protein	Homo sapiens
166 7	AF217973_1	329	68	AF217973 unknown	Homo sapiens
166 7	AK000496	330	66	unnamed protein product	Homo sapiens
166 7	AK090511	352	64	unnamed protein product	Homo sapiens
166 8	AK000917	2276	100	unnamed protein product	Homo sapiens
166 8	BC025560	2156	94	Similar to hypothetical protein FLJ10055	Mus musculus
166 8	BC039867	2259	99	hypothetical protein FLJ10055	Homo sapiens
166 9	AB039886	1071	100	down-regulated in gastric cancer	Homo sapiens
166 9	AY139182	995	100	18 kDa antrum mucosa protein	Homo sapiens
166 9	AY139184	995	100	18 kDa antrum mucosa protein	Homo sapiens
167 0	BC033721	3540	99	Unknown (protein for MGC:45264)	Homo sapiens
167 0	X82157	3543	100	hevin	Homo sapiens
167 0	X86693	3504	99	Hevin-like protein	Homo sapiens
167 1	M84472	1675	100	17-beta-hydroxysteroid dehydrogenase	Homo sapiens
167 1	U34879	1675	100	17-beta-hydroxysteroid dehydrogenase	Homo sapiens
167 1	X13440	1675	100	17-HSD protein (AA 1 - 328)	Homo sapiens
167 2	AAH12612	1812	99	BC012612 Similar to cathepsin L	Homo sapiens
167	M20496	1816	100	preprocathepsin L precursor	Homo sapiens

SEQ ID NO:	Genbank Accession Number	BLAST Score	Percent Identity	Annotation	Organism
2					
167 2	X12451	1816	100	pro-(cathepsin L)	Homo sapiens
167 3	AAH12355	3449	100	BC012355 Similar to solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Homo sapiens
167 3	U36341	3449	100	creatine transporter	Homo sapiens
167 3	Z66539	3449	100	creatine transporter	Homo sapiens
167 4	AF267852_1	749	100	AF267852 placental protein 13-like protein	Homo sapiens
167 4	AF367430	571	100	placental protein 13-like	Homo sapiens
167 4	BC022257	731	98	Similar to placental protein 13-like protein	Homo sapiens
167 5	AB001636	4072	99	ATP-dependent RNA helicase #46	Homo sapiens
167 5	AF279891_1	4162	100	AF279891 dead box protein 15	Homo sapiens
167 5	BC035974	4162	100	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15	Homo sapiens
167 6	AAH17321	687	100	BC017321 Unknown (protein for MGC:29768)	Homo sapiens
167 6	BC002079	687	100	Similar to ribosomal protein S12	Mus musculus
167 6	BC018362	687	100	Unknown (protein for MGC:19264)	Mus musculus
167 7	AAH20619	1123	99	BC020619 glutathione S-transferase A3	Homo sapiens
167 7	AF508266_1	1127	100	AF508266 glutathione transferase A3-3	Homo sapiens
167 7	AL121969	1127	100	dJ214M20.1 (glutathione S-transferase A3)	Homo sapiens
167 8	AAH00359	923	100	BC000359 signal peptidase complex (18kD)	Homo sapiens
167 8	AAH14508	923	100	BC014508 Similar to signal peptidase complex (18kD)	Homo sapiens
167 8	AF061737	923	100	microsomal signal peptidase	Homo sapiens
167 9	AF179890_1	598	100	AF179890 DNA polymerase delta smallest subunit p12	Homo sapiens
167 9	AF515709_1	492	83	AF515709 small subunit DNA polymerase delta p12	Mus musculus
167 9	BC028520	492	83	Unknown (protein for MGC:41275)	Mus musculus
168 0	AC005067_2	1340	73	AC005067 Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and genscan	Homo sapiens
168 0	AF226732_1	2286	100	AF226732 NPD007	Homo sapiens
168 0	BC018360	1199	68	Unknown (protein for MGC:18730)	Mus musculus
168 1	AAH19040	897	100	BC019040 Unknown (protein for MGC:20769)	Homo sapiens
168 2	AK023767	960	100	unnamed protein product	Homo sapiens
168 2	AL080169	979	100	hypothetical protein	Homo sapiens
168 2	BC016647	960	100	Unknown (protein for MGC:16844)	Homo sapiens
168 3	AF309646_1	1147	88	AF309646 Rab6-like protein WTH3	Homo sapiens
168 3	AF498941_1	1058	100	AF498941 small GTP binding protein RAB6C	Homo sapiens
168 3	AL136727	1147	88	hypothetical protein	Homo sapiens

SEQ ID NO:	Genbank Accesssion Number	BLAST Score	Percent Identity	Annotation	Organism
1684	AC005095_1	1373	100	AC005095 pantophysin	Homo sapiens
1684	S72481	1373	100	pantophysin	Homo sapiens
1684	X68194	1373	100	h-Sp1	Homo sapiens
1685	D14665	3850	99	KIAA0021 protein	Homo sapiens
1685	U41765	3814	83	metalloprotease/disintegrin/cysteine rich protein precursor	Mus musculus
1685	U41766	4476	100	metalloprotease/disintegrin/cysteine-rich protein precursor	Homo sapiens
1686	U20770	1412	100	cell surface glycoprotein	Homo sapiens
1686	U67274	1412	100	metastasis suppressor	Homo sapiens
1686	X53795	1412	100	inducible membrane protein	Homo sapiens
1687	AF517934_1	2980	100	AF517934 interleukin 2 receptor, beta	Homo sapiens
1687	AL022314	2980	100	dJ1170K4.3 (Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen))	Homo sapiens
1687	BC025691	2980	100	interleukin 2 receptor, beta	Homo sapiens
1688	AF072242	2167	100	methyl-CpG binding protein MBD2	Homo sapiens
1688	AF120994	2167	100	methyl-CpG binding protein 2	Homo sapiens
1688	BC032638	2167	100	methyl-CpG binding domain protein 2	Homo sapiens
1689	AAH00486	607	100	BC000486 small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	Homo sapiens
1689	AAH01930	607	100	BC001930 small nuclear ribonucleoprotein D2 polypeptide (16.5kD)	Homo sapiens
1689	AC007191_1	607	100	AC007191 SMD2_HUMAN; SNRNP CORE PROTEIN D2; SM-D2	Homo sapiens
1690	AAH18180	870	100	BC018180 CGI-121 protein	Homo sapiens
1690	AF151879_1	870	100	AF151879 CGI-121 protein	Homo sapiens
1690	BC029492	870	100	CGI-121 protein	Homo sapiens
1691	U52373	4063	99	MNB	Homo sapiens
1691	U58497	4037	99	mp86	Mus musculus
1691	X79769	4052	99	Dual Specificity Yak1-related Kinase (Dyrk)	Rattus norvegicus

EXAMPLE 3

Initial Determination of Differential Regulation of Polynucleotides of the Invention in Pre-eclampsia

A plurality of polynucleotide sequences were obtained from cDNA libraries obtained from both normal and pre-eclamptic placental tissues, using SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon
5 membrane filters and screened with oligonucleotide probes (for example, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequences of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye
10 terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases, RACE (Rapid Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

Relative expression of the gene may be approximated by a relative abundance of a transcript (number of copies of mRNA) of the gene in question in the cytoplasm of the cells of the tissues in
15 question. Relative abundance of a transcript is calculated as an absolute number of cDNA clones from that transcript in the library created from the total mRNAs of the analyzed tissue over a total number of cDNA clones analyzed per tissue (e.g. 100,000 was the total number of cDNA clones analyzed per tissue. For example, if a gene was represented by 25,000 clones in a given placental library - i.e. its cDNA cluster comprised 25,000 clones, relative expression of that gene is 25%,
20 since 25% of all clones analyzed belong to that one gene.

Differential expression may be calculated for heterogeneous cDNA clusters which are clusters obtained through clustering of clones from two or more different libraries together. A cluster may be heterogeneous even if it's made up of clones from one library only, provided clustering was done for more than one library. More precisely, heterogeneity is the qualifier of the
25 clustering experiment, rather than the qualifier of the cluster. For example, if two or more libraries were used in the clustering experiment, and a cluster comprises clones from only one of the two libraries, it can still be characterized as heterogeneous, with zero clones from all but one libraries. In this case pairwise comparisons were performed where two libraries were clustered at a time. For given initial conditions (100,000 clones per library, 200,000 total per clustering experiment), clusters
30 of a size of 8 clones or greater were selected for further consideration. Out of these only those showing a differential ratio of clones of 2 times and above were selected as of statistically significant differential expression, thus keeping the confidence level at greater than or equal to 90%. This

number measures the probability that the given cluster shows real differential expression. Note that since both libraries in the pair at hand were of the same initial size, therefore, no normalization of the cluster size on the total library size was necessary.

The following table shows the results of this process, indicating which polynucleotides of the invention are designated as up-regulated in pre-eclamptic placental tissues, and which are down-regulated in pre-eclamptic placental tissues.

TABLE 2

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
1	UP	434	7	11
2	UP	376	108	148
3	UP	6623	6	10
4	UP	1996	6	15
5	UP	12951	17	32
6	UP	4704	18	23
7	UP	3930	0	8
8	UP	12138	25	29
9	UP	703	126	212
10	DOWN	305	190	180
11	DOWN	8	2878	1125
12	UP	2498	20	40
13	DOWN	12700	8	0
14	DOWN	6779	28	10
15	DOWN	1037	9	3
16	UP	8238	1	8
17	UP	11051	10	12
18	DOWN	9165	22	1
19	DOWN	8265	9	2
20	DOWN	39852	8	0
21	DOWN	13238	16	1
22	UP	3184	2	9
23	DOWN	15366	43	2
24	DOWN	32470	8	1
25	DOWN	6195	16	1
26	UP	69	3	14
27	DOWN	1550	14	4
28	DOWN	1544	9	3
29	DOWN	3129	23	18
30	DOWN	39826	11	0
31	DOWN	39825	11	0
32	DOWN	12237	42	26
33	DOWN	39614	14	0
34	DOWN	22223	8	1
35	DOWN	8274	8	2
36	DOWN	8993	16	1
37	DOWN	16337	11	1
38	DOWN	5959	18	16

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
39	DOWN	39367	10	1
40	DOWN	7336	23	4
41	UP	1052	22	73
42	DOWN	6260	18	1
43	DOWN	7782	8	0
44	DOWN	14057	8	0
45	UP	5438	14	27
46	DOWN	9433	15	2
47	DOWN	9442	18	8
48	DOWN	1722	36	10
49	DOWN	2710	31	9
50	DOWN	10245	14	11
51	DOWN	24399	15	2
52	UP	4592	2	10
53	DOWN	9466	23	3
54	DOWN	40893	9	0
55	DOWN	9639	9	1
56	DOWN	7143	10	1
57	UP	571	20	45
58	UP	396	2	30
59	UP	1195	10	17
60	UP	6656	2	9
61	UP	2970	2	10
62	DOWN	2929	21	18
63	DOWN	10556	37	17
64	DOWN	1033	55	42
65	UP	115	28	62
66	UP	1907	18	22
67	UP	326	5	32
68	UP	4657	12	30
69	UP	2228	78	145
70	UP	3061	2	8
71	UP	2145	55	154
72	UP	4072	21	31
73	DOWN	101	77	15
74	DOWN	1307	19	18
75	UP	2602	1	23
76	UP	2675	16	55
77	UP	5131	28	39
78	DOWN	2663	20	16
79	DOWN	3485	56	12
80	UP	4189	30	43
81	DOWN	2880	19	7
82	UP	3514	8	35
83	UP	1184	24	92
84	DOWN	1047	20	5
85	UP	37	33	76
86	DOWN	2085	17	4
87	UP	2655	1	16
88	DOWN	13007	8	1
89	UP	920	3	25
90	DOWN	50	71	11
91	DOWN	3413	97	25

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
92	UP	3610	5	17
93	DOWN	3705	10	2
94	DOWN	303	18	1
95	DOWN	6875	14	1
96	UP	4791	29	33
97	UP	1514	5	10
98	UP	848	6	29
99	DOWN	1305	27	7
100	UP	2659	29	79
101	DOWN	4498	37	14
102	UP	14168	13	18
103	DOWN	3391	8	1
104	UP	3013	10	15
105	UP	1182	2	32
106	DOWN	1177	103	7
107	UP	5258	4	11
108	DOWN	1739	20	1
109	UP	95	10	30
110	UP	664	19	20
111	UP	12341	1	8
112	UP	99	14	119
113	UP	168	23	53
114	DOWN	1492	32	11
115	DOWN	769	26	23
116	UP	87	6	16
117	UP	1314	1	27
118	DOWN	1147	126	100
119	UP	4205	6	23
120	DOWN	2994	19	9
121	UP	843	21	36
122	UP	1220	4	12
123	DOWN	482	23	3
124	UP	1061	2	9
125	UP	2205	10	42
126	DOWN	1730	21	18
127	DOWN	5983	51	11
128	UP	10559	23	94
129	DOWN	2158	28	5
130	UP	252	13	135
131	DOWN	4956	38	27
132	DOWN	7031	17	2
133	DOWN	1670	9	1
134	DOWN	30049	23	2
135	DOWN	27955	8	0
136	DOWN	7679	8	1
137	UP	2741	9	15
138	DOWN	7542	11	4
139	UP	8179	6	9
140	UP	7089	4	14
141	UP	6968	13	17
142	UP	7166	3	34
143	UP	7378	9	34
144	DOWN	6954	25	5

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
145	DOWN	3051	16	1
146	DOWN	5485	14	5
147	UP	5128	6	25
148	UP	6749	4	18
149	DOWN	5070	15	11
150	UP	1059	8	10
151	UP	4885	18	21
152	UP	4643	30	100
153	DOWN	5058	15	9
154	UP	5980	5	21
155	UP	2089	6	11
156	DOWN	5490	28	22
157	UP	4821	52	95
158	UP	61	13	27
159	UP	4710	7	37
160	DOWN	8083	8	1
161	UP	4878	9	43
162	DOWN	1857	25	21
163	DOWN	5346	11	3
164	UP	5124	21	55
165	UP	4804	41	123
166	DOWN	6555	10	3
167	DOWN	6869	8	2
168	DOWN	7961	13	8
169	DOWN	6854	58	13
170	UP	13272	3	15
171	UP	4796	66	85
172	UP	258	12	13
173	UP	5334	1	9
174	UP	10290	0	24
175	DOWN	5245	37	5
176	DOWN	12521	8	2
177	UP	1382	79	148
178	DOWN	12566	9	0
179	UP	6354	7	10
180	UP	4945	14	65
181	DOWN	5491	72	25
182	DOWN	10400	22	2
183	UP	5702	7	25
184	DOWN	3050	22	17
185	DOWN	6201	20	9
186	UP	4884	3	27
187	DOWN	7725	8	1
188	UP	5988	43	71
189	UP	11831	3	16
190	DOWN	4855	16	3
191	UP	786	25	27
192	UP	5263	4	19
193	UP	5556	16	20
194	UP	7758	1	8
195	UP	9188	1	17
196	DOWN	4698	18	16
197	UP	5654	0	8

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
198	UP	4937	3	10
199	UP	5890	2	18
200	UP	3983	5	46
201	DOWN	7240	45	19
202	UP	5555	3	8
203	UP	5276	4	9
204	DOWN	6687	49	22
205	UP	3547	31	93
206	UP	3513	14	54
207	DOWN	10446	8	1
208	UP	10774	8	13
209	UP	10793	1	7
210	DOWN	10988	26	1
211	UP	4366	1	8
212	DOWN	6243	119	96
213	DOWN	7248	8	0
214	UP	8984	2	10
215	UP	561	5	26
216	DOWN	10657	13	11
217	UP	9847	5	12
218	UP	10184	9	14
219	UP	5279	6	16
220	UP	12109	8	22
221	UP	3955	7	16
222	UP	8885	2	10
223	UP	10365	2	21
224	UP	1178	5	30
225	UP	4066	5	17
226	UP	1760	11	11
227	UP	5969	12	45
228	DOWN	4883	8	1
229	UP	5163	17	38
230	UP	10739	3	8
231	DOWN	12507	52	17
232	DOWN	1812	35	30
233	UP	134	0	18
234	DOWN	3197	10	2
235	UP	9077	8	12
236	DOWN	10016	21	17
237	UP	3788	3	11
238	DOWN	10011	8	1
239	UP	9599	3	9
240	DOWN	6566	64	1
241	DOWN	9865	19	1
242	UP	10885	17	26
243	UP	12292	5	22
244	DOWN	12390	45	22
245	DOWN	13573	49	4
246	DOWN	1203	35	4
247	UP	9768	19	33
248	UP	6552	3	12
249	DOWN	10363	9	4
250	UP	649	15	27

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
251	UP	12635	0	10
252	DOWN	464	17	6
253	DOWN	12809	21	2
254	UP	2868	11	34
255	DOWN	6423	136	7
256	UP	8249	6	13
257	DOWN	4665	24	14
258	DOWN	3521	18	17
259	UP	3001	18	25
260	DOWN	11740	8	2
261	UP	13122	5	16
262	UP	2177	48	72
263	UP	8444	11	24
264	DOWN	2187	57	5
265	UP	6962	61	148
266	DOWN	12538	7	2
267	UP	443	44	67
268	DOWN	13257	14	5
269	DOWN	13549	19	0
270	DOWN	4087	11	2
271	UP	45	3	20
272	DOWN	12290	13	9
273	UP	3570	11	49
274	UP	7142	2	9
275	DOWN	13596	37	12
276	UP	1975	34	251
277	DOWN	901	16	6
278	UP	5652	77	107
279	DOWN	10591	11	2
280	DOWN	11910	9	2
281	UP	12090	6	26
282	DOWN	4495	167	33
283	UP	3739	5	32
284	UP	5064	2	18
285	DOWN	10511	23	2
286	UP	1750	2	9
287	DOWN	2968	16	4
288	UP	12172	7	31
289	UP	11685	9	13
290	UP	12822	4	14
291	UP	4732	9	12
292	UP	12971	1	8
293	UP	12180	4	8
294	UP	6618	8	13
295	DOWN	12247	23	4
296	UP	9086	10	23
297	UP	11765	20	33
298	UP	12767	2	38
299	DOWN	2136	13	12
300	UP	1110	1	8
301	UP	10099	26	75
302	DOWN	4800	10	2
303	DOWN	13652	8	1

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
304	UP	4762	3	13
305	UP	1519	0	8
306	UP	223	1	17
307	UP	13680	1	8
308	UP	11884	1	8
309	DOWN	1681	16	13
310	UP	11800	16	36
311	UP	6565	111	125
312	UP	13555	9	11
313	DOWN	7878	15	4
314	DOWN	11630	12	3
315	DOWN	8596	29	12
316	DOWN	8005	17	8
317	DOWN	5037	29	12
318	UP	644	29	38
319	UP	7190	1	7
320	UP	12055	9	26
321	DOWN	4714	44	9
322	UP	4330	2	10
323	UP	6773	14	53
324	DOWN	9057	81	26
325	DOWN	2907	9	1
326	UP	2910	3	17
327	DOWN	9989	10	3
328	UP	1713	2	8
329	UP	3618	23	67
330	UP	2252	6	17
331	DOWN	12013	13	2
332	UP	6673	24	38
333	DOWN	2091	64	11
334	DOWN	11539	43	28
335	DOWN	14305	8	1
336	UP	8835	14	53
337	DOWN	12824	15	5
338	DOWN	13661	14	5
339	UP	8290	22	24
340	DOWN	12559	8	1
341	UP	10192	21	34
342	UP	8540	3	17
343	DOWN	563	18	8
344	UP	5319	3	11
345	DOWN	1131	19	13
346	DOWN	10034	25	18
347	UP	10644	0	8
348	DOWN	6564	15	10
349	UP	656	5	10
350	DOWN	13465	16	11
351	DOWN	13564	20	8
352	UP	9110	26	61
353	DOWN	6594	80	42
354	UP	1637	13	44
355	UP	13262	3	26
356	UP	484	16	69

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
357	DOWN	10314	63	11
358	DOWN	9880	8	0
359	DOWN	10993	17	4
360	UP	5788	7	18
361	DOWN	9892	109	54
362	UP	1602	38	83
363	UP	1191	21	44
364	DOWN	128	125	47
365	UP	239	166	949
366	DOWN	1202	111	90
367	DOWN	3724	22	3
368	UP	1080	1	9
369	UP	2376	33	94
370	UP	190	508	774
371	UP	3866	11	65
372	DOWN	27995	12	1
373	UP	4199	1	7
374	UP	311	2	21
375	DOWN	3585	20	14
376	DOWN	6583	9	2
377	UP	5646	9	33
378	UP	4746	1	27
379	DOWN	8891	33	2
380	UP	13605	8	13
381	UP	4479	16	118
382	UP	7523	2	9
383	UP	7575	1	16
384	DOWN	4842	18	3
385	UP	2071	31	72
386	UP	6828	1	24
387	UP	9973	18	38
388	DOWN	2141	104	61
389	UP	9003	10	16
390	DOWN	12691	25	2
391	DOWN	13237	19	6
392	UP	220	1	8
393	UP	5371	10	33
394	UP	12723	25	39
395	DOWN	9954	31	13
396	UP	1461	48	51
397	DOWN	10742	10	2
398	UP	5189	23	54
399	UP	2862	21	97
400	UP	12888	1	9
401	UP	8225	4	21
402	DOWN	5829	16	5
403	DOWN	1238	36	31
404	UP	2234	50	55
405	UP	10464	5	13
406	UP	1439	16	19
407	DOWN	6353	39	17
408	UP	8356	8	12
409	UP	12863	3	18

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
410	UP	5391	14	17
411	DOWN	660	29	3
412	UP	12828	3	19
413	DOWN	6367	16	1
414	UP	7641	16	30
415	UP	10503	2	10
416	UP	3687	10	17
417	DOWN	5524	37	15
418	DOWN	15	2577	450
419	DOWN	6087	11	7
420	DOWN	337	56	13
421	UP	38	11	24
422	UP	1940	55	67
423	DOWN	1002	22	7
424	DOWN	1922	22	10
425	DOWN	6192	58	24
426	UP	2041	33	60
427	DOWN	9351	31	1
428	UP	1758	10	16
429	UP	2954	8	35
430	UP	4097	34	66
431	DOWN	487	82	7
432	DOWN	6228	25	8
433	UP	235	45	99
434	UP	690	24	48
435	UP	1362	4	28
436	UP	1978	48	93
437	UP	691	2	8
438	DOWN	3805	11	1
439	UP	3639	98	115
440	DOWN	6919	8	1
441	DOWN	585	84	35
442	DOWN	4436	18	1
443	UP	8923	27	31
444	UP	24	226	377
445	UP	1211	67	106
446	DOWN	5473	8	0
447	UP	380	218	454
448	DOWN	2785	13	6
449	UP	6090	16	16
450	UP	177	23	34
451	DOWN	3632	25	11
452	UP	6400	2	10
453	DOWN	1660	49	13
454	UP	1934	24	95
455	UP	2680	1	12
456	UP	136	10	91
457	DOWN	9445	306	47
458	DOWN	4763	82	43
459	DOWN	1068	40	33
460	DOWN	1797	32	19
461	DOWN	8275	56	2
462	UP	265	0	8

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
463	UP	6547	2	11
464	UP	9244	12	36
465	UP	5676	9	15
466	UP	96	43	67
467	UP	6047	3	26
468	UP	3559	1	9
469	UP	6182	4	9
470	DOWN	8377	139	58
471	UP	1265	13	48
472	DOWN	12747	15	5
473	DOWN	14061	21	5
474	UP	365	89	367
475	UP	2363	68	88
476	UP	10195	14	18
477	DOWN	4520	42	12
478	DOWN	12435	12	3
479	UP	884	9	22
480	UP	4138	5	18
481	UP	1154	3	19
482	UP	2778	47	71
483	DOWN	852	16	15
484	DOWN	7188	110	20
485	DOWN	12168	9	1
486	UP	11591	1	15
487	UP	10039	2	12
488	UP	5194	11	32
489	UP	10061	1	7
490	DOWN	1994	30	20
491	UP	11941	8	78
492	DOWN	5733	12	8
493	DOWN	1299	12	4
494	UP	86	9	25
495	UP	292	123	155
496	UP	3644	1	19
497	DOWN	11458	19	13
498	UP	12641	1	7
499	DOWN	11674	75	9
500	UP	3089	0	8
501	DOWN	8552	9	3
502	DOWN	4808	25	1
503	UP	6540	16	33
504	UP	3966	13	33
505	DOWN	886	10	2
506	UP	3167	23	25
507	UP	1246	4	12
508	UP	3018	23	25
509	UP	506	2	8
510	UP	4683	4	20
511	UP	1165	41	78
512	DOWN	8148	8	0
513	UP	5746	4	9
514	DOWN	865	83	74
515	UP	3235	18	37

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
516	DOWN	5271	61	5
517	DOWN	4605	38	22
518	UP	517	64	95
519	UP	1341	23	35
520	DOWN	8858	32	13
521	DOWN	8205	10	1
522	UP	6977	12	22
523	DOWN	12678	15	9
524	DOWN	931	24	8
525	DOWN	12947	38	11
526	UP	8955	17	39
527	DOWN	9418	8	1
528	UP	1113	29	129
529	DOWN	3617	25	23
530	UP	5243	10	14
531	UP	4246	22	49
532	UP	8909	5	31
533	UP	1213	18	49
534	UP	13318	2	10
535	UP	574	1	7
536	DOWN	9166	9	1
537	UP	6211	5	37
538	UP	2771	1	15
539	UP	341	38	74
540	DOWN	4688	204	84
541	UP	3219	1	7
542	UP	6056	14	32
543	DOWN	6739	97	65
544	UP	629	172	487
545	UP	3239	62	106
546	DOWN	4958	1096	5
547	DOWN	2735	14	3
548	UP	6224	4	40
549	UP	3142	6	23
550	DOWN	2098	57	34
551	UP	1554	25	128
552	UP	2424	2	13
553	UP	127	2	8
554	DOWN	212	28	3
555	UP	4776	4	10
556	DOWN	327	18	1
557	UP	12520	1	10
558	DOWN	4604	11	4
559	DOWN	9810	16	1
560	UP	360	0	11
561	DOWN	10867	9	1
562	UP	1912	97	214
563	DOWN	751	123	120
564	UP	175	33	250
565	DOWN	5049	16	6
566	UP	65	115	329
567	UP	2609	17	42
568	UP	11967	5	16

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
569	UP	9230	12	30
570	UP	3946	33	96
571	UP	752	21	58
572	UP	4767	12	127
573	DOWN	9958	8	1
574	UP	1133	91	100
575	UP	5087	1	8
576	UP	12332	9	12
577	UP	383	11	45
578	UP	10259	4	18
579	DOWN	524	51	21
580	DOWN	11813	46	9
581	DOWN	6060	8	1
582	DOWN	923	196	162
583	DOWN	6619	8	1
584	DOWN	4150	16	10
585	UP	4185	25	30
586	UP	3764	16	19
587	DOWN	11835	47	8
588	UP	222	16	39
589	UP	393	7	37
590	UP	4352	26	90
591	UP	5384	30	50
592	DOWN	3019	20	16
593	UP	5001	4	17
594	UP	3370	14	31
595	DOWN	7069	24	19
596	DOWN	5126	59	33
597	UP	3532	2	10
598	UP	12	1645	2225
599	UP	193	21	22
600	UP	8086	20	24
601	UP	2586	47	299
602	UP	8780	23	72
603	DOWN	13928	45	22
604	DOWN	11269	24	1
605	DOWN	7070	58	37
606	UP	1557	42	97
607	UP	11999	5	19
608	UP	11661	22	33
609	DOWN	70	650	611
610	DOWN	498	20	16
611	DOWN	917	16	13
612	UP	8974	8	11
613	UP	2067	105	268
614	UP	2443	8	17
615	UP	91	53	98
616	UP	1585	9	34
617	DOWN	1283	14	10
618	UP	1977	59	112
619	DOWN	6535	8	1
620	UP	9417	19	32
621	DOWN	8959	18	17

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
622	UP	8095	3	22
623	DOWN	10468	8	1
624	UP	6664	13	18
625	DOWN	2971	15	4
626	UP	4386	19	50
627	DOWN	3843	321	16
628	UP	6223	2	9
629	DOWN	9914	12	4
630	DOWN	3261	8	1
631	UP	12511	12	48
632	UP	1883	2	8
633	UP	1918	3	32
634	DOWN	9695	63	4
635	UP	8882	10	28
636	DOWN	2315	300	277
637	UP	1286	33	46
638	UP	6004	81	149
639	UP	2236	44	83
640	UP	12400	2	9
641	DOWN	6716	130	7
642	UP	3715	9	9
643	DOWN	6931	20	14
644	DOWN	5278	82	13
645	UP	7811	1	15
646	DOWN	3783	124	76
647	DOWN	724	42	34
648	UP	13530	1	7
649	UP	666	1	9
650	UP	741	3	23
651	DOWN	7002	402	1
652	DOWN	9722	14	7
653	DOWN	8831	11	1
654	UP	100	25	63
655	UP	185	101	105
656	UP	13050	2	8
657	UP	1215	161	339
658	UP	1493	27	42
659	UP	2647	0	11
660	UP	11865	2	9
661	UP	335	2	29
662	DOWN	9974	9	1
663	UP	4325	0	8
664	UP	5859	9	25
665	DOWN	10755	7	2
666	DOWN	8227	27	7
667	UP	3716	7	46
668	UP	3304	5	24
669	UP	3045	3	12
670	DOWN	2017	13	2
671	DOWN	12994	8	0
672	UP	2386	54	111
673	DOWN	8884	98	11
674	UP	3949	30	58

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
675	DOWN	11971	21	19
676	DOWN	8080	8	1
677	UP	1932	37	71
678	UP	1735	1	8
679	UP	10004	5	14
680	UP	2313	2	8
681	UP	413	12	25
682	UP	824	51	102
683	UP	5494	87	133
684	UP	11842	11	49
685	UP	888	17	38
686	DOWN	9904	27	13
687	UP	6	141	4273
688	DOWN	4933	180	33
689	DOWN	4859	12	5
690	DOWN	7568	55	35
691	DOWN	10505	44	27
692	DOWN	2383	34	20
693	UP	182	2065	3955
694	DOWN	6129	143	40
695	UP	10187	9	21
696	UP	3	647	666
697	UP	3315	8	10
698	DOWN	12014	17	4
699	UP	1	2954	7028
700	UP	1206	16	233
701	UP	2821	30	83
702	UP	11882	2	9
703	UP	608	89	201
704	DOWN	2261	20	2
705	UP	7728	25	26
706	UP	5	3558	3991
707	DOWN	5075	66	0
708	DOWN	1709	8	0
709	UP	2058	10	19
710	UP	8913	14	33
711	DOWN	2605	23	3
712	DOWN	6388	8	0
713	UP	398	29	125
714	UP	146	17	54
715	UP	4	257	812
716	UP	5626	14	21
717	UP	2099	31	123
718	UP	9142	24	25
719	UP	11744	14	29
720	UP	123	198	1192
721	UP	2775	33	83
722	UP	2949	2	9
723	UP	3244	53	97
724	UP	153	3	16
725	UP	1034	11	48
726	DOWN	3515	14	6
727	UP	143	138	265

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
728	DOWN	9234	10	3
729	DOWN	60	264	83
730	UP	5906	9	26
731	UP	1288	13	23
732	UP	915	1	9
733	DOWN	9891	9	2
734	UP	33	40	272
735	DOWN	11571	74	13
736	UP	1023	2	20
737	DOWN	670	61	59
738	UP	5187	9	29
739	UP	2096	80	87
740	DOWN	5360	62	17
741	DOWN	12680	36	10
742	UP	5239	3	29
743	DOWN	6926	11	4
744	UP	4793	73	144
745	UP	167	2	10
746	UP	7706	5	11
747	DOWN	4344	20	9
748	UP	2896	57	115
749	UP	2766	6	15
750	UP	1652	20	45
751	UP	1295	5	15
752	UP	1733	11	17
753	UP	1728	65	176
754	UP	1958	3	25
755	UP	1092	32	225
756	UP	5222	27	59
757	DOWN	8928	130	10
758	UP	7681	14	15
759	DOWN	3953	21	6
760	DOWN	9050	7	1
761	DOWN	3793	72	53
762	DOWN	10133	8	1
763	UP	584	5	8
764	DOWN	12494	9	2
765	UP	4129	58	78
766	UP	3727	9	20
767	DOWN	5730	9	2
768	UP	2340	45	198
769	UP	4532	16	22
770	UP	1198	94	277
771	DOWN	10387	39	7
772	DOWN	12955	15	7
773	UP	10	4481	8914
774	DOWN	2895	69	50
775	UP	3498	21	25
776	UP	8557	11	26
777	UP	6368	53	105
778	UP	2195	53	143
779	UP	716	84	203
780	DOWN	3192	42	10

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
781	UP	215	33	284
782	UP	3858	11	26
783	UP	9024	22	24
784	UP	497	5	38
785	DOWN	503	102	93
786	UP	449	56	83
787	UP	789	26	34
788	DOWN	11806	28	16
789	DOWN	1262	11	6
790	UP	4113	17	30
791	UP	1638	108	330
792	UP	985	18	38
793	DOWN	4070	21	8
794	UP	109	177	272
795	UP	1561	55	135
796	UP	3164	17	47
797	UP	31	448	557
798	DOWN	1397	20	14
799	UP	2	550	1174
800	UP	5322	11	78
801	DOWN	4813	36	6
802	DOWN	7099	105	12
803	UP	10758	6	32
804	DOWN	4950	22	7
805	UP	9211	9	11
806	UP	4718	6	30
807	DOWN	2581	11	2
808	UP	338	21	28
809	UP	2850	69	161
810	UP	5703	0	17
811	UP	1736	102	110
812	DOWN	9390	10	3
813	UP	7952	14	19
814	DOWN	3792	10	3
815	DOWN	9887	31	6
816	DOWN	27	12	4
817	DOWN	3451	9	0
818	UP	3047	2	34
819	DOWN	5186	145	24
820	UP	34	67	81
821	UP	1508	7	38
822	DOWN	11292	211	13
823	UP	2430	6	19
824	UP	2554	55	63
825	DOWN	10869	9	0
826	UP	9553	16	25
827	DOWN	8832	19	4
828	DOWN	5761	22	2
829	DOWN	2378	7	1
830	DOWN	8304	8	1
831	UP	4823	11	19
832	DOWN	4229	8	1
833	UP	2722	2	7

SEQ ID NO:	REGULATION	Cluster_ID	Expression in Normal Placenta	Expression in Pre-eclamptic Placenta
834	UP	13325	4	8
835	UP	1114	1	22
836	UP	6459	1	7
837	UP	2953	3	11
838	UP	807	31	73
839	UP	2040	1	9
840	UP	1336	58	290
841	UP	6796	6	15
842	UP	1455	7	22
843	UP	2576	29	145
844	UP	1293	19	117
845	DOWN	3518	18	1
846	DOWN	3819	10	9
847	UP	4734	22	38
848	UP	10265	0	9
849	UP	10344	4	23
850	DOWN	12491	18	11
851	UP	11621	2	18
852	UP	8384	7	20

EXAMPLE 4
Pfam Annotation of Polypeptides of the Invention

Using the Pfam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference), the polypeptides of the invention (SEQ ID NO: 853 through 1704) we determined. Further description of the Pfam models can be found at <http://pfam.wustl.edu/>.

The following table lists the polypeptides of SEQ ID NO 853 through 1704 that had significant Pfam model hits:

TABLE 3

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
853	TPR	1/1	297-330	14.0	0.036	TPR Domain
854	Sterol_desat	1/1	24-214	268.2	2.9e-81	Sterol desaturase
856	ras	1/1	8-194	335.5	1.4e-98	Ras family
857	thyroglobulin_1	1/1	7-86	140.8	2.5e-38	Thyroglobulin type-1 repeat
860	thioredo	2/2	65-173	131.1	3.3e-38	Thioredoxin
861	GP120	1/1	21-44	5.6	0.81	Envelope glycoprotein GP120
861	TIMP	1/1	69-246	484.3	1.9e-176	Tissue inhibitor of metalloproteinase
863	globin	1/1	20-160	203.0	4.6e-57	Globin
864	COX1	1/1	5-461	867.8	3.4e-257	Cytochrome C and Quinol oxidase polypeptide

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
866	PGAM	1/1	13-241	436.5	2.3e-127	Phosphoglycerate mutase family
869	2OG-FeII_Oxy	1/1	117-146	15.5	0.005	2OG-Fe(II) oxygenase superfamily
870	LIM	1/1	281-337	78.5	8.5e-21	LIM domain
870	PDZ	1/1	30-109	86.7	3e-23	PDZ domain (Also known as DHR or GLGF)
873	GDPD	1/1	243-324	73.6	4.1e-21	Glycerophosphoryl diester phosphodiester
874	rrm	1/3	204-274	48.1	1.1e-12	RNA recognition motif. (a.k.a. RRM, RBD,
874	rrm	2/3	301-372	112.3	1.3e-31	RNA recognition motif. (a.k.a. RRM, RBD,
874	rrm	3/3	496-552	20.9	0.00011	RNA recognition motif. (a.k.a. RRM, RBD,
875	DUF232	1/1	396-433	9.7	0.36	Putative transcriptional regulator
875	bZIP	1/2	233-274	9.9	0.27	bZIP transcription factor
875	bZIP	2/2	408-430	9.2	0.44	bZIP transcription factor
875	filament	1/1	181-496	550.9	8.8e-162	Intermediate filament protein
878	Zip	1/1	209-354	168.7	9.9e-47	ZIP Zinc transporter
879	OATP_C	1/1	78-445	669.4	1.9e-197	Organic Anion Transporter Polypeptide (OATP
879	OATP_N	1/1	520-662	180.8	2.2e-50	Organic Anion Transporter Polypeptide (OATP
879	kazal	1/1	471-498	14.8	0.051	Kazal-type serine protease inhibitor domain
880	G-gamma	1/1	13-67	98.2	1.1e-30	GGL domain
881	JNK	1/1	55-311	495.0	1.1e-156	Jun-like transcription factor
881	PspA_IM30	1/1	344-382	9.1	0.32	PspA/IM30 family
881	bZIP	1/1	320-384	77.5	1.6e-20	bZIP transcription factor
882	chloroa_b-bind	1/1	69-93	28.3	5.6e-07	Chlorophyll A-B binding protein
883	chloroa_b-bind	1/1	82-133	103.6	1.1e-28	Chlorophyll A-B binding protein
884	Glyco_transf_25	1/1	35-219	252.2	7.1e-72	Glycosyltransferase family 25 (LPS bi
885	chloroa_b-bind	1/1	78-120	84.7	3.1e-23	Chlorophyll A-B binding protein
888	DEP	1/1	454-528	120.9	2.4e-32	Domain found in Dishevelled, Egl-10, and
888	DIX	1/1	33-114	196.2	5.1e-55	DIX domain
888	Dishevelled	1/1	174-245	138.7	1.7e-46	Dishevelled

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						specific domain
888	PDZ	1/1	281-368	87.8	1.5e-23	PDZ domain (Also known as DHR or GLGF)
889	DUF232	1/2	282-316	8.5	0.72	Putative transcriptional regulator
889	K-box	1/1	176-193	7.8	0.52	K-box region
889	filament	1/1	158-474	527.7	8.2e-155	Intermediate filament protein
890	ank	2/3	84-116	11.9	0.14	Ankyrin repeat
890	ank	3/3	117-149	20.6	0.00046	Ankyrin repeat
891	Herpes_HEPA	1/1	85-99	3.4	0.86	Herpesvirus DNA helicase/primase complex
891	actin	1/1	77-279	440.8	9.4e-134	Actin
892	ig	1/4	41-100	36.7	1.6e-08	Immunoglobulin domain
892	ig	2/4	175-236	30.1	1.1e-06	Immunoglobulin domain
892	ig	3/4	274-333	19.2	0.0012	Immunoglobulin domain
893	Ribosomal_L14	1/1	32-153	218.5	9.7e-62	Ribosomal protein L14p/L23e
894	PMP22_Claudin	1/1	73-223	278.8	6.8e-80	PMP-22/EMP/MP20/Claudin family
895	alk_phosphatase	1/1	41-512	1065.8	0	Alkaline phosphatase
897	CPSF_A	1/1	821-1105	508.3	5.8e-149	CPSF A subunit region
898	Neur_chan_memb	1/2	29-124	93.3	1.2e-26	Neurotransmitter-gated ion-channel tra
898	Neur_chan_memb	2/2	220-245	20.5	3.4e-05	Neurotransmitter-gated ion-channel tra
899	G-patch	1/1	2311-2355	70.7	3.9e-19	G-patch domain
899	dsrm	1/1	2378-2414	38.2	2.9e-09	Double-stranded RNA binding motif
900	serpin	1/1	9-423	515.3	1e-151	Serpin (serine protease inhibitor)
901	Lipoprotein_X	1/21	224-246	10.2	0.086	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	10/21	477-501	11.6	0.035	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	11/21	502-521	13.8	0.0086	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	12/21	523-541	12.8	0.017	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	13/21	543-566	18.6	0.00042	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	14/21	567-596	21.7	5.8e-05	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	15/21	597-621	13.7	0.0092	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	16/21	622-649	21.5	6.5e-05	Mycoplasma MG185/MG260

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						protein
901	Lipoprotein_X	17/21	652-671	12.5	0.021	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	18/21	672-696	15.6	0.0027	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	2/21	247-271	11.9	0.03	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	20/21	725-754	8.5	0.25	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	3/21	273-298	20.2	0.00015	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	4/21	303-329	17.8	0.0007	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	5/21	332-356	16.5	0.0016	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	6/21	357-386	19.5	0.00023	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	7/21	387-419	23.1	2.3e-05	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	8/21	422-446	17.8	0.0007	Mycoplasma MG185/MG260 protein
901	Lipoprotein_X	9/21	447-476	18.8	0.00035	Mycoplasma MG185/MG260 protein
902	Seryl_tRNA_N	1/1	27-78	76.9	4.2e-19	Seryl-tRNA synthetase N-terminal domain
902	tRNA-synt_2b	1/1	224-391	201.2	9e-59	tRNA synthetase class II core domain (G,
903	CH	1/1	81-196	41.3	5.2e-10	Calponin homology (CH) domain
903	IQ	1/3	730-750	23.4	0.00011	IQ calmodulin-binding motif
903	IQ	2/3	760-780	22.6	0.00018	IQ calmodulin-binding motif
903	IQ	3/3	790-810	13.7	0.063	IQ calmodulin-binding motif
903	Peptidase_C57	1/1	1233-1240	5.8	0.74	Vaccinia virus I7 processing peptidase
903	RasGAP	1/1	977-1190	341.7	8.1e-99	GTPase-activator protein for Ras-like G
903	RasGAP_C	1/1	1405-1540	227.6	1.8e-64	RasGAP C-terminus
903	WW	1/1	650-664	13.9	0.041	WW domain
904	Alpha_L_fucos	1/1	20-414	1057.3	0	Alpha-L-fucosidase
906	hormone	1/1	19-106	61.2	2.3e-22	Somatotropin hormone family
907	rrm	1/1	307-378	84.1	2.8e-23	RNA recognition motif. (a.k.a. RRM, RBD, or
911	cyclin	1/1	75-202	169.3	6.5e-47	Cyclin, N-terminal domain
911	cyclin_C	1/1	204-332	78.7	6.1e-20	Cyclin, C-terminal domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
912	RIIa	1/1	54-91	63.4	3.5e-16	Regulatory subunit of type II PKA R-subu
912	cNMP_binding	1/2	181-269	106.8	7.1e-29	Cyclic nucleotide-binding domain
912	cNMP_binding	2/2	299-393	117.7	5.9e-32	Cyclic nucleotide-binding domain
913	DSBA	1/1	61-76	12.5	0.023	DSBA oxidoreductase
913	RNA_pol_L	1/1	35-127	200.3	4.6e-60	RNA polymerases L / 13 to 16 kDa subunit
914	Collagen	1/21	602-650	37.1	1.1e-08	Collagen triple helix repeat (20 copies)
914	Collagen	10/21	941-971	19.6	0.00068	Collagen triple helix repeat (20 copies)
914	Collagen	11/21	984-1012	14.7	0.015	Collagen triple helix repeat (20 copies)
914	Collagen	17/21	1249-1269	8.0	1	Collagen triple helix repeat (20 copies)
914	Collagen	21/21	1473-1517	34.0	7.4e-08	20/21 1434 1446 .. 1 13
914	Collagen	3/21	676-735	49.9	3.2e-12	Collagen triple helix repeat (20 copies)
914	Collagen	4/21	736-780	39.1	3e-09	Collagen triple helix repeat (20 copies)
914	Collagen	5/21	781-840	51.4	1.2e-12	Collagen triple helix repeat (20 copies)
914	Collagen	6/21	854-885	17.1	0.0033	Collagen triple helix repeat (20 copies)
914	Seryl_tRNA_N	1/1	520-537	12.5	0.13	Seryl-tRNA synthetase N-terminal domain
915	GNT-I	1/1	45-477	1084.9	0	GNT-I family
916	CBM_14	2/6	922-942	9.2	0.14	Chitin binding Peritrophin-A domain
916	CBM_14	4/6	1763-1783	10.7	0.047	3/6 1643 1665 .. 35 58
916	CBM_14	5/6	1923-1943	11.4	0.028	3/6 1643 1665 .. 35 58
916	EGF	10/47	748-783	31.4	3.7e-07	EGF-like domain
916	EGF	11/47	858-894	41.8	4.1e-10	EGF-like domain
916	EGF	12/47	900-936	37.7	5.9e-09	EGF-like domain
916	EGF	13/47	942-976	27.1	6e-06	EGF-like domain
916	EGF	14/47	1045-1081	37.0	9.4e-09	EGF-like domain
916	EGF	15/47	1163-1199	31.6	3.1e-07	EGF-like domain
916	EGF	16/47	1205-1242	17.7	0.0026	EGF-like domain
916	EGF	17/47	1248-1284	28.1	3.1e-06	EGF-like domain
916	EGF	18/47	1290-1326	27.1	6e-06	EGF-like domain
916	EGF	19/47	1332-1367	22.5	0.00012	EGF-like domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
916	EGF	2/47	250-276	18.0	0.0021	EGF-like domain
916	EGF	20/47	1373-1409	31.9	2.5e-07	EGF-like domain
916	EGF	21/47	1415-1446	29.2	1.5e-06	EGF-like domain
916	EGF	22/47	1457-1492	26.5	8.7e-06	EGF-like domain
916	EGF	23/47	1498-1533	27.5	4.6e-06	EGF-like domain
916	EGF	24/47	1539-1575	33.4	1e-07	EGF-like domain
916	EGF	25/47	1581-1616	25.9	1.3e-05	EGF-like domain
916	EGF	26/47	1622-1657	25.6	1.6e-05	EGF-like domain
916	EGF	27/47	1741-1777	36.3	1.5e-08	EGF-like domain
916	EGF	28/47	1783-1818	15.9	0.0086	EGF-like domain
916	EGF	29/47	1901-1937	30.4	6.8e-07	EGF-like domain
916	EGF	3/47	281-308	16.9	0.0045	EGF-like domain
916	EGF	30/47	1943-1976	29.5	1.3e-06	EGF-like domain
916	EGF	31/47	1984-2020	21.0	0.00031	EGF-like domain
916	EGF	32/47	2026-2059	17.6	0.0029	EGF-like domain
916	EGF	33/47	2065-2102	37.8	5.5e-09	EGF-like domain
916	EGF	34/47	2108-2142	25.1	2.2e-05	EGF-like domain
916	EGF	35/47	2148-2184	32.8	1.4e-07	EGF-like domain
916	EGF	36/47	2262-2295	22.9	9e-05	EGF-like domain
916	EGF	37/47	2301-2335	23.8	5.1e-05	EGF-like domain
916	EGF	38/47	2341-2376	26.0	1.2e-05	EGF-like domain
916	EGF	39/47	2382-2420	20.0	0.00061	EGF-like domain
916	EGF	4/47	381-417	20.2	0.00051	EGF-like domain
916	EGF	40/47	2426-2462	25.7	1.5e-05	EGF-like domain
916	EGF	41/47	2537-2573	30.4	6.9e-07	EGF-like domain
916	EGF	42/47	2579-2614	33.5	9e-08	EGF-like domain
916	EGF	43/47	2620-2650	18.0	0.0022	EGF-like domain
916	EGF	44/47	2659-2696	32.4	1.9e-07	EGF-like domain
916	EGF	45/47	2702-2736	16.6	0.0054	EGF-like domain
916	EGF	46/47	2742-2777	20.6	0.00041	EGF-like domain
916	EGF	47/47	2783-2817	13.8	0.034	EGF-like domain
916	EGF	5/47	423-459	30.1	8.6e-07	EGF-like domain
916	EGF	6/47	584-614	24.5	3.2e-05	EGF-like domain
916	EGF	7/47	625-659	23.3	6.8e-05	EGF-like domain
916	EGF	8/47	665-701	38.3	4e-09	EGF-like domain
916	EGF	9/47	707-742	42.0	3.7e-10	EGF-like domain
916	TB	1/10	324-366	72.5	2.4e-21	TB domain
916	TB	10/10	2477-2520	76.0	1.9e-22	TB domain
916	TB	2/10	474-519	69.6	2e-20	TB domain
916	TB	3/10	799-841	75.9	2e-22	TB domain
916	TB	4/10	991-1032	59.3	3.6e-17	TB domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
916	TB	6/10	1096-1138	71.2	6.2e-21	TB domain
916	TB	7/10	1678-1719	79.2	1.8e-23	TB domain
916	TB	8/10	1835-1878	79.5	1.5e-23	TB domain
916	TB	9/10	2199-2241	73.0	1.7e-21	TB domain
916	wnt	1/1	434-445	3.4	0.78	wnt family
917	Fragilysin	1/1	448-495	6.8	0.39	Fragilysin metalloproteinase (M10C) en
917	Peptidase M10	1/1	160-266	276.2	4.1e-79	Matrixin
917	Peptidase_M10_N	1/1	80-154	141.4	1.3e-48	Matrix metalloproteinase, N-terminal do
917	UPF0143	1/1	540-560	6.2	0.89	Uncharacterised protein family (UPF01
917	fn2	1/3	281-322	92.4	3.9e-34	Fibronectin type II domain
917	fn2	2/3	339-380	91.9	6.1e-34	Fibronectin type II domain
917	fn2	3/3	397-438	104.0	1.4e-38	Fibronectin type II domain
917	hemopexin	1/4	523-566	42.4	2.7e-11	Hemopexin
917	hemopexin	2/4	568-611	54.2	6.8e-15	Hemopexin
917	hemopexin	3/4	616-663	73.0	1.3e-20	Hemopexin
917	hemopexin	4/4	665-708	31.9	4.4e-08	Hemopexin
918	CD36	1/1	28-468	797.9	3.8e-236	CD36 family
920	TSC22	1/1	141-200	146.4	4.8e-46	TSC-22/dip/bun family
921	AMOP	1/1	483-646	319.0	7e-96	AMOP domain
921	tsp_1	1/1	417-457	25.2	4.8e-06	Thrombospondin type 1 domain
923	Peptidase_C1	1/1	85-334	393.4	3.7e-117	Papain family cysteine protease
926	secY	1/3	87-108	11.6	0.013	eubacterial secY protein
926	secY	3/3	278-472	28.2	1.7e-07	eubacterial secY protein
927	DUF173	1/1	583-629	16.4	0.0014	Uncharacterized ACR, COG1354
928	arf	1/1	24-202	423.3	2.1e-123	ADP-ribosylation factor family
930	EF1BD	1/1	175-261	198.7	1.5e-56	EF-1 guanine nucleotide exchange domain
931	Myc-LZ	1/1	360-390	8.5	0.75	Myc leucine zipper domain
931	bZIP	1/1	327-391	21.5	0.00014	bZIP transcription factor
933	CAP	1/1	13-483	1121.9	0	CAP protein
934	7tm_1	1/1	179-431	255.5	4.1e-82	7 transmembrane receptor (rhodopsin family)
935	NadA	1/1	18-38	7.9	0.78	Quinolinate synthetase A protein
935	RrnaAD	1/1	133-169	5.2	0.78	Ribosomal RNA adenine dimethylase
935	efhand	1/4	34-62	39.6	4.8e-09	EF hand
935	efhand	2/4	70-98	38.4	1e-08	EF hand
935	efhand	3/4	107-135	42.1	9.8e-10	EF hand
935	efhand	4/4	143-171	41.2	1.7e-09	EF hand

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
936	rrm	1/2	107-176	59.4	5e-16	RNA recognition motif. (a.k.a. RRM, RBD, or
936	rrm	2/2	194-237	43.0	3.4e-11	RNA recognition motif. (a.k.a. RRM, RBD, or
939	Vps55	1/1	26-154	54.2	2.2e-14	Vacuolar protein sorting 55
940	SH2	1/1	110-191	53.8	2.3e-17	SH2 domain
943	CH	1/1	57-169	79.5	1.4e-20	Calponin homology (CH) domain
943	calponin	1/1	206-231	51.5	2e-14	Calponin family repeat
946	PSI_PsaJ	1/1	185-220	7.8	0.76	Photosystem I reaction centre subunit IX / P
947	YT521-B	1/1	436-526	210.7	2.2e-59	YT521-B-like family
950	HSP20	1/1	80-176	73.5	4.9e-19	Hsp20/alpha crystallin family
951	CH	1/2	55-158	99.5	4.2e-26	Calponin homology (CH) domain
951	CH	2/2	168-273	127.8	2e-34	Calponin homology (CH) domain
951	efhand	1/2	777-805	22.5	0.00025	EF hand
951	efhand	2/2	818-846	20.1	0.0012	EF hand
951	spectrin	1/4	299-409	62.5	7.6e-16	Spectrin repeat
951	spectrin	2/4	419-524	108.6	1.2e-28	Spectrin repeat
951	spectrin	3/4	535-646	56.3	4.1e-14	Spectrin repeat
951	spectrin	4/4	657-760	56.3	4.2e-14	Spectrin repeat
952	abhydrolase	1/1	172-407	50.2	2.1e-14	alpha/beta hydrolase fold
953	NIF	1/1	164-338	358.8	1.4e-104	NLI interacting factor
954	PMP22_Claudin	1/1	12-127	149.3	5.1e-42	PMP-22/EMP/MP20/Claudin family
955	Exo_endo_phos	1/1	400-699	140.8	2.4e-38	Endonuclease/Exonuclease/phosphatase fa
956	rrm	1/1	49-115	78.6	1.1e-21	RNA recognition motif. (a.k.a. RRM, RBD, or
956	zf-CCHC	1/1	140-157	20.4	0.00095	Zinc knuckle
958	SH3	1/1	365-413	52.4	9.2e-13	SH3 domain
959	ELH	1/1	247-273	4.4	0.71	Egg-laying hormone precursor
959	TGF-beta	1/1	337-445	218.2	1.3e-62	Transforming growth factor beta like
959	TGFb_propeptide	1/1	61-293	194.0	2.3e-54	TGF-beta propeptide
959	Tub	1/1	255-264	2.3	0.33	Tub family
960	Hydrolase	2/3	347-379	13.2	0.026	haloacid dehalogenase-like hydrolase
961	PABP	1/1	544-615	166.7	3.8e-46	Poly-adenylate binding protein, unique
961	rrm	1/4	14-85	98.4	1.7e-27	RNA recognition motif. (a.k.a. RRM, RBD
961	rrm	2/4	102-171	90.8	2.8e-25	RNA recognition motif. (a.k.a.

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						RRM, RBD
961	rrm	3/4	194-264	110.9	3.6e-31	RNA recognition motif. (a.k.a. RRM, RBD)
961	rrm	4/4	297-366	86.5	5.3e-24	RNA recognition motif. (a.k.a. RRM, RBD)
962	bZIP	1/1	672-735	17.2	0.0023	bZIP transcription factor
964	COLFI	1/1	948-1165	561.6	5.7e-219	Fibrillar collagen C-terminal domain
964	Collagen	1/13	105-142	20.6	0.00035	Collagen triple helix repeat (20 copies)
964	Collagen	10/13	657-716	44.5	9.7e-11	Collagen triple helix repeat (20 copies)
964	Collagen	11/13	717-776	56.8	4e-14	Collagen triple helix repeat (20 copies)
964	Collagen	12/13	780-839	56.3	5.6e-14	Collagen triple helix repeat (20 copies)
964	Collagen	13/13	840-896	58.7	1.2e-14	Collagen triple helix repeat (20 copies)
964	Collagen	2/13	171-230	64.5	3e-16	Collagen triple helix repeat (20 copies)
964	Collagen	3/13	237-296	76.5	1.6e-19	Collagen triple helix repeat (20 copies)
964	Collagen	4/13	297-356	66.3	9.5e-17	Collagen triple helix repeat (20 copies)
964	Collagen	5/13	357-416	65.2	1.9e-16	Collagen triple helix repeat (20 copies)
964	Collagen	6/13	417-476	65.6	1.5e-16	Collagen triple helix repeat (20 copies)
964	Collagen	7/13	477-536	61.9	1.6e-15	Collagen triple helix repeat (20 copies)
964	Collagen	8/13	537-596	67.3	5.2e-17	Collagen triple helix repeat (20 copies)
964	Collagen	9/13	597-656	47.1	1.8e-11	Collagen triple helix repeat (20 copies)
964	DNA_pol3_beta	1/1	925-947	9.3	0.39	DNA polymerase III beta subunit, N-term
965	DEAD	1/1	205-430	273.3	4.3e-83	DEAD/DEAH box helicase
965	helicase_C	1/1	477-548	130.3	1.4e-35	Helicase conserved C-terminal domain
966	zf-RanBP	1/1	85-114	32.7	2.8e-07	Zn-finger in Ran binding protein and others
967	DUF343	1/1	12-131	158.7	3.2e-44	Protein of unknown function (DUF343)
969	UPF0005	1/1	281-347	19.4	0.00018	Uncharacterized protein family

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						UPF0005
970	GSHPx	1/1	45-159	245.6	7e-70	Glutathione peroxidase
970	RTX	1/1	48-57	5.2	0.22	RTX N-terminal domain
971	Insulin	1/1	122-179	84.7	1.8e-21	Insulin/IGF/Rel axin family
972	2OG-FeII_Oxy	1/1	353-451	52.8	1.7e-13	2OG-Fe(II) oxygenase superfamily
975	ank	2/7	61-93	33.7	8.2e-08	Ankyrin repeat
975	ank	3/7	94-126	22.1	0.00017	Ankyrin repeat
975	ank	4/7	127-159	29.4	1.4e-06	Ankyrin repeat
975	ank	5/7	160-192	44.2	8.8e-11	Ankyrin repeat
975	ank	6/7	193-225	38.0	4.9e-09	Ankyrin repeat
979	Glyco_transf_29	1/1	86-373	419.0	4.3e-122	Glycosyltransferase family 29 (sialyl)
980	TIM	1/1	82-254	383.9	3.8e-124	Triosephosphate isomerase
981	adh_short	1/1	60-308	297.7	1.4e-85	short chain dehydrogenase
982	Ribosomal_L24e	1/1	40-110	177.5	2.5e-51	Ribosomal protein L24e
985	annexin	1/4	63-130	116.8	4.1e-31	Annexin
985	annexin	2/4	135-202	109.0	9e-29	Annexin
985	annexin	3/4	219-287	88.8	1.1e-22	Annexin
985	annexin	4/4	295-362	106.8	4.2e-28	Annexin
989	Fz	1/1	147-266	213.2	6.3e-72	Fz domain
989	NTR	1/1	298-402	80.9	1.2e-20	NTR/C345C module
990	WW	1/1	151-180	48.0	1e-11	WW domain
991	Glyco_hydro_35	1/1	6-66	89.4	4.7e-26	Glycosyl hydrolases family 35
993	PKI	1/1	15-84	98.0	1.2e-27	cAMP-dependent protein kinase inhibitor
994	RWP-RK	1/1	63-74	8.4	0.71	RWP-RK domain
994	Stathmin	1/1	26-165	311.6	9.2e-90	Stathmin family
999	Peptidase_M1	1/1	235-619	659.8	6.6e-228	Peptidase family M1
1000	Peptidase_C1	1/1	256-483	323.3	3.8e-96	Papain family cysteine protease
1001	IF-2B	1/1	15-298	436.2	3e-127	Initiation factor 2 subunit family
1002	Cu_amine_oxid	1/2	315-722	751.6	3.3e-222	Copper amine oxidase, enzyme domain
1002	Cu_amine_oxid	2/2	723-759	61.9	1.3e-16	Copper amine oxidase, enzyme domain
1002	Cu_amine_oxidN2	1/1	58-145	115.9	2.5e-32	Copper amine oxidase, N2 domain
1002	Cu_amine_oxidN3	1/1	161-261	99.6	1.4e-28	Copper amine oxidase, N3 domain
1003	DUF279	1/1	98-110	6.8	1	Eukaryotic protein of unknown function
1003	TRAPP_Bet3	1/1	58-238	418.5	6.1e-122	Transport protein particle (TRAPP) com
1004	zf-CCCH	1/2	114-140	49.6	2.8e-13	Zinc finger C-x8-C-x5-C-x3-H

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						type (and simil
1004	zf-CCCH	2/2	152-178	48.1	8e-13	Zinc finger C-x8-C-x5-C-x3-H type (and simil
1007	Peptidase_M13	1/1	544-750	262.3	4.3e-81	Peptidase family M13
1007	Peptidase_M4	1/1	582-594	11.6	0.079	Thermolysin metallopeptidase, catalytic
1008	Cadherin_C_term	1/1	661-817	280.3	2.5e-80	Cadherin cytoplasmic region
1008	cadherin	1/5	92-182	62.9	5.1e-17	Cadherin domain
1008	cadherin	2/5	196-289	109.3	1.3e-30	Cadherin domain
1008	cadherin	3/5	303-404	122.1	2.2e-34	Cadherin domain
1008	cadherin	4/5	417-510	94.1	3.7e-26	Cadherin domain
1008	cadherin	5/5	523-616	42.1	6.5e-11	Cadherin domain
1010	KH	1/3	32-78	57.3	5.9e-15	KH domain
1010	KH	2/3	116-165	63.1	1.2e-16	KH domain
1010	KH	3/3	298-346	58.3	3e-15	KH domain
1011	Glyco_hydro_2_N	1/1	78-101	19.8	0.00014	Glycosyl hydrolases family 2, sugar b
1012	C2	1/3	158-241	86.9	1.3e-23	C2 domain
1012	C2	3/3	724-757	21.5	9.4e-05	C2 domain
1013	PA28_alpha	1/1	32-95	155.4	1e-42	Proteasome activator pa28 alpha subunit
1013	PA28_beta	1/1	126-275	409.9	2.4e-119	Proteasome activator pa28 beta subunit
1013	biopterin_H	1/1	59-69	6.8	0.18	Biopterin-dependent aromatic amino acid h
1014	ras	1/1	27-129	80.3	8.8e-23	Ras family
1015	Rhabdo_glycop	1/1	392-439	10.6	0.019	Rhabdovirus spike glycoprotein
1015	ig	1/3	90-174	22.9	0.00011	Immunoglobulin domain
1015	ig	3/3	308-362	23.1	9.7e-05	Immunoglobulin domain
1016	EGF	1/5	264-300	15.1	0.014	EGF-like domain
1016	EGF	2/5	306-343	35.3	2.9e-08	EGF-like domain
1016	EGF	3/5	349-380	20.9	0.00033	EGF-like domain
1016	EGF	4/5	389-425	19.1	0.0011	EGF-like domain
1016	EGF	5/5	431-467	15.5	0.011	EGF-like domain
1016	TIL	1/2	297-349	9.9	0.094	Trypsin Inhibitor like cysteine rich do
1016	Tissue fac	1/1	583-625	20.1	0.00014	Tissue factor
1016	Xlink	1/1	33-64	7.8	0.008	Extracellular link domain
1016	lectin_c	1/1	47-103	20.3	0.00082	Lectin C-type domain
1018	FH2	1/1	1-59	57.2	9.5e-15	Formin Homology 2 Domain
1019	GoLoco	1/1	64-84	33.6	1.4e-08	LGN motif, putative GEF specific for G-alpha
1019	Rap_GAP	1/1	277-464	424.3	1.1e-123	Rap/ran-GAP
1020	Cys_knot	1/1	297-394	114.6	1.8e-30	Cystine-knot domain
1020	IGFBP	1/1	77-148	115.5	1.4e-31	Insulin-like growth factor binding protein

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1020	tsp_1	1/1	249-290	56.2	2.7e-15	Thrombospondin type 1 domain
1020	vwc	2/2	151-214	102.8	1.9e-28	von Willebrand factor type C domain
1021	rrm	1/2	9-72	77.8	1.9e-21	RNA recognition motif. (a.k.a. RRM, RBD, or
1021	rrm	2/2	208-274	49.7	3.5e-13	RNA recognition motif. (a.k.a. RRM, RBD, or
1022	Ets	1/1	409-492	206.7	3.5e-58	Ets-domain
1023	CRF	1/1	192-230	70.0	9.6e-19	Corticotropin-releasing factor family
1024	Exonuclease	1/1	64-236	103.6	1.5e-27	Exonuclease
1026	OPR	1/1	59-88	50.1	9.8e-13	Octicosapeptide repeat
1027	SSF	1/2	112-279	28.8	1.7e-07	Sodium:solute symporter family
1027	SSF	2/2	400-514	12.4	0.0086	Sodium:solute symporter family
1029	Ribosomal_S9	1/1	19-151	294.9	3.2e-91	Ribosomal protein S9/S16
1031	actin	1/1	24-399	942.3	2.3e-286	Actin
1032	gln-synt	1/1	249-502	364.6	1.1e-105	Glutamine synthetase, catalytic domain
1032	gln-synt_N	1/1	163-244	128.6	1.6e-37	Glutamine synthetase, beta-Grasp domain
1034	sushi	1/3	71-117	12.5	0.15	Sushi domain (SCR repeat)
1034	sushi	2/3	137-192	54.2	1.5e-12	Sushi domain (SCR repeat)
1034	sushi	3/3	199-252	54.9	9.6e-13	Sushi domain (SCR repeat)
1034	trypsin	1/1	515-786	155.7	1.2e-48	Trypsin
1034	vwa	1/1	304-502	221.2	7.1e-64	von Willebrand factor type A domain
1036	efhand	1/6	90-118	19.0	0.0023	EF hand
1036	efhand	2/6	126-154	9.6	0.91	EF hand
1036	efhand	4/6	210-238	21.3	0.00053	EF hand
1036	efhand	6/6	287-315	9.8	0.81	EF hand
1037	bZIP	1/1	75-135	78.1	1.1e-20	bZIP transcription factor
1038	AhpC-TSA	1/1	16-165	310.5	2e-89	AhpC/TSA family
1039	IBR	1/1	340-389	7.3	0.81	IBR domain
1039	zf-C2H2	1/5	319-344	13.5	0.26	Zinc finger, C2H2 type
1039	zf-C2H2	2/5	350-374	22.3	0.0018	Zinc finger, C2H2 type
1039	zf-C2H2	3/5	380-402	26.1	0.00019	Zinc finger, C2H2 type
1039	zf-C2H2	4/5	408-430	25.7	0.00024	Zinc finger, C2H2 type
1039	zf-C2H2	5/5	438-461	23.5	0.00085	Zinc finger, C2H2 type
1040	EGF	2/2	664-691	13.2	0.052	EGF-like domain
1040	FAD_binding_7	1/1	388-412	6.0	1	FAD binding domain of DNA photolyase
1040	Pep_M12B_propep	1/1	86-201	164.7	7.6e-46	Reprolysin family

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						propeptide
1040	Reprolysin	1/1	218-420	400.8	1.3e-116	Reprolysin (M12B) family zinc metallo
1040	disintegrin	1/1	437-512	102.0	8.2e-33	Disintegrin
1041	Na_H_antiporter	1/1	477-523	8.8	0.26	Na+/H+ antiporter family
1041	Na_sulph_symp	1/2	19-174	124.1	1.3e-34	Sodium:sulfate symporter transmembran
1041	Na_sulph_symp	2/2	225-585	200.5	2.5e-56	Sodium:sulfate symporter transmembran
1042	MDM2	1/1	177-189	11.1	0.017	p53-associated protein (MDM2)
1042	NAD_binding_1	1/1	65-160	48.5	1.5e-12	Oxidoreductase NAD-binding domain
1043	trypsin	1/1	95-331	330.0	4e-104	Trypsin
1045	EGF	1/18	83-110	27.0	6.3e-06	EGF-like domain
1045	EGF	10/18	803-838	26.0	1.2e-05	EGF-like domain
1045	EGF	11/18	844-879	21.2	0.00027	EGF-like domain
1045	EGF	12/18	885-921	24.5	3.3e-05	EGF-like domain
1045	EGF	13/18	927-963	24.7	2.9e-05	EGF-like domain
1045	EGF	14/18	969-1006	22.1	0.00015	EGF-like domain
1045	EGF	15/18	1107-1144	20.2	0.00053	EGF-like domain
1045	EGF	16/18	1150-1185	30.4	6.7e-07	EGF-like domain
1045	EGF	17/18	1304-1339	30.8	5.2e-07	EGF-like domain
1045	EGF	18/18	1345-1384	31.5	3.5e-07	EGF-like domain
1045	EGF	2/18	310-345	30.6	6.1e-07	EGF-like domain
1045	EGF	4/18	556-592	29.8	1e-06	EGF-like domain
1045	EGF	5/18	598-634	28.1	3.2e-06	EGF-like domain
1045	EGF	6/18	640-661	9.2	0.68	EGF-like domain
1045	EGF	8/18	721-756	24.6	3e-05	EGF-like domain
1045	EGF	9/18	762-797	26.4	9.3e-06	EGF-like domain
1045	Fanconia	1/1	9-31	5.6	0.94	Fanconi anaemia group A protein
1045	TB	1/4	246-289	54.5	1.1e-15	TB domain
1045	TB	2/4	367-407	70.6	9.5e-21	TB domain
1045	TB	3/4	1036-1079	74.2	7.2e-22	TB domain
1045	TB	4/4	1213-1255	76.3	1.5e-22	TB domain
1045	VSP	1/3	660-681	7.4	0.3	
1045	VSP	3/3	907-927	6.9	0.41	
1045	granulin	1/2	621-636	7.4	0.58	Granulin
1048	CSD	1/8	53-118	77.9	1.8e-20	'Cold-shock' DNA-binding domain
1048	CSD	3/8	213-276	89.0	1.3e-23	2/8 180 207 .. 44 71
1048	CSD	4/8	337-365	9.7	0.31	2/8 180 207 .. 44 71
1048	CSD	5/8	376-424	28.5	1.6e-06	2/8 180 207 .. 44 71
1048	CSD	6/8	514-538	11.3	0.11	2/8 180 207 .. 44 71
1048	CSD	7/8	546-610	76.5	4.6e-20	2/8 180 207 .. 44 71
1048	CSD	8/8	701-766	74.9	1.2e-19	2/8 180

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						207 .. 4471
1050	DIL	1/1	451-557	160.9	2.2e-44	DIL domain
1050	FHA	1/1	92-158	50.0	1.5e-11	FHA domain
1050	PDZ	1/1	675-758	86.3	4e-23	PDZ domain (Also known as DHR or GLGF)
1051	Lamp	1/1	65-438	832.2	1.7e-246	Lysosome-associated membrane glycoprotein
1052	pp-binding	1/1	103-170	69.7	1.1e-17	Phosphopantetheine attachment site
1053	START	1/1	174-324	58.6	4.1e-16	START domain
1055	HSP70	1/1	620-643	4.7	0.87	Hsp70 protein
1055	helicase_C	1/1	643-732	50.3	8.6e-13	Helicase conserved C-terminal domain
1056	Calpain_III	1/1	385-542	387.0	2.6e-113	Calpain large subunit, domain III
1056	Peptidase_C2	1/1	75-374	739.1	1.9e-218	Calpain family cysteine protease
1056	Porin_2	1/1	683-706	5.9	0.69	Porin subfamily
1056	efhand	2/4	609-637	14.7	0.036	EF hand
1056	efhand	3/4	639-667	16.6	0.01	EF hand
1057	KOW	1/1	135-169	34.8	1.3e-07	KOW motif
1058	TGF-beta	1/1	260-367	121.4	2.7e-34	Transforming growth factor beta like domain
1062	ig	1/2	65-142	13.7	0.039	Immunoglobulin domain
1062	ig	2/2	172-235	21.2	0.00032	Immunoglobulin domain
1063	EGF	2/2	436-451	12.1	0.1	EGF-like domain
1063	Glyco_hydro_56	1/1	38-376	785.1	2.7e-232	Hyaluronidase
1064	DUF232	1/2	278-329	14.6	0.017	Putative transcriptional regulator
1064	KE2	1/1	315-347	9.6	0.39	KE2 family protein
1064	filament	1/1	97-409	568.1	5.6e-167	Intermediate filament protein
1067	PKD	1/2	280-319	25.1	9.2e-07	PKD domain
1067	PKD	2/2	448-476	7.0	0.5	PKD domain
1068	zf-B_box	1/1	228-268	55.4	1.2e-12	B-box zinc finger
1069	ras	1/1	25-216	372.2	1.9e-109	Ras family
1070	IRS	1/1	234-336	206.5	3.9e-58	PTB domain (IRS-1 type)
1070	PH	1/1	71-184	47.1	7.1e-12	PH domain
1071	Peptidase_M16	1/1	98-246	240.8	2e-68	Insulinase (Peptidase family M16)
1072	CBM_20	1/1	279-356	31.5	4e-07	Starch binding domain
1073	PRA1	1/1	80-240	280.6	2e-80	Prenylated rab acceptor (PRA1)
1075	CLN3	1/1	48-449	889.8	8.1e-264	CLN3 protein
1075	FA_desaturase	1/1	52-83	11.7	0.019	Fatty acid desaturase
1076	UPF0146	1/1	2989-3007	7.2	0.81	Uncharacterised protein family (UPF0146)
1076	laminin_B	2/2	1715-1851	83.2	7.3e-22	Laminin B (Domain IV)

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1076	laminin_EGF	1/22	322-378	30.1	4.1e-07	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	10/22	798-848	43.0	8.4e-11	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	11/22	851-883	29.0	8.8e-07	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	12/22	1460-1508	58.1	4e-15	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	14/22	1550-1596	44.6	2.9e-11	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	15/22	1599-1647	65.4	3.1e-17	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	16/22	1853-1883	15.1	0.0083	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	17/22	1886-1932	51.9	2.2e-13	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	18/22	1935-1988	51.4	3.2e-13	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	19/22	1991-2042	65.3	3.3e-17	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	2/22	381-448	45.4	1.6e-11	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	20/22	2045-2089	45.4	1.7e-11	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	21/22	2092-2136	47.8	3.5e-12	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	22/22	2139-2167	16.0	0.0048	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	3/22	451-493	34.1	3e-08	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	4/22	516-560	47.1	5.7e-12	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	5/22	563-606	40.4	4.5e-10	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	6/22	609-651	51.4	3.3e-13	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	7/22	654-696	40.6	4e-10	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	8/22	699-747	45.0	2.2e-11	Laminin EGF-like (Domains III and V)
1076	laminin_EGF	9/22	766-795	38.7	1.4e-09	Laminin EGF-like (Domains III and V)
1076	laminin_G	1/4	2898-2933	9.0	0.27	Laminin G domain
1076	laminin_G	3/4	3392-3524	45.2	1.3e-11	Laminin G domain
1076	laminin_G	4/4	3571-3698	60.6	5.7e-16	Laminin G domain
1076	laminin_Nterm	1/1	67-320	285.9	3.8e-86	Laminin N-

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						terminal (Domain VI)
1077	KOW	1/1	12-47	31.2	1.2e-06	KOW motif
1077	Ribosomal_L27e	1/1	59-143	213.6	7.4e-74	Ribosomal L27e protein family
1078	arf	1/1	64-240	144.3	1e-39	ADP-ribosylation factor family
1080	UPF0005	1/1	99-279	137.6	9.1e-39	Uncharacterized protein family UPF0005
1081	cyclin	1/1	81-208	163.2	4.4e-45	Cyclin, N-terminal domain
1081	cyclin_C	1/1	210-339	73.0	2.1e-18	Cyclin, C-terminal domain
1082	Oxysterol_BP	1/1	442-858	772.2	2.1e-228	Oxysterol-binding protein
1082	PH	1/1	150-242	87.5	2.9e-23	PH domain
1083	DUF348	1/1	110-129	11.6	0.14	Domain of unknown function (DUF348)
1083	rnaseH	1/1	600-733	28.5	1e-06	RNase H
1083	rve	1/1	863-963	27.5	9.7e-07	Integrase core domain
1083	rvp	1/1	63-84	25.9	7.8e-06	Retroviral aspartyl protease
1083	rvt	1/1	185-357	46.1	1.4e-11	Reverse transcriptase (RNA-dependent DNA pol
1084	MAP1_LC3	1/1	40-143	255.6	6.1e-75	Microtubule associated protein 1A/1B, light
1085	7tm_1	1/2	50-88	8.2	0.045	7 transmembrane receptor (rhodopsin family)
1089	SlyX	1/1	273-283	6.3	0.019	SlyX
1090	aa_permeases	2/2	359-410	12.5	0.012	
1092	adh_short	1/1	28-228	149.0	4.1e-41	short chain dehydrogenase
1094	Clusterin	1/1	16-463	1269.5	0	Clusterin
1094	Thymidylate_kin	1/1	338-380	9.1	0.024	Thymidylate kinase
1096	COLFI	1/1	1248-1466	568.8	9.2e-222	Fibrillar collagen C-terminal domain
1096	Collagen	1/18	112-161	27.3	5e-06	Collagen triple helix repeat (20 copies)
1096	Collagen	10/18	659-718	60.6	3.6e-15	Collagen triple helix repeat (20 copies)
1096	Collagen	11/18	719-778	70.2	8.4e-18	Collagen triple helix repeat (20 copies)
1096	Collagen	12/18	782-841	68.4	2.7e-17	Collagen triple helix repeat (20 copies)
1096	Collagen	13/18	842-901	60.4	4e-15	Collagen triple helix repeat (20 copies)
1096	Collagen	14/18	902-961	59.2	8.9e-15	Collagen triple helix repeat (20 copies)
1096	Collagen	15/18	962-1021	62.6	9.9e-16	Collagen triple helix repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						(20 copies)
1096	Collagen	16/18	1023-1081	54.4	1.8e-13	Collagen triple helix repeat (20 copies)
1096	Collagen	17/18	1082-1141	73.9	8.1e-19	Collagen triple helix repeat (20 copies)
1096	Collagen	18/18	1142-1195	40.5	1.2e-09	Collagen triple helix repeat (20 copies)
1096	Collagen	2/18	180-238	50.4	2.3e-12	Collagen triple helix repeat (20 copies)
1096	Collagen	3/18	239-298	75.7	2.5e-19	Collagen triple helix repeat (20 copies)
1096	Collagen	4/18	299-358	64.9	2.4e-16	Collagen triple helix repeat (20 copies)
1096	Collagen	5/18	359-418	61.6	1.9e-15	Collagen triple helix repeat (20 copies)
1096	Collagen	6/18	419-478	61.1	2.6e-15	Collagen triple helix repeat (20 copies)
1096	Collagen	7/18	479-538	63.9	4.4e-16	Collagen triple helix repeat (20 copies)
1096	Collagen	8/18	539-598	64.6	2.9e-16	Collagen triple helix repeat (20 copies)
1096	Collagen	9/18	599-658	62.1	1.4e-15	Collagen triple helix repeat (20 copies)
1098	DUF410	1/1	66-315	513.5	1.6e-150	Protein of unknown function (DUF410)
1098	v110	1/1	306-326	8.7	0.55	Viral family 110
1100	G-alpha	1/1	59-407	820.0	8.4e-243	G-protein alpha subunit
1100	arf	1/1	244-279	25.6	4e-06	ADP-ribosylation factor family
1101	ECH	1/1	367-539	73.0	1.4e-20	Enoyl-CoA hydratase/isomerase family
1101	chromo	1/1	77-113	53.3	3.5e-14	'chromo' (Chromatin Organization Modifiers)
1102	MAM	1/1	27-184	212.9	4.7e-60	MAM domain
1102	Y_phosphatase	1/2	923-1153	432.5	3.9e-126	Protein-tyrosine phosphatase
1102	Y_phosphatase	2/2	1213-1447	326.5	3.1e-94	Protein-tyrosine phosphatase
1102	bromodomain	1/1	1008-1024	7.8	0.79	Bromodomain
1102	fn3	1/4	281-367	32.1	8e-08	Fibronectin type III domain
1102	fn3	2/4	379-470	8.2	0.67	Fibronectin type III domain
1102	fn3	3/4	482-575	42.5	8e-11	Fibronectin type III domain
1102	ig	1/1	199-262	23.1	9.9e-05	Immunoglobulin domain
1104	PWWP	1/1	114-186	123.0	4.9e-34	PWWP domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1105	Bcl-2	1/1	233-332	165.6	2.1e-66	Apoptosis regulator proteins, Bcl-2 family
1106	sugar_tr	1/1	15-468	661.4	4.6e-195	Sugar (and other) transporter
1107	C2	1/1	521-600	52.4	1.1e-13	C2 domain
1107	Calpain_III	1/1	353-498	269.1	1.9e-78	Calpain large subunit, domain III
1107	Peptidase_C2	1/1	29-347	283.1	3.5e-81	Calpain family cysteine protease
1108	DSPc	1/1	317-457	244.7	1.3e-69	Dual specificity phosphatase, catalytic
1108	Rhodanese	1/2	130-167	27.7	5.9e-07	Rhodanese-like domain
1108	Y_phosphatase	1/1	387-436	6.3	0.81	Protein-tyrosine phosphatase
1109	UPF0128	1/1	467-482	6.5	0.99	Uncharacterised protein family (UPF0128)
1109	WH2	1/1	1160-1180	14.6	0.023	WH2 motif
1110	rrm	1/2	420-474	13.8	0.013	RNA recognition motif. (a.k.a. RRM, RBD, or
1110	rrm	2/2	504-572	26.8	2e-06	RNA recognition motif. (a.k.a. RRM, RBD, or
1112	Fork_head	1/1	55-191	93.0	6.1e-24	Fork head domain
1113	thyroglobulin_1	1/1	156-228	104.2	2.6e-27	Thyroglobulin type-1 repeat
1114	E1_DerP2_DerF2	1/1	51-178	185.6	8e-52	ML domain
1115	ENV_polyprotein	1/1	2-28	17.1	0.00015	ENV polyprotein (coat polyprotein)
1116	heme_1	1/1	104-184	53.8	6.5e-14	Heme/Steroid binding domain
1117	IGFBP	1/1	87-145	99.4	5.7e-27	Insulin-like growth factor binding pr
1117	thyroglobulin_1	1/1	234-309	142.1	1e-38	Thyroglobulin type-1 repeat
1119	EGF	2/6	181-216	26.3	9.7e-06	EGF-like domain
1119	EGF	3/6	222-256	23.6	5.9e-05	EGF-like domain
1119	EGF	4/6	262-296	20.1	0.00056	EGF-like domain
1119	EGF	5/6	302-329	12.5	0.078	EGF-like domain
1119	TIL	1/4	203-222	10.7	0.051	Trypsin Inhibitor like cysteine rich domain
1119	TIL	2/4	241-262	15.7	0.0014	Trypsin Inhibitor like cysteine rich domain
1119	VSP	2/2	282-304	10.4	0.045	1/2 242 266 .. 1 29
1120	ZU5	1/1	989-1093	218.3	1.1e-61	ZU5 domain
1120	ank	10/24	340-372	32.1	2.4e-07	Ankyrin repeat
1120	ank	11/24	373-405	35.8	2.2e-08	Ankyrin repeat
1120	ank	12/24	406-438	45.1	4.7e-11	Ankyrin repeat
1120	ank	13/24	439-471	37.2	8.7e-09	Ankyrin repeat
1120	ank	14/24	472-504	37.4	7.3e-09	Ankyrin repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1120	ank	15/24	505-537	38.3	4.1e-09	Ankyrin repeat
1120	ank	16/24	538-570	42.1	3.4e-10	Ankyrin repeat
1120	ank	17/24	571-603	40.2	1.2e-09	Ankyrin repeat
1120	ank	18/24	604-636	35.9	2e-08	Ankyrin repeat
1120	ank	19/24	637-669	44.4	7.4e-11	Ankyrin repeat
1120	ank	2/24	80-112	40.3	1.1e-09	Ankyrin repeat
1120	ank	20/24	670-702	29.0	1.9e-06	Ankyrin repeat
1120	ank	21/24	703-735	41.2	6.2e-10	Ankyrin repeat
1120	ank	22/24	736-768	38.5	3.7e-09	Ankyrin repeat
1120	ank	23/24	769-801	39.1	2.5e-09	Ankyrin repeat
1120	ank	3/24	113-145	42.6	2.4e-10	Ankyrin repeat
1120	ank	4/24	146-178	39.2	2.2e-09	Ankyrin repeat
1120	ank	5/24	179-202	20.6	0.00046	Ankyrin repeat
1120	ank	6/24	212-240	10.0	0.46	Ankyrin repeat
1120	ank	7/24	241-273	32.9	1.4e-07	Ankyrin repeat
1120	ank	8/24	274-306	44.7	6.2e-11	Ankyrin repeat
1120	ank	9/24	307-339	34.1	6.6e-08	Ankyrin repeat
1120	death	1/1	4098-4181	109.4	1e-30	Death domain
1121	LIM	1/2	30-87	77.0	2.2e-20	LIM domain
1121	LIM	2/2	90-147	40.0	6.9e-10	LIM domain
1121	PDZ	1/1	170-256	70.0	1.8e-18	PDZ domain (Also known as DHR or GLGF)
1121	pkinase	1/1	349-626	213.8	2.5e-60	Protein kinase domain
1122	Yippee	1/1	23-131	263.8	2.2e-75	Yippee putative zinc-binding protein
1123	Kunitz_BPTI	1/1	29-79	94.2	1.6e-29	Kunitz/Bovine pancreatic trypsin inhibitor
1125	NHL	1/1	73-100	33.7	8e-08	NHL repeat
1126	PUF	1/8	861-895	33.8	4.8e-08	Pumilio-family RNA binding repeat
1126	PUF	2/8	897-931	32.3	1.4e-07	Pumilio-family RNA binding repeat
1126	PUF	3/8	933-967	33.2	7.5e-08	Pumilio-family RNA binding repeat
1126	PUF	4/8	969-1003	40.3	6.7e-10	Pumilio-family RNA binding repeat
1126	PUF	5/8	1005-1039	37.1	5.4e-09	Pumilio-family RNA binding repeat
1126	PUF	6/8	1041-1075	45.2	2.6e-11	Pumilio-family RNA binding repeat
1126	PUF	7/8	1077-1112	28.1	2.2e-06	Pumilio-family RNA binding repeat
1126	PUF	8/8	1120-1154	31.0	3.3e-07	Pumilio-family RNA binding repeat
1127	Ribosomal_L7Ae	1/1	30-112	35.4	3.5e-09	Ribosomal protein L7Ae/L30e/S12e/Gadd4
1128	S10_plectin	1/1	21-118	254.1	1.9e-72	Plectin/S10 domain
1133	CBM_14	2/2	1273-1302	11.4	0.028	Chitin binding Peritrophin-A domain
1133	Cys_knot	2/2	2823-2919	100.4	3.4e-26	Cystine-knot domain
1133	EB	2/3	914-927	11.8	0.19	

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1133	TIL	1/5	401-454	41.0	1.5e-11	Trypsin Inhibitor like cysteine rich do
1133	TIL	2/5	758-813	42.4	5.6e-12	Trypsin Inhibitor like cysteine rich do
1133	TIL	3/5	882-933	27.5	2.6e-07	Trypsin Inhibitor like cysteine rich do
1133	TIL	4/5	1252-1302	34.9	1.3e-09	Trypsin Inhibitor like cysteine rich do
1133	vwa	1/3	1383-1559	173.2	9.1e-50	von Willebrand factor type A domain
1133	vwa	2/3	1604-1770	203.6	1e-58	von Willebrand factor type A domain
1133	vwa	3/3	1797-1970	184.6	3.9e-53	von Willebrand factor type A domain
1133	vwc	1/12	456-494	14.5	0.0079	von Willebrand factor type C domain
1133	vwc	11/12	2688-2750	79.2	1.3e-21	von Willebrand factor type C domain
1133	vwc	3/12	935-974	25.8	4.1e-06	von Willebrand factor type C domain
1133	vwc	4/12	1305-1341	8.5	0.43	von Willebrand factor type C domain
1133	vwc	6/12	2363-2431	89.2	1.7e-24	von Willebrand factor type C domain
1133	vwc	9/12	2537-2600	90.6	6.4e-25	von Willebrand factor type C domain
1133	vwd	1/4	141-285	133.1	5.4e-37	von Willebrand factor type D domain
1133	vwd	2/4	494-647	183.4	2e-51	von Willebrand factor type D domain
1133	vwd	3/4	973-1119	153.1	1e-42	von Willebrand factor type D domain
1133	vwd	4/4	2056-2208	138.7	1.3e-38	von Willebrand factor type D domain
1134	thioered	1/1	88-151	44.0	6.3e-12	Thioredoxin
1137	pkinase	1/1	78-352	279.4	4.6e-80	Protein kinase domain
1138	FGGY	1/1	84-111	11.3	0.051	FGGY family of carbohydrate kinases, N-termi
1138	HSP70	1/1	85-683	1382.0	0	Hsp70 protein
1139	Anti_proliferat	1/1	61-221	345.4	6.3e-100	BTG1 family
1140	EMP70	1/1	11-72	125.3	9.5e-38	Endomembrane protein 70
1141	Transglut_core	1/1	338-427	185.8	7.1e-52	Transglutaminas e-like superfamily
1141	Transglutamin_C	1/2	547-651	107.0	2.6e-30	Transglutaminas

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						e family, C-terminal i
1141	Transglutamin_C	2/2	659-756	108.8	7.2e-31	Transglutaminase family, C-terminal i
1141	Transglutamin_N	1/1	74-195	221.3	1.4e-64	Transglutaminase family
1143	PCI	1/1	433-513	57.3	3.8e-15	PCI domain
1144	PCI	1/1	781-864	106.1	2.7e-29	PCI domain
1145	RTX	1/1	916-952	3.3	1	RTX N-terminal domain
1145	SMC_C	1/1	1090-1291	410.9	5.9e-121	SMC family, C-terminal domain
1145	SMC_N	1/1	93-271	289.6	3.8e-83	RecF/RecN/SMC N terminal domain
1145	SlyX	1/1	340-351	3.6	0.4	SlyX
1146	PGM_PMM	1/1	512-622	159.5	1.3e-44	Phosphoglucomutase/phosphomannomutase, C-
1146	PGM_PMM_I	1/1	82-233	186.9	3.3e-52	Phosphoglucomutase/phosphomannomutase, al
1146	PGM_PMM_II	1/1	264-374	193.6	7e-62	Phosphoglucomutase/phosphomannomutase, al
1146	PGM_PMM_III	1/1	376-491	174.2	1.7e-48	Phosphoglucomutase/phosphomannomutase, al
1147	C2	1/2	101-165	49.6	7.2e-13	C2 domain
1148	ig	1/2	99-169	29.0	2.3e-06	Immunoglobulin domain
1148	ig	2/2	205-273	40.2	1.8e-09	Immunoglobulin domain
1151	efhand	1/2	254-280	10.6	0.48	EF hand
1151	efhand	2/2	304-332	10.6	0.48	EF hand
1152	SNase	1/5	137-230	56.1	3.4e-14	Staphylococcal nuclease homologue
1152	SNase	2/5	303-392	34.5	3e-08	Staphylococcal nuclease homologue
1152	SNase	3/5	405-560	54.9	7e-14	Staphylococcal nuclease homologue
1152	SNase	4/5	589-724	77.1	5.5e-20	Staphylococcal nuclease homologue
1152	SNase	5/5	914-959	20.9	0.00017	Staphylococcal nuclease homologue
1152	TUDOR	1/1	741-861	137.2	3e-37	Tudor domain
1154	filament	1/1	133-440	581.6	4.8e-171	Intermediate filament protein
1155	Calsequestrin	1/1	27-62	5.4	0.4	Calsequestrin
1155	EGF	11/16	1557-1569	11.9	0.12	EGF-like domain
1155	EGF	13/16	3876-3908	44.1	9.5e-11	EGF-like domain
1155	EGF	14/16	3916-3949	31.3	3.7e-07	EGF-like domain
1155	EGF	15/16	4136-4168	31.5	3.4e-07	EGF-like domain
1155	EGF	16/16	4175-4203	24.9	2.5e-05	EGF-like domain
1155	EGF	3/16	758-770	10.9	0.22	EGF-like domain
1155	EGF	5/16	870-879	9.8	0.44	EGF-like domain
1155	SEA	1/1	106-220	105.7	2.6e-30	SEA domain
1155	ig	1/22	447-508	35.8	3e-08	Immunoglobulin domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1155	ig	10/22	2479-2533	44.3	1.3e-10	Immunoglobulin domain
1155	ig	11/22	2576-2630	39.3	3.1e-09	Immunoglobulin domain
1155	ig	12/22	2672-2726	41.8	6.5e-10	Immunoglobulin domain
1155	ig	13/22	2769-2823	43.0	3e-10	Immunoglobulin domain
1155	ig	14/22	2869-2923	40.8	1.2e-09	Immunoglobulin domain
1155	ig	15/22	2967-3021	44.4	1.2e-10	Immunoglobulin domain
1155	ig	16/22	3064-3121	26.2	1.3e-05	Immunoglobulin domain
1155	ig	17/22	3155-3215	27.0	8e-06	Immunoglobulin domain
1155	ig	18/22	3254-3308	31.6	4.4e-07	Immunoglobulin domain
1155	ig	19/22	3341-3395	37.4	1.1e-08	Immunoglobulin domain
1155	ig	2/22	1719-1776	32.6	2.2e-07	Immunoglobulin domain
1155	ig	20/22	3442-3496	30.4	9.1e-07	Immunoglobulin domain
1155	ig	21/22	3531-3585	31.0	6.5e-07	Immunoglobulin domain
1155	ig	22/22	3617-3671	32.3	2.7e-07	Immunoglobulin domain
1155	ig	3/22	1814-1870	33.9	1e-07	Immunoglobulin domain
1155	ig	4/22	1908-1963	27.2	6.9e-06	Immunoglobulin domain
1155	ig	5/22	1998-2055	45.0	8.5e-11	Immunoglobulin domain
1155	ig	6/22	2093-2147	47.6	1.6e-11	Immunoglobulin domain
1155	ig	7/22	2194-2248	45.0	8.5e-11	Immunoglobulin domain
1155	ig	8/22	2287-2341	37.2	1.2e-08	Immunoglobulin domain
1155	ig	9/22	2383-2437	42.5	4.2e-10	Immunoglobulin domain
1155	laminin_B	1/3	623-757	78.0	2.1e-20	Laminin B (Domain IV)
1155	laminin_B	2/3	1018-1152	136.4	5.2e-37	Laminin B (Domain IV)
1155	laminin_B	3/3	1424-1556	133.7	3.4e-36	Laminin B (Domain IV)
1155	laminin_EGF	10/15	1591-1638	61.5	4e-16	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	11/15	1641-1696	29.9	4.6e-07	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	12/15	3883-3910	9.4	0.37	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	15/15	4191-4205	10.4	0.19	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	2/15	792-839	61.8	3.2e-16	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	3/15	842-897	37.8	2.5e-09	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	4/15	919-949	22.6	5.8e-05	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	5/15	1153-	10.7	0.16	Laminin EGF-

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
			1184			like (Domains III and V)
1155	laminin_EGF	6/15	1187-1234	67.3	9e-18	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	7/15	1237-1291	32.9	6.5e-08	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	8/15	1303-1350	55.4	2.3e-14	Laminin EGF-like (Domains III and V)
1155	laminin_EGF	9/15	1557-1576	14.6	0.012	Laminin EGF-like (Domains III and V)
1155	laminin_G	1/3	3720-3859	111.4	2e-30	Laminin G domain
1155	laminin_G	2/3	3985-4116	128.9	2.2e-35	Laminin G domain
1155	laminin_G	3/3	4262-4395	131.0	5.5e-36	Laminin G domain
1155	ldl_recept_a	1/4	223-262	47.2	8.4e-13	Low-density lipoprotein receptor domain
1155	ldl_recept_a	2/4	309-347	54.8	4e-15	Low-density lipoprotein receptor domain
1155	ldl_recept_a	3/4	349-387	57.1	8.3e-16	Low-density lipoprotein receptor domain
1155	ldl_recept_a	4/4	392-431	44.0	8e-12	Low-density lipoprotein receptor domain
1158	PX	1/1	134-173	20.1	0.00098	PX domain
1158	pkinase	1/1	210-467	304.7	1.1e-87	Protein kinase domain
1158	pkinase_C	1/1	468-542	56.0	5.6e-16	Protein kinase C terminal domain
1161	DUF260	1/1	56-82	3.3	0.95	Protein of unknown function DUF260
1163	K-box	1/2	83-110	6.9	1	K-box region
1163	Retrotrans_gag	1/1	193-286	78.5	2.9e-21	Retrotransposon gag protein
1163	zf-CCHC	1/1	367-384	16.7	0.011	Zinc knuckle
1164	7tm_2	1/1	474-723	376.5	6.9e-112	7 transmembrane receptor (Secretin family)
1164	DsbB	1/1	475-504	6.7	0.91	Disulfide bond formation protein DsbB
1164	EGF	2/3	91-120	12.5	0.077	EGF-like domain
1164	EGF	3/3	143-175	16.2	0.0072	EGF-like domain
1164	GPS	1/1	421-472	84.0	7.2e-22	Latrophilin/CL-1-like GPS domain
1165	sugar_tr	1/1	39-492	661.0	6.1e-195	Sugar (and other) transporter
1167	MBD	1/1	14-67	86.9	2.1e-22	Methyl-CpG binding domain
1168	aa_permeases	1/1	356-408	8.3	0.18	Amino acid permease
1170	Reticulon	1/1	223-414	368.1	2e-112	Reticulon
1172	FKBP	1/1	41-135	179.4	9.1e-54	FKBP-type peptidyl-prolyl cis-trans isomeras
1174	abhydrolase	1/2	47-104	28.9	7e-08	alpha/beta

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						hydrolase fold
1174	abhydrolase	2/2	120-186	7.6	0.24	alpha/beta hydrolase fold
1174	abhydrolase_2	1/1	173-194	7.3	0.61	Phospholipase/C arboxylesterase
1176	DUF357	1/1	449-465	8.6	0.48	Protein of unknown function (DUF357)
1176	Furin-like	1/1	627-644	8.0	0.23	Furin-like cysteine rich region
1176	P	1/1	470-601	250.4	2.5e-71	Proprotein convertase P-domain
1176	Peptidase_S8	1/1	153-458	436.3	2.8e-127	Subtilase family
1176	VSP	2/2	667-690	6.4	0.56	1/2 242 266 .. 1 29
1179	Exostosin	1/1	217-503	327.6	1.4e-94	Exostosin family
1182	COLFI	1/1	1661-1872	488.9	1.5e-190	Fibrillar collagen C-terminal domain
1182	Collagen	10/20	1009-1068	53.8	2.6e-13	Collagen triple helix repeat (20 copies)
1182	Collagen	11/20	1069-1104	26.4	9.2e-06	Collagen triple helix repeat (20 copies)
1182	Collagen	12/20	1105-1161	42.5	3.5e-10	Collagen triple helix repeat (20 copies)
1182	Collagen	13/20	1162-1221	54.6	1.6e-13	Collagen triple helix repeat (20 copies)
1182	Collagen	14/20	1222-1281	54.2	2e-13	Collagen triple helix repeat (20 copies)
1182	Collagen	15/20	1285-1344	42.9	2.6e-10	Collagen triple helix repeat (20 copies)
1182	Collagen	16/20	1345-1404	55.5	9.3e-14	Collagen triple helix repeat (20 copies)
1182	Collagen	17/20	1405-1457	34.2	6.5e-08	Collagen triple helix repeat (20 copies)
1182	Collagen	18/20	1459-1518	57.2	3.1e-14	Collagen triple helix repeat (20 copies)
1182	Collagen	19/20	1528-1587	59.0	9.7e-15	Collagen triple helix repeat (20 copies)
1182	Collagen	2/20	505-553	41.4	6.8e-10	Collagen triple helix repeat (20 copies)
1182	Collagen	20/20	1588-1607	11.1	0.14	Collagen triple helix repeat (20 copies)
1182	Collagen	3/20	593-648	34.1	6.9e-08	Collagen triple helix repeat (20 copies)
1182	Collagen	4/20	649-708	59.8	6e-15	Collagen triple helix repeat (20 copies)
1182	Collagen	5/20	709-768	58.8	1.1e-14	Collagen triple helix repeat (20 copies)

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1182	Collagen	6/20	769-828	40.8	9.7e-10	Collagen triple helix repeat (20 copies)
1182	Collagen	7/20	832-887	34.5	5.5e-08	Collagen triple helix repeat (20 copies)
1182	Collagen	8/20	889-948	41.9	4.9e-10	Collagen triple helix repeat (20 copies)
1182	Collagen	9/20	949-1008	57.9	2e-14	Collagen triple helix repeat (20 copies)
1182	TSPN	1/1	75-266	290.0	1.7e-83	Thrombospondin N-terminal - like domain
1182	laminin_G	1/1	195-218	14.6	0.0071	Laminin G domain
1185	fibrinogen_C	1/2	235-335	156.5	1e-43	Fibrinogen beta and gamma chains, C-term
1185	fibrinogen_C	2/2	377-451	67.0	3.5e-18	Fibrinogen beta and gamma chains, C-term
1187	SH3	1/1	335-389	78.3	6.8e-20	SH3 domain
1188	AT hook	1/1	73-85	8.9	1	AT hook motif
1188	Vinculin	1/1	43-891	1728.4	0	Vinculin family
1189	annexin	1/2	13-67	67.1	1e-16	Annexin
1189	annexin	2/2	75-142	109.4	6.9e-29	Annexin
1190	Heme oxygenase	1/1	35-272	639.9	1.4e-188	Heme oxygenase
1192	DED	1/1	35-112	19.8	0.00037	Death effector domain
1193	proteasome	1/1	38-226	230.9	1.9e-65	Proteasome A-type and B-type
1194	adh_short	1/1	88-380	244.7	1.3e-69	short chain dehydrogenase
1195	V-ATPase_G	1/1	13-118	205.7	6.9e-58	Vacuolar (H ⁺)-ATPase G subunit
1197	BTB	2/2	490-594	81.6	4.7e-21	BTB/POZ domain
1197	ras	2/2	231-250	6.2	0.92	Ras family
1198	AMP-binding	1/1	1-245	224.3	1.8e-63	AMP-binding enzyme
1199	gla	1/1	39-80	67.3	2.6e-19	Vitamin K-dependent carboxylation/gamma-
1200	PDZ	1/2	119-198	49.1	1.6e-12	PDZ domain (Also known as DHR or GLGF)
1200	PDZ	2/2	203-277	25.2	1.1e-05	PDZ domain (Also known as DHR or GLGF)
1201	EPH_lbd	1/1	20-200	399.0	3.8e-117	Ephrin receptor ligand binding domain
1201	SAM	1/1	908-972	93.9	3.6e-25	SAM domain (Sterile alpha motif)
1201	fn3	1/2	327-417	39.0	8.6e-10	Fibronectin type III domain
1201	fn3	2/2	437-522	68.4	2.7e-18	Fibronectin type III domain
1201	pkinase	1/1	618-874	256.1	4.6e-73	Protein kinase domain
1202	GTF2I	1/6	230-305	172.6	6.9e-55	GTF2I-like repeat
1202	GTF2I	2/6	438-513	172.9	5.3e-55	GTF2I-like repeat
1202	GTF2I	3/6	543-618	182.0	6.2e-58	GTF2I-like repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1202	GTF2I	4/6	648-723	183.6	1.8e-58	GTF2I-like repeat
1202	GTF2I	5/6	810-885	177.3	2e-56	GTF2I-like repeat
1202	GTF2I	6/6	945-1020	165.2	1.7e-52	GTF2I-like repeat
1202	ribonuc_red_sm	1/1	869-898	6.0	0.57	Ribonucleotide reductase, small chain
1203	GRAM	1/1	13-96	65.5	1.1e-17	GRAM domain
1204	FlpD	1/1	607-622	5.5	1	Methyl-viologen-reducing hydrogenase,
1204	crystall	1/6	971-997	23.0	0.00046	Beta/Gamma crystallin
1204	crystall	2/6	1072-1119	49.7	6.5e-11	Beta/Gamma crystallin
1204	crystall	3/6	1133-1226	95.3	1.2e-24	Beta/Gamma crystallin
1204	crystall	4/6	1234-1317	62.7	8.2e-15	Beta/Gamma crystallin
1204	crystall	5/6	1330-1409	59.9	5.5e-14	Beta/Gamma crystallin
1204	crystall	6/6	1417-1497	84.0	3.1e-21	Beta/Gamma crystallin
1204	gpdh	1/1	498-508	5.1	0.055	Glyceraldehyde 3-phosphate dehydrogenase
1205	hormone	1/1	2-143	124.6	6.8e-46	Somatotropin hormone family
1206	histone	1/1	30-146	188.4	1.1e-52	Core histone H2A/H2B/H3/H4
1208	Gal-bind_lectin	1/1	67-198	277.2	2.1e-79	Galactoside-binding lectin
1209	ENV_polyprotein	1/1	1097-1140	63.8	2.4e-18	ENV polyprotein (coat polyprotein)
1209	rnaseH	1/1	662-769	70.8	2.1e-18	RNase H
1209	rve	1/1	885-1039	126.3	3.5e-35	Integrase core domain
1209	rvp	1/1	20-117	72.3	7.6e-19	Retroviral aspartyl protease
1209	rvt	1/1	203-380	110.8	2.1e-29	Reverse transcriptase (RNA-dependent)
1211	Peptidase_C1	1/1	302-513	353.9	2.6e-105	Papain family cysteine protease
1211	gpdh	1/1	430-439	3.6	0.25	Glyceraldehyde 3-phosphate dehydrogenase
1212	ANATO	1/1	63-71	7.4	0.033	Anaphylotoxin-like domain
1214	kazal	1/1	18-56	22.2	0.00062	Kazal-type serine protease inhibitor domain
1215	p34-Arc	1/1	16-73	35.7	1e-08	Arp2/3 complex, 34kD subunit p34-Arc
1216	EGF	2/3	64-100	25.9	1.3e-05	EGF-like domain
1216	EGF	3/3	106-140	13.2	0.05	EGF-like domain
1217	kazal	1/1	39-87	36.5	1.4e-07	Kazal-type serine protease inhibitor domain
1218	filament	1/1	13-76	134.7	1.6e-36	Intermediate filament

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						protein
1219	pkinese	1/1	99-361	290.7	1.8e-83	Protein kinase domain
1221	transmembrane4	1/1	22-70	52.3	1.5e-15	Tetraspanin family
1222	ferritin	1/1	1-109	177.7	1.8e-49	Ferritin-like domain
1223	DUF260	1/1	33-68	4.8	0.23	Protein of unknown function DUF260
1223	bZIP	1/1	16-51	10.2	0.22	bZIP transcription factor
1224	hormone	1/1	4-107	119.8	4.2e-44	Somatotropin hormone family
1225	sushi	1/1	16-43	27.4	1.7e-05	Sushi domain (SCR repeat)
1227	L15	1/1	66-92	44.5	3.2e-10	Ribosomal protein L15
1229	Dynein_heavy	1/1	11-127	91.5	2.6e-26	Dynein heavy chain
1231	dCMP_cyt_deam	1/1	34-140	98.5	1.3e-26	Cytidine and deoxycytidylate deaminase
1232	adh_short	1/1	38-146	99.8	3.4e-27	short chain dehydrogenase
1233	ldh	1/1	44-129	143.7	3.2e-39	lactate/malate dehydrogenase, NAD binding d
1234	HMG_box	1/2	1-66	59.4	4.5e-15	HMG (high mobility group) box
1234	HMG_box	2/2	82-145	88.0	4.4e-23	HMG (high mobility group) box
1236	EGF	1/3	2-27	13.7	0.037	EGF-like domain
1236	EGF	2/3	33-68	30.1	8.6e-07	EGF-like domain
1236	EGF	3/3	74-110	28.1	3.1e-06	EGF-like domain
1236	PSI	1/1	19-47	6.7	0.78	Plexin repeat
1237	cystatin	1/1	2-93	124.3	5.4e-35	Cystatin domain
1239	cadherin	1/1	36-62	9.5	0.22	Cadherin domain
1240	bZIP	1/1	226-282	16.8	0.003	bZIP transcription factor
1242	IF_tail	1/1	1-85	167.1	1.9e-46	Intermediate filament tail domain
1244	Ribosomal_S15	1/1	88-149	14.6	0.0094	Ribosomal protein S15
1246	ldh	1/1	1-42	82.0	4.4e-21	lactate/malate dehydrogenase, NAD binding do
1246	ldh_C	1/1	44-130	163.1	4.9e-45	lactate/malate dehydrogenase, alpha/beta C-t
1249	W2	1/1	35-99	97.3	5.1e-29	eIF4-gamma/eIF5/eIF2-epsilon
1251	Pep_M12B_propep	1/1	120-198	75.4	2.7e-20	Reprolysin family propeptide
1251	Reprolysin	2/3	352-449	31.3	5.6e-07	Reprolysin (M12B) family zinc metallo
1251	Tfb2	1/1	312-330	3.3	0.1	Transcription factor Tfb2
1251	tsp_1	2/4	595-645	43.1	2.3e-11	Thrombospondin type 1 domain
1251	tsp_1	3/4	888-941	12.4	0.032	Thrombospondin type 1 domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1251	tsp_1	4/4	947-998	24.6	7.2e-06	Thrombospondin type 1 domain
1253	ANATO	1/1	60-66	4.4	0.46	Anaphylotoxin-like domain
1255	UPF0005	1/1	15-144	58.8	6.8e-16	Uncharacterized protein family UPF0005
1256	actin	1/1	1-145	358.0	1.5e-108	Actin
1258	OSCP	1/1	37-209	257.9	1.9e-75	ATP synthase delta (OSCP) subunit
1259	PA28_alpha	1/1	9-72	135.5	9.4e-37	Proteasome activator pa28 alpha subunit
1259	PA28_beta	1/1	90-239	387.7	1.1e-112	Proteasome activator pa28 beta subunit
1260	WD40	1/5	166-205	31.0	5.2e-07	WD domain, G-beta repeat
1260	WD40	2/5	216-255	24.2	4.5e-05	WD domain, G-beta repeat
1260	WD40	3/5	262-301	40.4	1.1e-09	WD domain, G-beta repeat
1260	WD40	4/5	306-345	33.9	7.8e-08	WD domain, G-beta repeat
1260	WD40	5/5	363-402	28.6	2.5e-06	WD domain, G-beta repeat
1261	WD40	1/5	6-38	13.2	0.059	WD domain, G-beta repeat
1261	WD40	2/5	42-80	41.8	4.4e-10	WD domain, G-beta repeat
1261	WD40	4/5	178-216	28.6	2.5e-06	WD domain, G-beta repeat
1261	WD40	5/5	275-313	24.1	4.6e-05	WD domain, G-beta repeat
1262	Big_1	1/3	1337-1373	8.9	0.16	Bacterial Ig-like domain (group 1)
1262	CH	1/2	72-177	97.6	1.3e-25	Calponin homology (CH) domain
1262	CH	2/2	195-297	78.2	3.2e-20	Calponin homology (CH) domain
1262	Filamin	1/24	306-399	127.4	2e-37	Filamin/ABP280 repeat
1262	Filamin	10/24	1185-1274	96.0	7.1e-28	Filamin/ABP280 repeat
1262	Filamin	11/24	1280-1374	120.5	2.5e-35	Filamin/ABP280 repeat
1262	Filamin	12/24	1380-1467	139.6	3.8e-41	Filamin/ABP280 repeat
1262	Filamin	13/24	1473-1563	137.8	1.3e-40	Filamin/ABP280 repeat
1262	Filamin	14/24	1569-1660	124.8	1.2e-36	Filamin/ABP280 repeat
1262	Filamin	15/24	1666-1756	121.9	9.1e-36	Filamin/ABP280 repeat
1262	Filamin	16/24	1812-1868	76.6	5.4e-22	Filamin/ABP280 repeat
1262	Filamin	17/24	1873-1960	145.4	6.6e-43	Filamin/ABP280 repeat
1262	Filamin	18/24	1971-2046	63.2	6.8e-18	Filamin/ABP280 repeat
1262	Filamin	19/24	2054-2141	135.8	5.4e-40	Filamin/ABP280 repeat
1262	Filamin	2/24	406-498	122.7	5.3e-36	Filamin/ABP280 repeat
1262	Filamin	20/24	2142-2237	78.2	1.8e-22	Filamin/ABP280 repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1262	Filamin	21/24	2245-2332	154.6	1e-45	Filamin/ABP280 repeat
1262	Filamin	22/24	2339-2427	95.4	1.1e-27	Filamin/ABP280 repeat
1262	Filamin	23/24	2436-2523	103.7	3.2e-30	Filamin/ABP280 repeat
1262	Filamin	24/24	2564-2653	112.4	7.5e-33	Filamin/ABP280 repeat
1262	Filamin	3/24	504-595	129.1	6.1e-38	Filamin/ABP280 repeat
1262	Filamin	4/24	601-688	106.5	4.4e-31	Filamin/ABP280 repeat
1262	Filamin	5/24	697-788	94.3	2.4e-27	Filamin/ABP280 repeat
1262	Filamin	6/24	794-891	128.8	7.3e-38	Filamin/ABP280 repeat
1262	Filamin	7/24	897-990	127.9	1.4e-37	Filamin/ABP280 repeat
1262	Filamin	8/24	996-1086	86.5	5.7e-25	Filamin/ABP280 repeat
1262	Filamin	9/24	1092-1179	163.5	2.1e-48	Filamin/ABP280 repeat
1262	Lipase_3	1/1	977-992	6.2	0.79	Lipase (class 3)
1263	CUE	1/1	296-337	45.9	5.6e-12	CUE domain
1264	fibrinogen_C	1/1	28-242	252.8	4.6e-72	Fibrinogen beta and gamma chains, C-term
1265	HLH	1/1	80-132	74.3	1.7e-18	Helix-loop-helix DNA-binding domain
1266	transmembrane4	1/1	11-221	270.7	2.9e-84	Tetraspanin family
1267	HSP70	1/1	39-91	5.5	0.5	Hsp70 protein
1267	PC_rep	1/8	409-442	18.5	0.0018	Proteasome/cyclosome repeat
1267	PC_rep	2/8	443-479	31.3	4e-07	Proteasome/cyclosome repeat
1267	PC_rep	3/8	480-514	30.5	6.9e-07	Proteasome/cyclosome repeat
1267	PC_rep	4/8	517-551	17.8	0.0029	Proteasome/cyclosome repeat
1267	PC_rep	5/8	560-589	11.4	0.19	Proteasome/cyclosome repeat
1267	PC_rep	7/8	692-723	17.5	0.0035	Proteasome/cyclosome repeat
1267	PC_rep	8/8	724-757	19.9	0.00071	Proteasome/cyclosome repeat
1268	annexin	1/4	18-85	111.4	1.8e-29	Annexin
1268	annexin	2/4	90-157	105.7	9e-28	Annexin
1268	annexin	3/4	173-241	108.0	1.8e-28	Annexin
1268	annexin	4/4	249-316	122.3	8.8e-33	Annexin
1269	PID	1/1	50-176	162.3	8e-45	Phosphotyrosine interaction domain (PTB/PID)
1270	globin	1/1	3-147	221.7	1.1e-62	Globin
1273	Connexin43	1/1	301-320	39.9	8.9e-10	Gap junction alpha-1 protein (Cx43)
1273	SMC_N	1/1	133-144	6.5	0.73	RecF/RecN/SMC N terminal domain
1273	connexin	1/1	9-239	576.9	1.2e-169	Connexin
1274	trypsin	1/1	9-231	318.0	2.6e-100	Trypsin
1276	MAGE	1/1	471-592	119.5	2e-32	MAGE family
1276	SpoA	1/1	518-535	8.3	0.88	Surface presentation of antigens (SPOA)
1277	SH3	1/1	68-124	42.0	6.7e-10	SH3 domain
1279	ATP1G1 PLM MAT8	1/1	20-75	128.7	1.7e-38	ATP1G1/PLM/MAT8

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						family
1280	PAP2	1/1	100-251	179.5	5.5e-50	PAP2 superfamily
1281	cpn60_TCP1	1/1	39-529	628.8	3.1e-185	TCP-1/cpn60 chaperonin family
1282	thiore	1/2	24-132	167.5	3.5e-49	Thioredoxin
1282	thiore	2/2	159-270	187.1	4.3e-55	Thioredoxin
1283	Astacin	1/1	561-572	7.5	0.22	Astacin (Peptidase family M12A)
1283	notch	1/3	416-441	13.5	0.09	Notch (DSL) domain
1283	notch	2/3	451-474	13.2	0.11	Notch (DSL) domain
1283	sushi	1/4	1215-1280	23.2	0.00022	Sushi domain (SCR repeat)
1283	sushi	2/4	1305-1342	15.8	0.02	Sushi domain (SCR repeat)
1283	sushi	3/4	1346-1410	32.5	7.9e-07	Sushi domain (SCR repeat)
1283	sushi	4/4	1415-1471	23.2	0.00022	Sushi domain (SCR repeat)
1284	BAG	1/1	175-255	84.6	1.4e-22	BAG domain
1284	ThiI	1/1	206-223	7.2	0.53	Thiamine biosynthesis protein (ThiI)
1284	Tropomyosin	1/1	160-183	8.4	0.2	Tropomyosin
1284	ubiquitin	1/1	99-151	27.6	3.3e-06	Ubiquitin family
1285	bZIP	1/1	186-250	35.3	1.6e-08	bZIP transcription factor
1286	HSP70	1/1	30-635	1403.0	0	Hsp70 protein
1286	Hydantoinase_A	1/1	213-236	7.6	0.13	Hydantoinase/oxoprolinase
1287	DSBA	1/2	49-69	7.1	0.73	DSBA oxidoreductase
1287	DSBA	2/2	357-426	7.8	0.48	DSBA oxidoreductase
1287	thiore	1/2	24-133	190.7	3.5e-56	Thioredoxin
1287	thiore	2/2	375-485	183.5	5.2e-54	Thioredoxin
1288	TNF	1/1	153-280	59.0	2.6e-15	TNF (Tumor Necrosis Factor) family
1289	Pyrophosphatase	1/1	45-229	440.3	1e-128	Inorganic pyrophosphatase
1290	LIM	1/3	384-442	56.5	1.5e-14	LIM domain
1290	LIM	2/3	444-501	58.1	5.2e-15	LIM domain
1290	LIM	3/3	504-570	37.3	4.2e-09	LIM domain
1292	isodh	1/1	56-379	301.7	2.7e-89	Isocitrate/isopropylmalate dehydrogenase
1293	cofilin_ADF	1/1	19-154	195.2	1e-54	Cofilin/tropomyosin-type actin-binding pr
1294	UQ_con	1/1	2-154	254.3	1.6e-72	Ubiquitin-conjugating enzyme
1295	ABC tran	1/1	7-22	10.3	0.081	ABC transporter
1295	APS_kinase	1/1	5-20	8.3	0.24	Adenylylsulfate kinase
1295	DUF258	1/1	8-25	8.4	0.19	Protein of unknown function, DUF258
1295	Guanylate_kin	1/1	40-144	212.8	5.2e-60	Guanylate kinase
1295	Rad17	1/1	9-28	6.3	0.48	Rad17 cell

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						cycle checkpoint protein
1295	SKI	1/1	5-20	9.1	0.2	Shikimate kinase
1295	Viral_helicase1	1/1	7-27	5.5	0.95	Viral (Superfamily 1) RNA helicase
1295	cobW	1/1	7-27	6.6	0.32	Cobalamin synthesis protein/P47K
1297	Gal-bind_lectin	1/1	117-247	215.3	2.8e-61	Galactoside-binding lectin
1299	Acetyltransf	1/1	157-175	12.0	0.0055	Acetyltransferase (GNAT) family
1299	PapB	1/1	98-112	8.1	0.39	Adhesin biosynthesis transcription regu
1303	CH	1/2	44-149	96.3	3.2e-25	Calponin homology (CH) domain
1303	CH	2/2	167-269	82.4	2.2e-21	Calponin homology (CH) domain
1303	Filamin	1/24	278-371	159.1	4.6e-47	Filamin/ABP280 repeat
1303	Filamin	10/24	1157-1246	153.3	2.7e-45	Filamin/ABP280 repeat
1303	Filamin	11/24	1252-1346	146.0	4.4e-43	Filamin/ABP280 repeat
1303	Filamin	12/24	1352-1439	163.3	2.3e-48	Filamin/ABP280 repeat
1303	Filamin	13/24	1445-1536	167.4	1.3e-49	Filamin/ABP280 repeat
1303	Filamin	14/24	1542-1633	165.4	5.5e-49	Filamin/ABP280 repeat
1303	Filamin	15/24	1639-1737	130.1	2.9e-38	Filamin/ABP280 repeat
1303	Filamin	16/24	1779-1857	97.6	2.3e-28	Filamin/ABP280 repeat
1303	Filamin	17/24	1862-1949	167.4	1.4e-49	Filamin/ABP280 repeat
1303	Filamin	18/24	1951-2036	101.7	1.3e-29	Filamin/ABP280 repeat
1303	Filamin	19/24	2044-2131	163.1	2.7e-48	Filamin/ABP280 repeat
1303	Filamin	2/24	378-471	155.3	6.3e-46	Filamin/ABP280 repeat
1303	Filamin	20/24	2132-2227	114.6	1.5e-33	Filamin/ABP280 repeat
1303	Filamin	21/24	2235-2322	161.0	1.2e-47	Filamin/ABP280 repeat
1303	Filamin	22/24	2329-2417	126.0	5.3e-37	Filamin/ABP280 repeat
1303	Filamin	23/24	2426-2513	135.5	6.7e-40	Filamin/ABP280 repeat
1303	Filamin	24/24	2554-2643	137.7	1.5e-40	Filamin/ABP280 repeat
1303	Filamin	3/24	477-567	148.6	7e-44	Filamin/ABP280 repeat
1303	Filamin	4/24	573-660	139.5	4.1e-41	Filamin/ABP280 repeat
1303	Filamin	5/24	669-760	165.5	5.3e-49	Filamin/ABP280 repeat
1303	Filamin	6/24	766-863	141.7	8.9e-42	Filamin/ABP280 repeat
1303	Filamin	7/24	869-962	154.5	1.1e-45	Filamin/ABP280 repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1303	Filamin	8/24	968-1058	113.1	4.6e-33	Filamin/ABP280 repeat
1303	Filamin	9/24	1064-1151	169.7	2.8e-50	Filamin/ABP280 repeat
1304	CMD	1/1	90-106	7.9	0.75	Carboxymuconolactone decarboxylase
1305	Ribosomal_L7Ae	1/1	21-121	74.5	7.4e-21	Ribosomal protein L7Ae/L30e/S12e/Gadd4
1306	Dynein_light	1/1	1-89	219.7	4.3e-62	Dynein light chain type 1
1308	ig	2/2	119-187	26.8	9.1e-06	Immunoglobulin domain
1309	Glypican	1/1	4-578	1207.6	0	Glypican
1310	Astacin	1/1	128-321	395.9	4.8e-122	Astacin (Peptidase family M12A)
1310	CUB	1/5	322-431	204.4	6.2e-59	CUB domain
1310	CUB	2/5	435-544	228.2	6.1e-66	CUB domain
1310	CUB	3/5	591-700	210.5	9.9e-61	CUB domain
1310	CUB	4/5	747-856	206.0	2.2e-59	CUB domain
1310	CUB	5/5	860-973	173.6	7.4e-50	CUB domain
1310	EGF	1/2	551-587	33.2	1.1e-07	EGF-like domain
1310	EGF	2/2	707-742	27.2	5.5e-06	EGF-like domain
1310	VSP	1/1	572-589	5.5	1	Giardia variant-specific surface protein
1311	HIT	1/1	14-125	223.0	4.4e-63	HIT family
1312	proteasome	1/1	56-238	165.7	3.1e-46	Proteasome A-type and B-type
1313	filament	1/1	71-381	335.6	5.5e-97	Intermediate filament protein
1314	Fasciclin	1/4	134-238	61.9	1.2e-16	Fasciclin domain
1314	Fasciclin	2/4	240-373	99.8	1.3e-27	Fasciclin domain
1314	Fasciclin	3/4	432-500	10.5	0.078	Fasciclin domain
1314	Fasciclin	4/4	502-634	235.2	9.5e-67	Fasciclin domain
1315	histone	1/1	6-122	165.0	1.3e-45	Core histone H2A/H2B/H3/H4
1317	ATP-grasp	1/1	173-252	9.9	0.085	ATP-grasp domain
1317	Biotin_carb_C	1/1	372-480	197.4	1.4e-56	Biotin carboxylase C-terminal domain
1317	CPSase_L_D2	1/1	151-365	437.0	1.7e-127	Carbamoyl-phosphate synthase L chain,
1317	CPSase_L_chain	1/1	37-149	205.2	9.8e-58	Carbamoyl-phosphate synthase L chain,
1317	HlyD	1/1	633-660	7.1	0.94	HlyD family secretion protein
1317	SLT_beta	1/1	551-605	10.1	0.1	Shiga-like toxin beta subunit
1317	biotin_lipoyl	1/1	635-702	105.4	3e-28	Biotin-requiring enzyme
1317	gpD	1/1	169-182	6.2	0.53	Bacteriophage scaffolding

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						protein D
1318	Tropomyosin	1/1	10-126	235.3	8.9e-67	Tropomyosin
1322	Mtp	1/1	36-233	438.5	5.7e-128	Golgi 4-transmembrane spanning transporter
1323	eIF5_eIF2B	1/1	182-310	281.2	1.3e-80	Domain found in IF2B/IF5
1325	BPL_C	1/1	151-171	8.5	0.78	Biotin protein ligase C terminal domain
1325	Mov34	1/1	87-196	149.7	5.1e-41	Mov34/MPN/PAD-1 family
1326	Ribosomal_L22	1/1	17-152	236.6	3.5e-67	Ribosomal protein L22p/L17e
1327	MAPEG	1/1	52-136	156.7	5.8e-45	MAPEG family
1328	proteasome	1/1	40-221	165.8	2.8e-46	Proteasome A-type and B-type
1329	C2	1/1	435-514	46.6	5.3e-12	C2 domain
1329	PH	1/1	314-416	90.8	3.3e-24	PH domain
1329	RasGAP	1/1	608-782	319.3	4.4e-92	GTPase-activator protein for Ras-like G
1329	SH2	1/2	20-95	112.0	1.4e-37	SH2 domain
1329	SH2	2/2	190-265	116.7	3.6e-39	SH2 domain
1329	SH3	1/1	121-178	45.0	9.8e-11	SH3 domain
1330	AAA	1/1	221-408	303.8	1.2e-90	ATPase family associated with various
1330	IstB	1/1	222-238	8.3	0.23	IstB-like ATP binding protein
1330	Parvo_NS1	1/1	222-240	7.8	0.17	Parvovirus non-structural protein NS1
1330	RNA helicase	1/1	222-242	12.8	0.016	RNA helicase
1331	serpin	1/1	51-415	283.6	3.8e-83	Serpin (serine protease inhibitor)
1332	TGF-beta	1/1	208-308	65.0	8.5e-18	Transforming growth factor beta like domain
1334	BRICHOS	1/1	137-231	132.0	5.2e-37	BRICHOS domain
1337	DUF232	1/1	14-149	155.4	9.8e-43	Putative transcriptional regulator
1339	Ribosomal_L27	1/1	31-101	71.7	5.3e-20	Ribosomal L27 protein
1340	TPR	1/1	313-336	10.4	0.38	TPR Domain
1342	sushi	1/4	36-94	50.1	1.8e-11	Sushi domain (SCR repeat)
1342	sushi	2/4	98-158	43.2	1.2e-09	Sushi domain (SCR repeat)
1342	sushi	3/4	163-220	56.2	4.4e-13	Sushi domain (SCR repeat)
1342	sushi	4/4	225-283	75.4	1.2e-18	Sushi domain (SCR repeat)
1345	UCR_hinge	1/1	27-91	162.6	1.5e-46	Ubiquinol-cytochrome C reductase hinge prot
1349	AAA	1/1	185-372	305.1	5e-91	ATPase family associated with various
1349	IstB	1/1	180-205	11.0	0.037	IstB-like ATP binding protein
1349	Parvo_NS1	1/1	186-207	15.6	0.00085	Parvovirus non-structural protein NS1

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1349	RNA_helicase	1/1	186-204	11.9	0.028	RNA helicase
1349	Sigma54_activat	1/1	186-203	10.4	0.049	Sigma-54 interaction domain
1351	Robl_LC7	1/1	3-94	113.6	3.8e-30	Roadblock/LC7 domain
1352	YT521-B	1/1	457-547	212.4	7e-60	YT521-B-like family
1353	AAA	1/1	211-398	291.4	6.7e-87	ATPase family associated with various ce
1353	RNA_helicase	1/1	212-232	8.5	0.25	RNA helicase
1354	WD40	1/6	3-41	19.4	0.001	WD domain, G-beta repeat
1354	WD40	2/6	47-87	40.1	1.3e-09	WD domain, G-beta repeat
1354	WD40	3/6	93-133	31.5	3.6e-07	WD domain, G-beta repeat
1354	WD40	4/6	140-195	42.6	2.5e-10	WD domain, G-beta repeat
1354	WD40	5/6	202-244	38.8	3.2e-09	WD domain, G-beta repeat
1354	WD40	6/6	253-290	14.7	0.023	WD domain, G-beta repeat
1355	zf-C3HC4	1/1	76-116	38.4	1.6e-10	Zinc finger, C3HC4 type (RING finger)
1358	UDPGP	1/1	43-462	892.9	9.5e-265	UTP--glucose-1-phosphate uridylyltransferase
1360	W2	1/1	336-416	120.2	3.6e-36	eIF4-gamma/eIF5/eIF2-epsilon
1362	Ribosomal_L34e	1/1	5-103	229.8	4e-65	Ribosomal protein L34e
1363	Ribosomal_L18p	1/1	26-99	118.5	1.3e-31	Ribosomal L18p/L5e family
1365	ATP-gua_Ptrans	1/1	148-414	655.9	2.1e-193	ATP:guanido phosphotransferase, C-ter
1365	ATP-gua_PtransN	1/1	52-135	192.8	5.3e-54	ATP:guanido phosphotransferase, N-ter
1366	DUF232	1/1	8-142	189.0	7.6e-53	Putative transcriptional regulator
1367	Triabin	1/1	119-136	12.1	0.017	Triabin
1367	lipocalin	1/1	38-186	149.1	3.9e-42	Lipocalin / cytosolic fatty-acid binding pr
1369	CSD	1/1	62-98	38.8	1.9e-09	'Cold-shock' DNA-binding domain
1370	60s_ribosomal	1/1	22-113	129.0	6.3e-37	60s Acidic ribosomal protein
1371	thioered	1/1	2-106	155.7	1.2e-45	Thioredoxin
1372	LIM	1/2	28-85	62.3	3.3e-16	LIM domain
1372	LIM	2/2	137-194	70.7	1.3e-18	LIM domain
1373	PX	1/1	137-265	143.5	3.8e-39	PX domain
1373	Sorting_nexin	1/1	2-134	295.9	3.3e-91	Sorting nexin, N-terminal domain
1374	rrm	1/1	18-82	65.6	7.7e-18	RNA recognition motif. (a.k.a. RRM, RBD, or
1375	NHL	2/2	256-284	9.8	0.6	NHL repeat
1375	Str_synth	1/1	40-408	325.7	2.8e-97	Strictosidine

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						synthase
1377	Cation_ATPase_C	1/1	834-1012	238.1	4.2e-71	Cation transporting ATPase, C-terminu
1377	Cation_ATPase_N	1/1	33-116	134.2	6.9e-37	Cation transporter/ATPase, N-terminus
1377	E1-E2_ATPase	1/1	135-366	391.6	5.1e-118	E1-E2 ATPase
1377	Hydrolase	1/2	370-633	31.3	3.4e-07	haloacid dehalogenase-like hydrolase
1377	Hydrolase	2/2	687-738	41.9	4.7e-10	haloacid dehalogenase-like hydrolase
1379	SCAMP	1/1	131-308	359.0	5e-104	SCAMP family
1380	COX4	1/1	26-169	242.1	7.7e-69	Cytochrome c oxidase subunit IV
1381	LIM	1/1	260-315	45.6	1.8e-11	LIM domain
1381	PDZ	1/1	3-84	96.2	5.8e-26	PDZ domain (Also known as DHR or GLGF)
1382	CoaE	1/1	21-38	9.0	0.11	Dephospho-CoA kinase
1382	PRK	1/1	22-229	230.6	2.3e-65	Phosphoribulokinase / Uridine kinase family
1383	ras	1/1	61-240	329.8	7e-97	Ras family
1384	Leptin	1/1	40-185	392.4	1.4e-120	Leptin
1385	DUF387	1/1	78-100	5.8	0.99	Putative transcriptional regulators (Yp
1385	Ribosomal_S25	1/1	1-113	262.3	6.5e-75	S25 ribosomal protein
1386	DEAD	1/1	51-254	242.3	1.5e-73	DEAD/DEAH box helicase
1386	helicase_C	1/1	301-372	127.9	6.6e-35	Helicase conserved C-terminal domain
1388	ank	2/5	110-142	32.6	1.8e-07	Ankyrin repeat
1388	ank	3/5	143-175	16.5	0.0069	Ankyrin repeat
1388	ank	4/5	182-214	39.5	1.9e-09	Ankyrin repeat
1388	ank	5/5	216-248	41.0	7.1e-10	Ankyrin repeat
1390	PX	1/1	505-626	95.6	9.9e-25	PX domain
1390	PXA	1/1	122-253	42.5	2.7e-10	PXA domain
1391	SUI1	1/1	9-109	225.9	6e-64	Translation initiation factor SUI1
1392	perilipin	1/1	2-396	813.3	6.8e-244	Perilipin family
1393	PRA1	1/1	8-55	15.3	0.0047	Prenylated rab acceptor (PRA1)
1395	ENV_polyprotein	1/1	265-486	159.2	1.6e-46	ENV polyprotein (coat polyprotein)
1396	LRR	1/10	82-105	16.8	0.007	Leucine Rich Repeat
1396	LRR	2/10	106-129	12.9	0.085	Leucine Rich Repeat
1396	LRR	3/10	130-149	14.8	0.025	Leucine Rich Repeat
1396	LRR	4/10	151-174	9.1	1	Leucine Rich Repeat
1396	LRR	7/10	222-245	17.1	0.0055	Leucine Rich Repeat
1396	LRR	8/10	246-269	9.8	0.65	Leucine Rich Repeat
1396	LRR	9/10	270-292	15.3	0.018	Leucine Rich Repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1396	LRRNT	1/2	53-80	43.3	2.8e-10	Leucine rich repeat N-terminal domain
1397	Ribosomal_S27	1/1	101-147	119.0	8.7e-32	Ribosomal protein S27a
1397	ubiquitin	1/1	1-74	153.1	4.8e-42	Ubiquitin family
1398	Kunitz_BPTI	1/3	36-86	93.6	2.6e-29	Kunitz/Bovine pancreatic trypsin inhibito
1398	Kunitz_BPTI	2/3	96-149	38.7	2.1e-11	Kunitz/Bovine pancreatic trypsin inhibito
1398	Kunitz_BPTI	3/3	158-208	85.3	1.3e-26	Kunitz/Bovine pancreatic trypsin inhibito
1398	kinesin	1/1	221-231	5.8	0.8	Kinesin motor domain
1399	proteasome	1/1	28-216	186.1	4.6e-52	Proteasome A-type and B-type
1401	AAA	1/1	169-356	316.0	2.7e-94	ATPase family associated with various
1401	IstB	1/1	170-186	7.9	0.31	IstB-like ATP binding protein
1401	Parvo_NS1	1/1	171-188	6.5	0.4	Parvovirus non-structural protein NS1
1401	RNA helicase	1/1	170-191	11.7	0.032	RNA helicase
1401	Sigma54_activat	1/1	171-187	7.1	0.44	Sigma-54 interaction domain
1403	TB	1/1	46-71	8.6	0.35	TB domain
1403	kazal	1/2	121-167	48.1	1.4e-10	Kazal-type serine protease inhibitor domain
1403	kazal	2/2	195-243	36.5	1.4e-07	Kazal-type serine protease inhibitor domain
1404	60s_ribosomal	1/1	17-114	114.8	1e-32	60s Acidic ribosomal protein
1404	Peptidase_M4_C	1/1	12-32	6.5	0.31	Thermolysin metallopeptidase, alpha-he
1406	zf-C3HC4	1/1	79-102	10.3	0.069	Zinc finger, C3HC4 type (RING finger)
1408	Adap_comp_sub	1/1	58-95	7.6	0.054	Adaptor complexes medium subunit famil
1408	Clat_adaptor_s	1/1	1-142	325.8	4.8e-94	Clathrin adaptor complex small chain
1409	Calsequestrin	2/2	235-348	20.2	1.6e-05	Calsequestrin
1409	DSBA	1/3	83-104	10.2	0.1	DSBA oxidoreductase
1409	DSBA	2/3	194-225	7.4	0.62	DSBA oxidoreductase
1409	DSBA	3/3	547-576	16.2	0.0021	DSBA oxidoreductase
1409	thioered	1/3	61-169	184.7	2.2e-54	Thioredoxin
1409	thioered	2/3	176-284	193.4	5.2e-57	Thioredoxin
1409	thioered	3/3	524-636	182.5	1e-53	Thioredoxin

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1410	APS_kinase	1/1	21-39	10.8	0.042	Adenylylsulfate kinase
1410	CoaE	1/1	20-198	321.3	5e-96	Dephospho-CoA kinase
1410	PRK	1/1	21-39	18.5	0.00032	Phosphoribulokinase / Uridine kinase
1410	UPF0042	1/1	19-48	7.4	0.33	Uncharacterised P-loop ATPase protein
1411	Fz	1/1	1-21	22.8	7.9e-07	Fz domain
1411	Zn_carbOpept	1/2	50-160	69.8	6.6e-18	Zinc carboxypeptidase
1411	Zn_carbOpept	2/2	172-431	90.9	1.3e-23	Zinc carboxypeptidase
1412	ANATO	1/3	36-69	41.2	5.9e-15	Anaphylotoxin-like domain
1412	ANATO	2/3	77-110	29.6	1.4e-10	Anaphylotoxin-like domain
1412	ANATO	3/3	112-144	37.0	2.3e-13	Anaphylotoxin-like domain
1412	EGF	1/8	180-214	16.3	0.0067	EGF-like domain
1412	EGF	3/8	312-354	19.9	0.00063	EGF-like domain
1412	EGF	4/8	360-397	40.6	8.8e-10	EGF-like domain
1412	EGF	5/8	403-439	25.9	1.3e-05	EGF-like domain
1412	EGF	6/8	445-479	13.2	0.05	EGF-like domain
1412	EGF	7/8	485-523	29.3	1.4e-06	EGF-like domain
1413	rrm	1/3	192-233	32.9	3.1e-08	RNA recognition motif. (a.k.a. RRM, RBD, or
1413	rrm	2/3	260-327	66.4	4.4e-18	RNA recognition motif. (a.k.a. RRM, RBD, or
1413	rrm	3/3	346-414	75.0	1.3e-20	RNA recognition motif. (a.k.a. RRM, RBD, or
1414	Ribosomal_S11	1/1	29-147	234.9	3.4e-72	Ribosomal protein S11
1415	Ribosomal_L29e	1/1	25-64	83.6	4.4e-23	Ribosomal L29e protein family
1416	Ribosomal_L1	1/1	5-213	348.7	6.4e-127	Ribosomal protein L1p/L10e family
1418	LRR	1/10	67-90	15.2	0.019	Leucine Rich Repeat
1418	LRR	10/10	305-330	13.9	0.044	Leucine Rich Repeat
1418	LRR	2/10	91-116	11.0	0.3	Leucine Rich Repeat
1418	LRR	4/10	138-159	16.1	0.011	Leucine Rich Repeat
1418	LRR	5/10	160-184	12.9	0.088	Leucine Rich Repeat
1418	LRR	6/10	185-204	16.6	0.0078	Leucine Rich Repeat
1418	LRR	7/10	206-229	17.1	0.0057	Leucine Rich Repeat
1418	LRR	8/10	230-253	9.7	0.71	Leucine Rich Repeat
1418	LRR	9/10	255-277	12.7	0.096	Leucine Rich Repeat
1418	LRRNT	1/1	36-66	40.5	1.7e-09	Leucine rich repeat N-terminal domain
1419	AhpC-TSA	1/1	81-230	247.7	1.6e-70	AhpC/TSA family
1419	Syndecan	1/1	18-49	6.4	0.062	Syndecan domain
1421	Triabin	1/1	120-135	17.7	0.00038	Triabin
1421	lipocalin	1/1	41-185	111.9	2.6e-31	Lipocalin /

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						cytosolic fatty-acid binding pr
1422	Ribosomal_L21e	1/1	2-100	241.6	1.1e-68	Ribosomal protein L21e
1423	Ribosomal_S10	1/1	19-114	193.7	2.8e-54	Ribosomal protein S10p/S20e
1424	Ribosomal_L23	1/1	74-153	112.4	5e-32	Ribosomal protein L23
1424	Ribosomal_L23eN	1/1	15-68	63.2	1.3e-16	Ribosomal protein L23, N-terminal dom
1425	DUF435	1/1	98-383	445.3	5.3e-130	Membrane protein of unknown function (D
1427	FeoB	1/1	247-262	12.0	0.0065	Ferrous iron transport protein B
1427	MMR_HSR1	1/1	118-393	172.0	9.9e-48	GTPase of unknown function
1429	Peptidase_C13	1/1	6-327	698.1	4.2e-206	Peptidase C13 family
1430	ER_lumen_recept	1/1	1-202	527.3	1.1e-154	ER lumen protein retaining receptor
1431	COLFI	1/1	1149-1365	538.4	6.8e-210	Fibrillar collagen C-terminal domain
1431	Collagen	1/19	33-72	26.5	8.5e-06	Collagen triple helix repeat (20 copies)
1431	Collagen	10/19	529-567	30.1	8.6e-07	Collagen triple helix repeat (20 copies)
1431	Collagen	11/19	568-627	47.1	1.9e-11	Collagen triple helix repeat (20 copies)
1431	Collagen	12/19	628-687	49.2	4.9e-12	Collagen triple helix repeat (20 copies)
1431	Collagen	13/19	691-750	61.7	1.8e-15	Collagen triple helix repeat (20 copies)
1431	Collagen	14/19	751-810	45.7	4.5e-11	Collagen triple helix repeat (20 copies)
1431	Collagen	15/19	811-870	42.8	2.7e-10	Collagen triple helix repeat (20 copies)
1431	Collagen	16/19	874-933	60.0	5.3e-15	Collagen triple helix repeat (20 copies)
1431	Collagen	17/19	934-990	41.1	8.1e-10	Collagen triple helix repeat (20 copies)
1431	Collagen	18/19	991-1050	51.5	1.1e-12	Collagen triple helix repeat (20 copies)
1431	Collagen	19/19	1051-1105	40.4	1.3e-09	Collagen triple helix repeat (20 copies)
1431	Collagen	2/19	90-147	42.6	3.1e-10	Collagen triple helix repeat (20 copies)
1431	Collagen	3/19	148-207	59.9	5.6e-15	Collagen triple helix repeat

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						(20 copies)
1431	Collagen	4/19	208-267	48.5	7.5e-12	Collagen triple helix repeat (20 copies)
1431	Collagen	5/19	268-327	52.4	6.6e-13	Collagen triple helix repeat (20 copies)
1431	Collagen	6/19	328-387	54.7	1.5e-13	Collagen triple helix repeat (20 copies)
1431	Collagen	7/19	388-415	19.4	0.00075	Collagen triple helix repeat (20 copies)
1431	Collagen	8/19	418-465	40.7	1.1e-09	Collagen triple helix repeat (20 copies)
1431	Collagen	9/19	469-528	55.6	8.3e-14	Collagen triple helix repeat (20 copies)
1432	DJ-1_PfpI	1/1	4-173	203.7	1.7e-57	DJ-1/PfpI family
1433	Gastrin	1/1	2-115	198.2	1.3e-55	Gastrin/cholecystokinin family
1435	LRR	1/7	41-63	14.2	0.038	Leucine Rich Repeat
1435	LRR	2/7	64-86	13.8	0.049	Leucine Rich Repeat
1435	LRR	3/7	87-109	11.7	0.19	Leucine Rich Repeat
1435	LRR	4/7	110-134	13.6	0.055	Leucine Rich Repeat
1435	LRR	5/7	135-157	15.6	0.015	Leucine Rich Repeat
1435	LRR	6/7	158-180	13.4	0.061	Leucine Rich Repeat
1435	LRR	7/7	181-203	17.7	0.0039	Leucine Rich Repeat
1436	DUF435	1/1	62-348	516.0	2.7e-151	Membrane protein of unknown function (DUF435)
1437	asp	1/1	39-427	645.9	2.2e-190	Eukaryotic aspartyl protease
1438	Clq	1/1	123-247	251.9	8.8e-72	Clq domain
1438	Collagen	1/2	33-68	27.2	5.4e-06	Collagen triple helix repeat (20 copies)
1438	Collagen	2/2	69-114	24.2	3.5e-05	Collagen triple helix repeat (20 copies)
1439	ras	1/1	7-193	319.3	9.6e-94	Ras family
1440	Rho_GDI	1/1	1-201	502.6	3e-147	RHO protein GDP dissociation inhibitor
1441	Clathrin_lg_ch	1/2	3-162	294.2	1.7e-84	Clathrin light chain
1441	Clathrin_lg_ch	2/2	163-217	124.0	2.7e-33	Clathrin light chain
1441	Myc-LZ	1/1	98-130	8.4	0.85	Myc leucine zipper domain
1443	HMG_box	1/2	6-79	63.4	3.4e-16	HMG (high mobility group) box
1443	HMG_box	2/2	95-163	129.7	5.5e-35	HMG (high mobility group) box
1444	IBN_NT	1/1	31-97	24.8	2.7e-05	Importin-beta N-terminal

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						domain
1445	EGF	1/1	146-181	23.8	5.2e-05	EGF-like domain
1447	Spermine_synth	1/1	109-366	384.7	7e-116	Spermine/spermidine synthase
1449	ig	1/1	34-116	14.2	0.029	Immunoglobulin domain
1451	Ribosomal_S6	1/1	3-96	17.8	0.00053	Ribosomal protein S6
1453	Ribosomal_S17	1/1	75-145	149.1	4e-43	Ribosomal protein S17
1454	DUF196	1/1	87-106	7.3	0.84	Uncharacterized ACR, COG1343
1454	ras	1/1	13-206	381.5	3e-112	Ras family
1455	Folate_rec	1/1	6-249	561.2	7e-165	Folate receptor family
1458	serpin	1/1	139-498	455.7	4.5e-134	Serpin (serine protease inhibitor)
1459	cytochrome_b_C	1/1	258-359	152.3	8.2e-42	Cytochrome b(C-terminal)/b6/pe tD
1459	cytochrome_b_N	1/1	1-204	376.5	1e-115	Cytochrome b(N-terminal)/b6/pe tB
1460	Ribosomal_L32e	1/1	16-125	267.6	1.4e-83	Ribosomal protein L32
1462	ECH	1/1	68-248	150.0	2.2e-43	Enoyl-CoA hydratase/isomerase family
1463	filament	1/1	83-394	595.8	2.5e-175	Intermediate filament protein
1464	DEAD	1/2	15-62	52.1	4.7e-15	DEAD/DEAH box helicase
1464	DEAD	2/2	281-444	93.8	7.2e-28	DEAD/DEAH box helicase
1464	SPRY	1/1	130-246	121.0	2e-32	SPRY domain
1464	helicase_C	1/1	539-610	108.3	2.6e-29	Helicase conserved C-terminal domain
1465	IGFBP	1/1	37-94	13.4	0.017	Insulin-like growth factor binding protein
1465	PDZ	1/1	370-465	50.8	5.4e-13	PDZ domain (Also known as DHR or GLGF)
1465	kazal	1/1	109-155	29.4	8.9e-06	Kazal-type serine protease inhibitor domain
1465	trypsin	1/1	205-364	74.5	7.7e-23	Trypsin
1466	zf-CCHC	1/7	4-21	32.6	3.4e-07	Zinc knuckle
1466	zf-CCHC	2/7	52-69	27.6	8.5e-06	Zinc knuckle
1466	zf-CCHC	3/7	72-89	30.5	1.3e-06	Zinc knuckle
1466	zf-CCHC	4/7	96-113	31.8	5.4e-07	Zinc knuckle
1466	zf-CCHC	5/7	117-134	30.8	1.1e-06	Zinc knuckle
1466	zf-CCHC	6/7	135-152	28.2	5.8e-06	Zinc knuckle
1466	zf-CCHC	7/7	156-173	31.3	7.9e-07	Zinc knuckle
1467	TIMP	1/1	22-194	472.6	3.7e-172	Tissue inhibitor of metalloproteinase
1468	efhand	1/5	27-55	21.1	0.00061	EF hand
1468	efhand	3/5	94-122	31.9	6.3e-07	EF hand
1468	efhand	4/5	130-158	10.4	0.54	EF hand
1468	efhand	5/5	160-176	9.8	0.82	EF hand
1469	KE2	1/1	23-130	128.8	1e-34	KE2 family protein
1470	Ribosomal_L11	1/1	161-229	106.5	5.2e-28	Ribosomal protein L11,

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						RNA binding do
1470	Ribosomal_L11_N	1/1	98-156	93.4	1.1e-25	Ribosomal protein L11, N-terminal dom
1471	Mov34	1/1	4-118	168.8	9.3e-47	Mov34/MPN/PAD-1 family
1472	Na_K-ATPase	1/1	1-274	477.9	7.9e-140	Sodium / potassium ATPase beta chain
1475	hexapep	1/3	26-43	13.4	0.11	Bacterial transferase hexapeptide (four rep
1475	hexapep	3/3	110-127	12.8	0.16	Bacterial transferase hexapeptide (four rep
1476	tubulin	1/1	45-244	374.8	1.4e-109	Tubulin/FtsZ family, GTPase domain
1476	tubulin_C	1/1	246-383	270.9	1.7e-77	Tubulin/FtsZ family, C-terminal domain
1477	Calpain_inhib	1/5	53-183	179.0	1.5e-51	Calpain inhibitor
1477	Calpain_inhib	2/5	186-317	197.8	4.3e-57	Calpain inhibitor
1477	Calpain_inhib	3/5	323-460	221.0	6.8e-64	Calpain inhibitor
1477	Calpain_inhib	4/5	466-597	233.3	1.6e-67	Calpain inhibitor
1478	DAD	1/1	1-113	258.5	5.9e-88	DAD family
1479	PSI	1/1	514-542	13.0	0.0067	Plexin repeat
1479	Sema	1/1	55-496	841.8	2.3e-249	Sema domain
1479	ig	1/1	584-645	22.3	0.00017	Immunoglobulin domain
1480	Glyco_hydro_2	1/1	226-327	140.8	1.8e-43	Glycosyl hydrolases family 2, immunog
1480	Glyco_hydro_2_C	1/1	329-631	597.7	6.8e-176	Glycosyl hydrolases family 2, TIM bar
1480	Glyco_hydro_2_N	1/1	22-224	379.7	3e-110	Glycosyl hydrolases family 2, sugar b
1481	F-box	1/1	232-279	22.4	0.00033	F-box domain
1481	WD40	1/5	359-395	17.5	0.0035	WD domain, G-beta repeat
1481	WD40	2/5	398-434	29.1	1.7e-06	WD domain, G-beta repeat
1483	ras	1/1	12-169	221.6	9.4e-65	Ras family
1484	MHC_II_beta	1/1	40-116	164.6	1.7e-45	Class II histocompatibility antigen,
1484	ig	1/1	136-201	40.6	1.4e-09	Immunoglobulin domain
1486	Gal-bind_lectin	1/1	5-137	105.1	2.8e-29	Galactoside-binding lectin
1487	NAP	1/1	75-348	644.5	5.8e-190	Nucleosome assembly protein (NAP)
1488	serpin	1/1	24-398	542.0	1.3e-159	Serpin (serine protease inhibitor)
1489	SRCR	1/1	27-124	129.9	2.4e-35	Scavenger receptor

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						cysteine-rich domain
1490	Ribosomal_L3	1/1	50-348	664.8	4.5e-196	Ribosomal protein L3
1491	tubulin	1/1	49-246	376.0	6.1e-110	Tubulin/FtsZ family, GTPase domain
1491	tubulin_C	1/1	248-393	270.6	2e-77	Tubulin/FtsZ family, C-terminal domain
1493	efhand	1/2	127-155	27.6	9.5e-06	EF hand
1493	efhand	2/2	163-191	22.3	0.00029	EF hand
1494	HEAT	1/15	6-42	14.2	0.015	HEAT repeat
1494	HEAT	10/15	357-395	39.8	3.4e-10	HEAT repeat
1494	HEAT	11/15	396-434	32.3	6e-08	HEAT repeat
1494	HEAT	12/15	435-473	25.9	4.9e-06	HEAT repeat
1494	HEAT	13/15	474-512	30.3	2.3e-07	HEAT repeat
1494	HEAT	14/15	513-551	50.2	2.6e-13	HEAT repeat
1494	HEAT	2/15	43-80	24.1	1.6e-05	HEAT repeat
1494	HEAT	3/15	82-119	26.3	3.8e-06	HEAT repeat
1494	HEAT	4/15	120-157	23.0	3.5e-05	HEAT repeat
1494	HEAT	5/15	158-196	44.6	1.3e-11	HEAT repeat
1494	HEAT	6/15	197-235	40.9	1.7e-10	HEAT repeat
1494	HEAT	7/15	236-274	33.5	2.6e-08	HEAT repeat
1494	HEAT	8/15	275-313	47.4	1.9e-12	HEAT repeat
1494	HEAT	9/15	318-356	28.7	6.9e-07	HEAT repeat
1495	ATP1G1_PLM_MAT8	1/1	133-177	70.5	1.7e-20	ATP1G1/PLM/MAT8 family
1496	PMP22_Claudin	1/1	1-160	297.8	1.3e-85	PMP-22/EMP/MP20/Claudin family
1497	BAH	1/2	755-880	142.7	6.4e-39	BAH domain
1497	BAH	2/2	966-1100	137.6	2.2e-37	BAH domain
1497	DNA_methylase	1/3	1139-1230	54.6	2.8e-14	C-5 cytosine-specific DNA methylase
1497	DNA_methylase	2/3	1258-1317	31.7	6.7e-08	C-5 cytosine-specific DNA methylase
1497	DNA_methylase	3/3	1519-1594	69.5	2.1e-18	C-5 cytosine-specific DNA methylase
1497	zf-CXXC	1/1	645-691	87.4	6.3e-36	CXXC zinc finger
1498	Adrenomedullin	1/1	21-185	433.5	1.9e-126	Adrenomedullin
1499	S_100	1/1	5-45	60.9	1.1e-15	S-100/ICaBP type calcium binding domain
1499	efhand	2/2	51-79	11.2	0.34	EF hand
1500	PMP22_Claudin	1/1	3-180	162.7	6.9e-46	PMP-22/EMP/MP20/Claudin family
1501	PNPase	1/1	18-28	7.2	0.065	Polyribonucleotide nucleotidyltransferase,
1501	RNase_PH	1/1	31-166	125.2	9.5e-35	3' exoribonuclease family, domain 1
1501	RNase_PH_C	1/1	191-258	42.4	1.1e-10	3' exoribonuclease family, domain 2
1502	WD40	1/4	42-80	35.1	3.6e-08	WD domain, G-beta repeat
1502	WD40	2/4	132-170	24.2	4.4e-05	WD domain, G-beta repeat
1503	homeobox	1/1	19-69	14.4	0.085	Homeobox domain
1504	Fe-ADH	1/2	4-205	121.3	4.4e-34	Iron-containing

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						alcohol dehydrogenase
1504	Fe-ADH	2/2	228-290	64.2	1.3e-17	Iron-containing alcohol dehydrogenase
1505	Ribosomal_L37ae	1/1	2-92	223.3	3.5e-63	Ribosomal L37ae protein family
1506	HATPase_c	1/1	35-188	64.9	4.5e-17	Histidine kinase-, DNA gyrase B-, and HSP90
1506	HSP90	1/1	191-724	1284.2	0	Hsp90 protein
1507	annexin	1/4	35-102	88.7	1.2e-22	Annexin
1507	annexin	2/4	107-174	129.7	5.3e-35	Annexin
1507	annexin	3/4	191-259	65.5	2.8e-16	Annexin
1507	annexin	4/4	267-334	108.4	1.3e-28	Annexin
1508	Ribosomal_L31e	1/1	16-110	230.5	2.5e-71	Ribosomal protein L31e
1509	Glyco_hydro_20	1/1	200-518	724.9	3.6e-214	Glycosyl hydrolase family 20, catalyt
1509	Glyco_hydro_20b	1/1	68-198	245.7	6.3e-70	Glycosyl hydrolase family 20, domain
1510	proteasome	1/1	50-237	183.3	2.9e-51	Proteasome A-type and B-type
1511	CBS	1/2	112-168	30.4	1.4e-06	CBS domain
1511	CBS	2/2	179-232	41.4	1.4e-09	CBS domain
1511	FMN_dh	1/1	358-387	15.5	0.00086	FMN-dependent dehydrogenase
1511	IMPDH	1/1	20-514	683.5	1e-201	IMP dehydrogenase / GMP reductase
1511	NPD	2/2	359-397	15.5	0.0008	1/2 52 91 .. 1 40
1512	Phage_terminase	1/1	44-71	3.9	0.92	Phage Terminase
1513	LRR	2/2	232-256	13.7	0.05	Leucine Rich Repeat
1513	NTF2	1/2	326-362	27.6	3.3e-06	Nuclear transport factor 2 (NTF2) domain
1513	NTF2	2/2	397-476	36.9	9.3e-09	Nuclear transport factor 2 (NTF2) domain
1513	TAP_C	1/1	496-559	141.0	3.9e-39	TAP C-terminal domain
1514	CH	1/1	800-905	110.2	4e-29	Calponin homology (CH) domain
1515	ig	1/1	34-115	12.6	0.079	Immunoglobulin domain
1516	synaptobrevin	1/1	2-90	118.1	1.1e-31	Synaptobrevin
1517	zf-MYND	1/1	11-34	9.7	0.079	MYND finger
1518	FAD_binding_6	1/1	48-155	199.9	4.1e-56	Oxidoreductase FAD-binding domain
1518	NAD_binding_1	1/1	176-290	160.8	1.8e-44	Oxidoreductase NAD-binding domain
1519	HSP70	1/1	6-612	1407.8	0	Hsp70 protein
1520	Glyco_hydro_20	1/1	167-489	702.5	2e-207	Glycosyl hydrolase family 20, catalyt
1520	Glyco_hydro_20b	1/1	35-165	215.6	7.6e-61	Glycosyl

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						hydrolase family 20, domain
1521	rrm	1/2	64-123	79.5	6e-22	RNA recognition motif. (a.k.a. RRM, RBD, or
1521	rrm	2/2	143-207	51.8	8.7e-14	RNA recognition motif. (a.k.a. RRM, RBD, or
1522	ferritin	1/1	14-155	194.0	2.3e-54	Ferritin-like domain
1523	APG9	1/1	230-608	894.2	1.7e-268	Autophagy protein Apg9
1523	Diphthamide_syn	1/1	552-577	6.9	0.32	Putative diphthamide synthesis protei
1524	Ribosomal_S15	1/1	61-151	111.8	8.6e-31	Ribosomal protein S15
1525	Herpes_HEPA	1/1	10-24	3.4	0.86	Herpesvirus DNA helicase/primase complex
1525	actin	1/1	1-377	925.9	2.2e-281	Actin
1526	aldo_ket_red	1/1	7-296	529.8	9.4e-156	Aldo/keto reductase family
1527	p450	1/1	48-488	355.7	1.2e-110	Cytochrome P450
1528	Metallophos	1/1	199-461	70.5	1.4e-17	Calcineurin-like phosphoesterase
1529	WD40	1/7	5-44	34.2	6.2e-08	WD domain, G-beta repeat
1529	WD40	2/7	53-91	46.5	2e-11	WD domain, G-beta repeat
1529	WD40	3/7	95-133	50.7	1.3e-12	WD domain, G-beta repeat
1529	WD40	4/7	138-178	40.3	1.2e-09	WD domain, G-beta repeat
1529	WD40	5/7	182-220	37.7	6.3e-09	WD domain, G-beta repeat
1529	WD40	6/7	224-260	22.5	0.00013	WD domain, G-beta repeat
1529	WD40	7/7	273-311	21.6	0.00024	WD domain, G-beta repeat
1530	Ribosomal_L7Ae	1/1	20-114	114.8	7.2e-33	Ribosomal protein L7Ae/L30e/S12e/Gadd4
1531	cpn60_TCP1	1/1	32-524	583.9	9.7e-172	TCP-1/cpn60 chaperonin family
1532	CUB	1/2	23-138	79.9	2.7e-22	CUB domain
1532	CUB	2/2	193-302	160.5	5.2e-46	CUB domain
1532	EGF	1/1	161-189	17.9	0.0023	EGF-like domain
1532	sushi	2/3	309-371	45.5	2.8e-10	Sushi domain (SCR repeat)
1532	sushi	3/3	376-447	50.7	1.2e-11	Sushi domain (SCR repeat)
1532	trypsin	1/1	464-697	189.7	1.7e-59	Trypsin
1533	CUB	1/2	18-127	71.8	6.9e-20	CUB domain
1533	CUB	2/2	175-287	150.5	4.7e-43	CUB domain
1533	EGF	1/1	135-171	33.5	9.3e-08	EGF-like domain
1533	sushi	1/2	294-354	53.3	2.6e-12	Sushi domain (SCR repeat)
1533	sushi	2/2	359-421	53.5	2.2e-12	Sushi domain (SCR repeat)
1533	trypsin	1/1	438-675	217.2	3.1e-68	Trypsin
1534	Ndr	1/1	40-322	644.1	7.5e-190	Ndr family
1534	abhydrolase	1/2	95-178	11.7	0.013	alpha/beta hydrolase fold

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1535	RrnaAD	1/1	111-147	5.2	0.78	Ribosomal RNA adenine dimethylase
1535	efhand	1/4	12-40	39.6	4.8e-09	EF hand
1535	efhand	2/4	48-76	38.4	1e-08	EF hand
1535	efhand	3/4	85-113	42.1	9.8e-10	EF hand
1535	efhand	4/4	121-149	41.2	1.7e-09	EF hand
1536	calreticulin	1/1	21-332	774.0	2.2e-238	Calreticulin family
1537	S_100	1/1	5-48	88.6	1.2e-23	S-100/ICaBP type calcium binding domain
1537	efhand	1/1	54-82	17.2	0.0073	EF hand
1538	UPAR_LY6	1/1	26-96	114.1	2.7e-30	u-PAR/Ly-6 domain
1539	Cys_knot	1/1	22-130	187.9	1.7e-52	Cystine-knot domain
1540	Kunitz_BPTI	1/3	54-104	88.8	9.4e-28	Kunitz/Bovine pancreatic trypsin inhibito
1540	Kunitz_BPTI	2/3	125-175	88.2	1.5e-27	Kunitz/Bovine pancreatic trypsin inhibito
1540	Kunitz_BPTI	3/3	217-267	90.8	2.1e-28	Kunitz/Bovine pancreatic trypsin inhibito
1541	Ribosomal_L13e	1/1	7-185	463.8	1.4e-135	Ribosomal protein L13e
1542	GILT	1/1	62-170	88.8	1.1e-22	Gamma interferon inducible lysosomal thiol r
1543	HSP20	1/1	60-162	164.4	2e-45	Hsp20/alpha crystallin family
1543	crystallin	1/1	1-59	136.2	3.7e-38	Alpha crystallin A chain, N terminal
1544	CK_II_beta	1/1	5-183	508.1	6.6e-149	Casein kinase II regulatory subunit
1545	fn1	1/12	81-116	64.8	1.2e-16	Fibronectin type I domain
1545	fn1	10/12	2204-2243	77.5	3e-20	Fibronectin type I domain
1545	fn1	11/12	2249-2286	72.3	9e-19	Fibronectin type I domain
1545	fn1	12/12	2293-2328	62.0	7.5e-16	Fibronectin type I domain
1545	fn1	2/12	126-164	73.9	3.1e-19	Fibronectin type I domain
1545	fn1	3/12	170-208	67.9	1.5e-17	Fibronectin type I domain
1545	fn1	4/12	215-254	80.4	4.5e-21	Fibronectin type I domain
1545	fn1	5/12	260-299	76.9	4.4e-20	Fibronectin type I domain
1545	fn1	6/12	337-371	51.4	7.8e-13	Fibronectin type I domain
1545	fn1	7/12	499-537	77.0	4.2e-20	Fibronectin type I domain
1545	fn1	8/12	547-584	63.8	2.3e-16	Fibronectin type I domain
1545	fn1	9/12	590-628	71.3	1.7e-18	Fibronectin type I domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1545	fn2	1/2	389-430	94.2	7.6e-35	Fibronectin type II domain
1545	fn2	2/2	449-490	100.1	4.1e-37	Fibronectin type II domain
1545	fn3	1/16	637-720	53.0	7.5e-14	Fibronectin type III domain
1545	fn3	10/16	1477-1559	101.6	7e-28	Fibronectin type III domain
1545	fn3	11/16	1571-1650	81.6	4.1e-22	Fibronectin type III domain
1545	fn3	12/16	1661-1740	62.3	1.5e-16	Fibronectin type III domain
1545	fn3	13/16	1751-1830	79.0	2.3e-21	Fibronectin type III domain
1545	fn3	14/16	1843-1921	83.0	1.7e-22	Fibronectin type III domain
1545	fn3	15/16	1932-2011	92.8	2.4e-25	Fibronectin type III domain
1545	fn3	16/16	2102-2179	31.5	1.2e-07	Fibronectin type III domain
1545	fn3	2/16	749-829	59.7	8.8e-16	Fibronectin type III domain
1545	fn3	3/16	840-918	96.0	2.8e-26	Fibronectin type III domain
1545	fn3	4/16	936-1015	84.6	5.8e-23	Fibronectin type III domain
1545	fn3	5/16	1026-1104	80.6	8.3e-22	Fibronectin type III domain
1545	fn3	6/16	1125-1191	32.6	5.9e-08	Fibronectin type III domain
1545	fn3	7/16	1203-1285	74.5	4.7e-20	Fibronectin type III domain
1545	fn3	8/16	1296-1376	82.9	1.8e-22	Fibronectin type III domain
1545	fn3	9/16	1387-1466	86.1	2.2e-23	Fibronectin type III domain
1546	p450	1/1	52-511	482.4	2.7e-150	Cytochrome P450
1548	GTP_EFTU	1/1	5-239	376.4	2.9e-109	Elongation factor Tu GTP binding domain
1548	GTP_EFTU_D2	1/1	251-327	100.6	8e-27	Elongation factor Tu domain 2
1548	GTP_EFTU_D3	1/1	333-442	213.3	3.5e-60	Elongation factor Tu C-terminal domain
1549	fibrinogen_C	1/1	175-415	532.0	4.2e-156	Fibrinogen beta and gamma chains, C-t
1550	PX	1/1	65-178	106.7	4.6e-28	PX domain
1551	lectin_c	1/1	114-222	48.8	2.9e-11	Lectin C-type domain
1552	lipocalin	1/1	32-178	129.6	1.8e-36	Lipocalin / cytosolic fatty-acid binding pr
1553	enolase	1/1	142-432	717.1	8.3e-212	Enolase, C-terminal TIM barrel domain
1553	enolase_N	1/1	2-134	280.0	3.1e-80	Enolase, N-terminal domain
1554	p450	1/1	44-498	543.8	1.6e-169	Cytochrome P450
1555	Ribosomal_S3Ae	1/1	12-222	518.5	5e-152	Ribosomal S3Ae family
1556	ldl_recept_a	1/3	34-61	24.8	5.7e-06	Low-density lipoprotein receptor domain
1556	ldl_recept_a	3/3	105-141	45.1	3.8e-12	Low-density lipoprotein receptor domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1557	Glyco_hydro_31	1/1	194-918	1402.0	0	Glycosyl hydrolases family 31
1557	trefoil	1/1	81-130	53.4	2.2e-13	Trefoil (P-type) domain
1558	globin	1/1	3-147	218.1	1.3e-61	Globin
1559	ANATO	1/1	96-102	5.5	0.18	Anaphylotoxin-like domain
1559	fn3	3/4	429-516	13.0	0.027	Fibronectin type III domain
1559	fn3	4/4	527-609	33.7	2.8e-08	Fibronectin type III domain
1560	IGFBP	1/1	40-99	97.4	2e-26	Insulin-like growth factor binding pr
1560	thyroglobulin_1	1/1	213-285	119.6	5.9e-32	Thyroglobulin type-1 repeat
1561	IGFBP	1/1	30-89	86.8	2.1e-23	Insulin-like growth factor binding pr
1561	thyroglobulin_1	1/1	176-251	144.3	2.1e-39	Thyroglobulin type-1 repeat
1562	histone	1/1	17-135	100.3	3.6e-27	Core histone H2A/H2B/H3/H4
1563	MHC_I	1/1	22-200	473.5	1.7e-138	Class I Histocompatibility antigen, domains
1563	ig	1/1	217-282	36.6	1.7e-08	Immunoglobulin domain
1564	AT hook	1/1	244-256	12.0	0.12	AT hook motif
1564	Ets	1/1	272-357	127.6	8.8e-35	Ets-domain
1564	SAM_PNT	1/1	48-132	123.5	4.9e-35	Sterile alpha motif (SAM)/Pointed domain
1565	MHC_I	1/1	25-203	481.8	5.6e-141	Class I Histocompatibility antigen, domains
1565	ig	1/1	220-285	33.3	1.4e-07	Immunoglobulin domain
1566	ubiquitin	1/2	3-78	28.4	2e-06	Ubiquitin family
1566	ubiquitin	2/2	82-155	84.4	3.8e-22	Ubiquitin family
1567	C2	1/2	310-396	92.2	3.8e-25	C2 domain
1567	C2	2/2	461-539	30.4	2.6e-07	C2 domain
1568	EMP24_GP25L	1/1	8-211	142.6	7.2e-39	emp24/gp25L/p24 family
1569	DSPc	1/1	173-311	261.6	1.1e-74	Dual specificity phosphatase, catalytic
1569	Rhodanese	1/1	9-131	92.1	6e-26	Rhodanese-like domain
1569	Y_phosphatase	1/1	237-290	19.8	0.00013	Protein-tyrosine phosphatase
1570	Ribosomal_S17e	1/1	1-122	305.6	2.5e-95	Ribosomal S17
1571	proteasome	1/1	29-215	145.9	1.4e-40	Proteasome A-type and B-type
1572	TCTP	1/1	1-135	287.4	4.2e-87	Translationally controlled tumor prot
1573	HATPase_c	1/1	1-96	27.5	1.8e-06	Histidine kinase-, DNA gyrase B-, and H
1573	HSP90	1/1	99-635	1270.1	0	Hsp90 protein

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1574	Alpha_adaptin_C	1/1	226-237	6.3	0.25	Alpha adaptin AP2, C-terminal domain
1574	Amino_oxidase	1/1	23-460	326.9	2.3e-94	Flavin containing amine oxidoreductas
1574	DAO	1/1	14-46	21.0	9.2e-05	FAD dependent oxidoreductase
1574	FAD_binding_3	1/1	16-48	31.1	7.2e-09	FAD binding domain
1574	GMC_oxred	1/1	14-44	8.1	0.11	GMC oxidoreductase
1574	Thi4	1/1	15-45	14.8	0.00093	Thi4 family
1574	TrkA-N	1/1	15-43	13.2	0.037	TrkA-N domain
1574	pyr_redox	1/1	15-50	21.8	1.6e-05	Pyridine nucleotide-disulphide oxidor
1575	MHC_I	1/1	25-203	482.4	3.5e-141	Class I Histocompatibil ity antigen, domains
1575	ig	1/1	220-285	36.3	2.2e-08	Immunoglobulin domain
1576	MHC_II_alpha	1/1	29-109	158.0	1.4e-46	Class II histocompatibil ity antigen, alp
1576	ig	1/1	125-190	32.0	3.4e-07	Immunoglobulin domain
1577	NDK	1/1	5-152	396.9	2e-115	Nucleoside diphosphate kinase
1578	AAA	1/1	140-157	12.4	0.01	ATPase family associated with various ce
1578	ras	1/2	140-154	14.4	0.0034	Ras family
1578	ras	2/2	213-321	96.7	1.2e-27	Ras family
1579	Ribosomal_L10e	1/1	1-176	465.4	3.7e-138	Ribosomal L10
1580	RHD	1/1	18-186	416.3	6.5e-125	Rel homology domain (RHD)
1580	TIG	1/1	194-289	80.1	4.5e-20	IP/TIG domain
1581	serpin	1/1	28-402	583.7	5.8e-172	Serpin (serine protease inhibitor)
1582	PCNA	1/1	1-125	319.7	3.3e-92	Proliferating cell nuclear antigen, N-termin
1582	PCNA_C	1/1	127-254	317.2	1.9e-91	Proliferating cell nuclear antigen, C-termin
1583	Herpes_glycop_D	1/1	352-386	7.7	0.43	Herpesvirus glycoprotein D
1583	ig	1/3	43-110	19.4	0.001	Immunoglobulin domain
1583	ig	2/3	165-209	18.5	0.0018	Immunoglobulin domain
1583	ig	3/3	251-328	26.9	8.5e-06	Immunoglobulin domain
1584	WD40	2/6	84-123	9.0	0.94	WD domain, G-beta repeat
1585	ig	1/4	85-121	10.1	0.39	Immunoglobulin domain
1585	ig	3/4	255-312	16.3	0.0076	Immunoglobulin domain
1585	ig	4/4	347-396	32.3	2.7e-07	Immunoglobulin domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1586	lipocalin	1/1	4-134	110.6	6e-31	Lipocalin / cytosolic fatty-acid binding pr
1587	Grp1_Fun34_YaaH	1/1	557-575	6.3	0.3	GPRI/FUN34/yaaH family
1587	IGA1	1/1	63-81	5.6	0.59	Immunoglobulin A1 protease
1587	ig	1/4	35-85	13.5	0.043	Immunoglobulin domain
1587	ig	2/4	217-280	31.4	4.9e-07	Immunoglobulin domain
1587	ig	4/4	412-487	22.3	0.00016	Immunoglobulin domain
1587	pkinase	1/1	582-910	253.7	2.5e-72	Protein kinase domain
1588	RNA_pol_Rpb7_N	1/1	1-77	135.3	2.5e-39	RNA polymerase Rpb7, N-terminal domain
1588	S1	1/1	78-161	69.4	1.4e-17	S1 RNA binding domain
1590	GATase	1/1	204-249	8.3	0.33	Glutamine amidotransferase class-I
1591	Ribosomal_S2	1/1	18-186	340.5	1.8e-98	Ribosomal protein S2
1592	Gelsolin	1/6	76-126	64.7	6.4e-17	Gelsolin repeat
1592	Gelsolin	2/6	198-238	70.6	1.3e-18	Gelsolin repeat
1592	Gelsolin	3/6	314-356	62.2	3.2e-16	Gelsolin repeat
1592	Gelsolin	4/6	453-504	73.6	1.7e-19	Gelsolin repeat
1592	Gelsolin	5/6	576-616	42.9	1.1e-10	Gelsolin repeat
1592	Gelsolin	6/6	679-721	63.4	1.5e-16	Gelsolin repeat
1593	ion_trans	1/1	239-410	59.6	5.4e-15	Ion transport protein
1594	ig	1/2	148-206	24.5	4.1e-05	Immunoglobulin domain
1594	ig	2/2	256-310	25.3	2.4e-05	Immunoglobulin domain
1595	DUF258	1/1	15-30	6.4	0.79	Protein of unknown function, DUF258
1595	ras	1/1	13-218	366.4	9.7e-108	Ras family
1596	Exonuc_V_gamma	1/1	187-229	5.0	0.51	Exodeoxyribonuclease V, gamma subunit
1596	Ribosomal_S6e	1/1	1-127	312.1	6.7e-90	Ribosomal protein S6e
1597	IL8	1/1	23-90	47.3	6.7e-12	Small cytokines (intecrine/chemokine), inter
1598	Exo_endo_phos	1/1	8-237	141.2	1.9e-38	Endonuclease/Exonuclease/phosphatase fa
1598	rvt	1/1	508-773	263.0	3.9e-75	Reverse transcriptase (RNA-dependent DN
1599	Mov34	1/1	26-139	173.8	2.9e-48	Mov34/MPN/PAD-1 family
1600	histone	1/1	19-137	100.3	3.6e-27	Core histone H2A/H2B/H3/H4
1601	2-Hacid_DH	1/1	44-137	133.7	2.6e-36	D-isomer specific 2-hydroxyacid dehydrog
1601	2-Hacid_DH_C	1/1	139-320	199.8	4.1e-81	D-isomer specific 2-hydroxyacid dehydrog

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1601	PDH	1/1	187-213	8.1	0.35	Prephenate dehydrogenase
1602	GST_C	1/1	127-217	11.9	0.048	Glutathione S-transferase, C-terminal
1603	proteasome	1/1	31-217	238.3	1.1e-67	Proteasome A-type and B-type
1604	Ribosomal_S8	1/1	5-130	192.1	6.6e-58	Ribosomal protein S8
1605	PAE	1/1	17-102	7.4	0.2	Pectinacetyl esterase
1606	PCI	1/1	328-408	80.5	7.2e-22	PCI domain
1607	Ribosomal_L6e	1/1	181-288	251.0	8e-73	Ribosomal protein L6e
1607	Ribosomal_L6e_N	1/1	34-96	128.0	1.2e-36	Ribosomal protein L6, N-terminal domain
1608	EF1G_domain	1/1	275-381	303.5	2.3e-87	Elongation factor 1 gamma, conserved domain
1608	GST_C	1/1	86-198	113.3	8.8e-31	Glutathione S-transferase, C-terminal domain
1608	GST_N	1/1	1-81	89.1	1.9e-24	Glutathione S-transferase, N-terminal domain
1609	CH	1/1	25-138	75.3	2e-19	Calponin homology (CH) domain
1609	calponin	1/1	175-200	51.8	1.7e-14	Calponin family repeat
1610	E7	1/1	1561-1570	6.3	0.41	E7 protein, Early protein
1610	Glyco_hydro_16	1/1	1773-1802	9.3	0.15	Glycosyl hydrolases family 16
1610	Mov34	1/1	2099-2205	99.9	5e-26	Mov34/MPN/PAD-1 family
1610	toxin_3	1/2	955-973	8.9	0.15	
1611	ATP-bind	1/1	488-526	6.9	0.49	Conserved hypothetical ATP binding protein
1611	Ku_C	1/1	471-559	143.1	4.9e-39	Ku70/Ku80 C-terminal arm
1611	Ku_N	1/1	37-256	337.7	1.3e-97	Ku70/Ku80 N-terminal alpha/beta domain
1611	SAP	1/1	573-607	39.5	1.5e-09	SAP domain
1611	ku	1/1	261-468	296.2	2.7e-92	Ku70/Ku80 beta-barrel domain
1612	Nop	1/1	197-345	201.6	1.2e-56	Putative snoRNA binding domain
1614	3Beta_HSD	1/2	5-26	8.8	0.15	3-beta hydroxysteroid dehydrogenase/i
1614	3Beta_HSD	2/2	84-135	8.4	0.18	3-beta hydroxysteroid dehydrogenase/i
1614	Epimerase	1/1	5-341	499.3	3e-146	NAD dependent epimerase/dehydratase f
1614	adh_short	1/1	1-33	11.7	0.029	short chain dehydrogenase
1616	ATP-synt_C	1/1	67-135	107.9	1.9e-28	ATP synthase subunit C
1618	Flavi_NS2A	1/1	332-354	8.3	0.74	Flavivirus non-structural protein NS2A

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1618	Lamp	1/1	1-354	612.3	2.8e-180	Lysosome-associated membrane glycoprote
1618	Peptidase_M50	1/1	3-341	6.7	0.82	Peptidase family M50
1619	A4_EXTRA	1/1	42-204	413.4	2e-209	Amyloid A4 extracellular domain
1619	Coproge_n_oxidas	1/1	164-182	5.4	0.13	Coproporphyrinogen III oxidase
1619	Kunitz_BPTI	1/1	310-360	95.4	6.6e-30	Kunitz/Bovine pancreatic trypsin inhi
1620	Ribosomal_L30	1/1	88-140	98.3	2.3e-28	Ribosomal protein L30p/L7e
1621	PX	1/1	26-148	128.2	1.5e-34	PX domain
1622	ig	1/7	90-109	9.4	0.59	Immunoglobulin domain
1622	ig	3/7	245-313	31.5	4.5e-07	Immunoglobulin domain
1622	ig	4/7	359-404	16.6	0.006	Immunoglobulin domain
1622	ig	6/7	570-638	31.6	4.4e-07	Immunoglobulin domain
1622	ig	7/7	675-733	45.6	5.8e-11	Immunoglobulin domain
1622	pkinase	1/1	827-1152	259.7	3.8e-74	Protein kinase domain
1624	zf-C3HC4	1/1	521-560	8.8	0.21	Zinc finger, C3HC4 type (RING finger)
1625	hormone6	1/1	21-116	202.4	7e-57	Glycoprotein hormone
1626	G-alpha	1/1	13-393	687.4	7.2e-203	G-protein alpha subunit
1626	arf	1/1	213-296	26.1	2.9e-06	ADP-ribosylation factor family
1627	rrm	1/2	16-86	84.2	2.5e-23	RNA recognition motif. (a.k.a. RRM, RBD, or
1627	rrm	2/2	107-177	91.0	2.4e-25	RNA recognition motif. (a.k.a. RRM, RBD, or
1628	HMG_box	1/1	1-36	34.8	3.8e-08	HMG (high mobility group) box
1629	OEP	1/1	92-130	7.6	0.42	Outer membrane efflux protein
1629	Ribosomal_L7Ae	1/1	122-216	102.0	4.7e-29	Ribosomal protein L7Ae/L30e/S12e/Gadd4
1630	Ribosomal_S24e	1/1	23-105	192.0	8.1e-55	Ribosomal protein S24e
1631	SAPA	1/2	21-54	85.7	5.9e-33	Saposin A-type domain
1631	SAPA	2/2	491-524	78.1	6.4e-30	Saposin A-type domain
1631	Surfactant_B	2/3	357-389	9.8	0.1	1/3 240 272 .. 45 78
1632	Tropomyosin	2/2	48-284	501.7	5.5e-147	Tropomyosin
1633	hormone	1/1	12-227	352.4	2.1e-130	Somatotropin hormone family
1635	DSPc	2/2	1806-1840	8.7	0.36	Dual specificity phosphatase,

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						catalytic
1635	Y_phosphatase	1/2	1365-1596	454.3	1.1e-132	Protein-tyrosine phosphatase
1635	Y_phosphatase	2/2	1654-1887	413.6	1.8e-120	Protein-tyrosine phosphatase
1635	fn3	1/8	309-391	73.7	8e-20	Fibronectin type III domain
1635	fn3	2/8	403-490	66.5	9.6e-18	Fibronectin type III domain
1635	fn3	3/8	502-584	70.5	6.7e-19	Fibronectin type III domain
1635	fn3	4/8	596-686	69.3	1.5e-18	Fibronectin type III domain
1635	fn3	5/8	698-799	58.7	1.7e-15	Fibronectin type III domain
1635	fn3	6/8	811-894	50.4	4.3e-13	Fibronectin type III domain
1635	fn3	7/8	905-990	67.0	6.8e-18	Fibronectin type III domain
1635	ig	1/3	37-99	29.7	1.4e-06	Immunoglobulin domain
1635	ig	2/3	139-199	23.2	9.1e-05	Immunoglobulin domain
1635	ig	3/3	236-290	26.7	1e-05	Immunoglobulin domain
1636	ATP-synt_ab	1/1	138-421	550.0	1.5e-161	ATP synthase alpha/beta family, nucleot
1636	ATP-synt_ab_C	1/1	423-531	138.7	9.9e-39	ATP synthase alpha/beta chain, C termin
1636	ATP-synt_ab_N	1/1	67-135	74.5	1e-23	ATP synthase alpha/beta family, beta-ba
1637	S_100	1/1	8-51	87.9	1.9e-23	S-100/ICaBP type calcium binding domain
1637	efhand	1/1	58-86	23.8	0.00011	EF hand
1638	GLTT	1/1	40-68	7.6	0.44	GLTT repeat (6 copies)
1639	PGK	1/1	2-418	1017.1	3.9e-302	Phosphoglycerate kinase
1640	C2	1/8	2-85	87.2	1.1e-23	C2 domain
1640	C2	2/8	222-302	52.5	1.1e-13	C2 domain
1640	C2	3/8	381-479	66.0	1.4e-17	C2 domain
1640	C2	4/8	1154-1244	90.3	1.3e-24	C2 domain
1640	C2	5/8	1338-1421	17.4	0.0014	C2 domain
1640	C2	6/8	1580-1663	79.2	2.2e-21	C2 domain
1640	C2	8/8	1904-1926	15.3	0.0059	C2 domain
1641	RNA_pol_A	1/2	246-895	1289.3	0	RNA polymerase alpha subunit
1641	RNA_pol_A2	1/1	1060-1477	762.0	2.4e-225	RNA polymerase A/beta'/A" subunit
1643	HATPase_c	1/1	96-254	54.7	3.4e-14	Histidine kinase-, DNA gyrase B-, and HSP90
1643	HSP90	1/1	257-783	1105.0	0	Hsp90 protein
1644	Ribosomal_L40e	1/1	77-128	111.5	1.6e-29	Ribosomal L40e family
1644	ubiquitin	1/1	1-74	153.1	4.8e-42	Ubiquitin family
1646	Ribosomal_S13	1/1	14-142	274.7	1.2e-78	Ribosomal

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
						protein S13/S18
1647	Ribosomal_L5	1/1	10-63	87.8	2.2e-22	Ribosomal protein L5
1647	Ribosomal_L5_C	1/1	67-166	210.1	1.7e-62	ribosomal L5P family C-terminus
1648	Armadillo_seg	1/2	1017-1044	10.7	0.3	Armadillo/beta-catenin-like repeat
1649	ig	1/1	38-102	33.8	1e-07	Immunoglobulin domain
1650	ICE_p10	1/1	244-329	180.7	2.3e-50	ICE-like protease (caspase) p10 domain
1650	ICE_p20	1/1	88-219	293.9	5.7e-88	ICE-like protease (caspase) p20 domain
1650	TAF	1/1	133-143	4.8	1	TATA box binding protein associated factor (
1651	Ribosomal_L6	1/2	12-87	84.5	1.9e-22	Ribosomal protein L6
1651	Ribosomal_L6	2/2	99-178	66.8	2e-17	Ribosomal protein L6
1652	Ribosomal_S12	1/1	7-142	279.8	3.4e-80	Ribosomal protein S12
1653	ubiquitin	1/1	1-74	116.3	4.1e-31	Ubiquitin family
1654	Fragilysin	1/1	212-238	11.4	0.019	Fragilysin metalloproteinase (M10C) en
1654	Peptidase_M10	1/1	98-204	163.6	3.3e-45	Matrixin
1654	Peptidase_M10_N	1/1	75-84	10.2	0.014	Matrix metalloproteinase , N-terminal do
1654	hemopexin	1/4	298-341	58.5	3.3e-16	Hemopexin
1654	hemopexin	2/4	343-384	48.6	3.6e-13	Hemopexin
1654	hemopexin	3/4	387-434	54.2	7.1e-15	Hemopexin
1654	hemopexin	4/4	436-480	53.4	1.3e-14	Hemopexin
1655	Sec61_beta	1/1	49-94	98.9	2.4e-26	Sec61beta family
1656	ras	1/1	66-134	36.7	7.9e-10	Ras family
1657	Hist_deacetyl	1/1	681-1028	374.2	1.3e-108	Histone deacetylase family
1658	RA	1/1	648-735	97.5	2.6e-25	Ras association (RalGDS/AF-6) domain
1658	RasGEF	1/1	240-462	194.3	1.9e-54	RasGEF domain
1658	RasGEFN	1/1	86-140	31.4	2.4e-07	Guanine nucleotide exchange factor for Ras-1
1659	UPF0023	1/1	5-244	332.7	4.1e-96	Uncharacterized protein family UPF0023
1660	NNMT_PNMT_TEMT	1/1	1-259	593.3	1.5e-174	NNMT/PNMT/TEMT family
1661	KH	1/1	47-95	22.7	6e-05	KH domain
1661	Ribosomal_S3_C	1/1	104-188	112.8	2.6e-34	Ribosomal protein S3, C-terminal domai
1663	Neurokinin_B	1/1	1-55	126.0	2.2e-37	Neurokinin B
1664	ig	1/4	85-121	9.2	0.71	Immunoglobulin domain
1664	ig	2/4	162-219	8.8	0.89	Immunoglobulin domain

SEQ ID NO:	Model	Repeats	Position	Score	E_value	Description
1664	ig	3/4	255-312	18.4	0.0019	Immunoglobulin domain
1664	ig	4/4	347-396	30.7	7.8e-07	Immunoglobulin domain
1665	Ran_BP1	1/1	37-161	306.1	4.3e-88	RanBP1 domain
1666	bromodomain	1/1	136-223	128.7	5e-36	Bromodomain
1668	WD40	1/2	171-205	12.4	0.098	WD domain, G-beta repeat
1669	BRICHOS	1/1	68-164	144.0	1.7e-40	BRICHOS domain
1670	Osteopontin	1/1	1-18	4.6	0.78	Osteopontin
1670	TILa	1/1	433-455	8.8	0.41	TILa domain
1670	efhand	1/1	626-654	10.9	0.4	EF hand
1670	kazal	1/2	456-509	71.9	1.3e-17	Kazal-type serine protease inhibitor domain
1671	adh_short	1/1	2-288	223.8	2.5e-63	short chain dehydrogenase
1672	Peptidase_C1	1/1	114-332	442.9	5.2e-132	Papain family cysteine protease
1673	SNF	1/1	52-597	1309.0	0	Sodium:neurotransmitter symporter family
1674	Gal-bind_lectin	1/1	5-137	103.2	1e-28	Galactoside-binding lectin
1675	helicase_C	1/1	382-477	53.7	9.4e-14	Helicase conserved C-terminal domain
1676	Ribosomal_L7Ae	1/1	16-111	143.0	2.8e-41	Ribosomal protein L7Ae/L30e/S12e/Gadd4
1677	GST_C	1/1	83-192	106.0	1e-28	Glutathione S-transferase, C-terminal domain
1677	GST_N	1/1	4-77	100.0	1.3e-27	Glutathione S-transferase, N-terminal domain
1678	Peptidase_S26	1/1	86-244	185.1	7.9e-56	Signal peptidase I
1679	DNA_pol_delta_4	1/1	1-107	207.1	9.2e-63	DNA polymerase delta, subunit 4
1680	Rhomboid	1/1	99-250	78.6	6.6e-21	Rhomboid family
1683	ras	1/1	24-217	301.2	2.2e-88	Ras family
1684	Synaptophysin	1/1	35-260	245.2	8.9e-70	Synaptophysin / synaptoporin
1685	Pep_M12B_propep	1/1	88-204	200.2	3.2e-56	Reprolysin family propeptide
1685	Reprolysin	1/1	220-414	367.1	1.9e-106	Reprolysin (M12B) family zinc metallo
1685	disintegrin	1/1	431-507	82.2	3.1e-26	Disintegrin
1686	transmembrane4	1/1	70-316	332.6	1e-103	Tetraspanin family
1688	MBD	1/1	207-260	100.1	4.5e-26	Methyl-CpG binding domain
1689	Sm	1/1	43-122	63.7	1.2e-16	Sm protein
1691	pkinase	1/2	162-383	183.1	4.5e-51	Protein kinase domain
1691	pkinase	2/2	455-482	22.9	2.9e-05	Protein kinase domain

EXAMPLE 5
eMatrix Annotation of Polypeptides of the Invention

Using the eMATRIX software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., vol. 6, pp. 219-235 (1999), herein incorporated by reference), the polypeptides of the invention (SEQ ID NO 853 through 1704) we analyzed. The following table describes the polypeptides of the invention that have significant eMatrix hits:

TABLE 4

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
856	BL01115A	10.22	6.705e-10	7-50	BL01115	GTP-binding nuclear protein ran proteins.
856	BL01115B	10.81	7.308e-09	87-130	BL01115	GTP-binding nuclear protein ran proteins.
856	PR00449A	13.20	3.045e-17	7-28	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
856	PR00449B	14.34	6.318e-11	30-46	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
856	PR00449C	17.27	2.895e-18	47-69	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
856	PR00449D	10.79	2.800e-15	109-122	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
856	PR00449E	13.50	9.100e-16	157-179	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
857	BL00222C	22.97	1.333e-26	38-65	BL00222	Insulin-like growth factor binding proteins.
857	BL00484B	9.04	2.385e-15	39-52	BL00484	Thyroglobulin type-1 repeat proteins proteins.
857	BL00484C	17.01	7.158e-15	63-77	BL00484	Thyroglobulin type-1 repeat proteins proteins.
860	BL00194	12.16	3.348e-13	86-98	BL00194	Thioredoxin family proteins.
860	PR00421B	11.40	2.241e-11	93-102	PR00421	THIOREDOXIN FAMILY SIGNATURE
860	PR00421C	13.60	5.500e-09	136-147	PR00421	THIOREDOXIN FAMILY SIGNATURE
861	BL00288A	17.47	2.059e-36	64-93	BL00288	Tissue inhibitors of metalloproteinases proteins.
861	BL00288B	9.44	7.000e-15	108-118	BL00288	Tissue inhibitors of metalloproteinases proteins.
861	BL00288C	14.62	6.500e-18	127-141	BL00288	Tissue inhibitors of metalloproteinases proteins.
861	BL00288D	25.76	1.000e-40	151-195	BL00288	Tissue inhibitors of metalloproteinases proteins.
861	BL00288E	17.24	1.667e-26	197-219	BL00288	Tissue inhibitors of metalloproteinases proteins.
862	BL00229A	23.57	9.182e-09	216-254	BL00229	Tau and MAP proteins tubulin-binding domain proteins.
862	BL00412D	16.54	3.296e-09	175-225	BL00412	Neuromodulin (GAP-43) proteins.
862	BL00412D	16.54	4.398e-09	103-153	BL00412	Neuromodulin (GAP-43) proteins.
862	BL00412D	16.54	4.717e-10	107-157	BL00412	Neuromodulin (GAP-43) proteins.
862	BL00412D	16.54	5.684e-09	128-178	BL00412	Neuromodulin (GAP-43) proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
862	BL00412D	16.54	9.724e-09	90-140	BL00412	Neuromodulin (GAP-43) proteins.
862	BL00826C	7.63	6.400e-09	197-223	BL00826	MARCKS family proteins.
863	BL01033A	16.94	3.250e-20	44-65	BL01033	Globins profile.
863	BL01033B	13.81	7.000e-14	106-117	BL01033	Globins profile.
863	PR00611A	15.91	5.829e-09	44-66	PR00611	ERYTHROCRUORIN FAMILY SIGNATURE
863	PR00612A	8.64	5.800e-14	34-46	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
863	PR00612B	10.92	1.000e-13	51-61	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
863	PR00612C	12.16	2.286e-13	66-75	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
863	PR00612D	9.76	3.400e-15	93-106	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
863	PR00612E	9.04	7.000e-19	141-157	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
864	BL00077A	19.44	6.478e-34	5-45	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077B	10.15	7.750e-36	67-112	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077C	18.98	1.000e-40	127-177	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077D	11.17	1.000e-40	200-254	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077E	13.71	5.179e-38	265-313	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077F	11.35	1.000e-40	348-398	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
864	BL00077G	15.93	1.000e-40	413-461	BL00077	Heme-copper oxidase catalytic subunit, copper B binding regio.
866	BL00175A	15.42	8.333e-20	15-34	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.
866	BL00175B	12.60	1.000e-12	64-76	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.
866	BL00175C	23.75	5.000e-25	88-119	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.
866	BL00175D	27.67	8.500e-40	173-224	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.
870	BL00478B	14.79	6.870e-14	300-314	BL00478	LIM domain proteins.
870	PD00289	9.97	6.276e-09	72-85	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.
873	PD01922B	21.83	7.328e-14	251-286	PD01922	PROTEIN PHOSPHODIESTERASE HYDROL.
874	BL00030A	14.39	6.294e-11	301-319	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
874	BL00030B	7.03	4.789e-09	340-349	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
874	BL00048	6.39	1.563e-09	122-148	BL00048	Protamine P1 proteins.
874	BL00048	6.39	1.563e-09	123-149	BL00048	Protamine P1 proteins.
874	BL00048	6.39	1.711e-10	106-132	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
874	BL00048	6.39	1.947e-10	117-143	BL00048	Protamine P1 proteins.
874	BL00048	6.39	2.125e-11	120-146	BL00048	Protamine P1 proteins.
874	BL00048	6.39	3.025e-09	121-147	BL00048	Protamine P1 proteins.
874	BL00048	6.39	3.132e-10	127-153	BL00048	Protamine P1 proteins.
874	BL00048	6.39	3.813e-09	110-136	BL00048	Protamine P1 proteins.
874	BL00048	6.39	4.197e-10	118-144	BL00048	Protamine P1 proteins.
874	BL00048	6.39	5.725e-09	108-134	BL00048	Protamine P1 proteins.
874	BL00048	6.39	6.329e-10	114-140	BL00048	Protamine P1 proteins.
874	BL00048	6.39	6.566e-10	116-142	BL00048	Protamine P1 proteins.
874	BL00048	6.39	6.963e-09	125-151	BL00048	Protamine P1 proteins.
874	BL00048	6.39	7.039e-10	119-145	BL00048	Protamine P1 proteins.
874	BL00048	6.39	7.075e-09	115-141	BL00048	Protamine P1 proteins.
874	BL00048	6.39	7.395e-10	112-138	BL00048	Protamine P1 proteins.
874	BL00048	6.39	7.618e-12	124-150	BL00048	Protamine P1 proteins.
874	BL00048	6.39	7.638e-09	126-152	BL00048	Protamine P1 proteins.
874	BL00048	6.39	9.213e-09	113-139	BL00048	Protamine P1 proteins.
874	BL00970C	14.80	9.168e-09	99-136	BL00970	Nuclear transition protein 2 proteins.
874	PR00308A	5.90	4.646e-10	14-28	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00308A	5.90	4.706e-09	16-30	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00308C	3.83	8.831e-09	17-26	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00308C	3.83	8.892e-10	18-27	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00308C	3.83	8.892e-10	19-28	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00308C	3.83	8.892e-10	20-29	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
874	PR00833H	2.30	6.250e-10	15-29	PR00833	POLLEN ALLERGEN POA PI SIGNATURE
875	BL00226A	12.77	4.484e-13	181-195	BL00226	Intermediate filaments proteins.
875	BL00226B	23.86	7.120e-33	282-329	BL00226	Intermediate filaments proteins.
875	BL00226B	23.86	8.744e-09	233-280	BL00226	Intermediate filaments proteins.
875	BL00226C	13.23	2.714e-24	348-378	BL00226	Intermediate filaments proteins.
875	BL00226D	19.10	2.216e-29	451-497	BL00226	Intermediate filaments proteins.
875	BL00970B	10.09	7.033e-09	11-36	BL00970	Nuclear transition protein 2 proteins.
879	BL00282	16.88	3.640e-09	478-500	BL00282	Kazal serine protease inhibitors family proteins.
880	BL50058	27.23	9.654e-33	17-64	BL50058	G-protein gamma subunit profile.
880	PR00321A	11.91	6.727e-14	16-31	PR00321	GAMMA G-PROTEIN (TRANSDUCIN) SIGNATURE
880	PR00321B	12.62	3.647e-14	32-46	PR00321	GAMMA G-PROTEIN (TRANSDUCIN) SIGNATURE
880	PR00321C	15.39	8.816e-	52-69	PR00321	GAMMA G-PROTEIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			16			(TRANSDUCIN) SIGNATURE
881	BL00036	9.02	3.571e-13	331-343	BL00036	bZIP transcription factors basic domain proteins.
881	BL00048	6.39	2.238e-09	6-32	BL00048	Protamine P1 proteins.
881	BL00048	6.39	5.145e-10	5-31	BL00048	Protamine P1 proteins.
881	PR00043A	9.07	1.600e-25	309-329	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
881	PR00043B	8.73	1.310e-22	331-347	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
881	PR00043C	10.55	6.824e-16	349-361	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
881	PR00043D	11.91	5.737e-17	364-378	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
881	PR00043E	8.20	1.947e-18	378-393	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
881	PR00308C	3.83	8.013e-09	210-219	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
881	PR00308C	3.83	8.892e-10	211-220	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
881	PR00649B	8.21	9.206e-10	212-229	PR00649	GPR6 ORPHAN RECEPTOR SIGNATURE
888	PD00289	9.97	8.560e-10	328-341	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.
888	PF00424A	14.34	6.266e-09	236-267	PF00424	REV protein (anti-repression transactivator protein).
889	BL00226A	12.77	4.960e-14	158-172	BL00226	Intermediate filaments proteins.
889	BL00226B	23.86	4.600e-33	263-310	BL00226	Intermediate filaments proteins.
889	BL00226C	13.23	8.125e-22	328-358	BL00226	Intermediate filaments proteins.
889	BL00226D	19.10	8.054e-29	429-475	BL00226	Intermediate filaments proteins.
889	PR00581E	3.48	6.494e-09	46-61	PR00581	PROSTANOID EP2 RECEPTOR SIGNATURE
891	BL00406A	9.95	1.000e-40	84-118	BL00406	Actins proteins.
891	BL00406B	5.47	1.000e-40	160-214	BL00406	Actins proteins.
891	PR00190A	7.24	1.375e-13	103-112	PR00190	ACTIN SIGNATURE
891	PR00190B	9.98	1.000e-15	126-137	PR00190	ACTIN SIGNATURE
891	PR00190C	11.49	4.789e-30	138-160	PR00190	ACTIN SIGNATURE
891	PR00190D	19.23	3.520e-24	161-179	PR00190	ACTIN SIGNATURE
891	PR00190E	7.16	1.450e-19	192-205	PR00190	ACTIN SIGNATURE
891	PR00190F	7.80	4.349e-21	217-236	PR00190	ACTIN SIGNATURE
892	PD02870B	18.83	8.094e-11	219-251	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
893	BL00049A	13.86	8.333e-19	32-54	BL00049	Ribosomal protein L14 proteins.
893	BL00049B	18.42	6.806e-24	67-98	BL00049	Ribosomal protein L14 proteins.
893	BL00049C	17.38	2.688e-28	105-140	BL00049	Ribosomal protein L14 proteins.
893	BL00049D	13.47	5.765e-12	142-152	BL00049	Ribosomal protein L14 proteins.
894	BL01221A	17.26	3.739e-27	73-100	BL01221	PMP-22 / EMP / MP20 family proteins.
894	BL01221B	13.29	7.231e-14	108-121	BL01221	PMP-22 / EMP / MP20 family proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
894	BL01221C	26.20	8.333e-38	131-175	BL01221	PMP-22 / EMP / MP20 family proteins.
894	BL01221C	26.20	8.405e-11	128-172	BL01221	PMP-22 / EMP / MP20 family proteins.
894	BL01221D	13.99	7.577e-28	202-228	BL01221	PMP-22 / EMP / MP20 family proteins.
895	BL00123A	10.80	6.786e-28	77-101	BL00123	Alkaline phosphatase proteins.
895	BL00123B	19.31	1.900e-40	115-157	BL00123	Alkaline phosphatase proteins.
895	BL00123C	24.61	1.000e-40	170-219	BL00123	Alkaline phosphatase proteins.
895	BL00123D	12.73	5.263e-15	241-253	BL00123	Alkaline phosphatase proteins.
895	BL00123E	22.25	1.000e-40	329-382	BL00123	Alkaline phosphatase proteins.
895	BL00123F	19.03	6.625e-33	389-423	BL00123	Alkaline phosphatase proteins.
895	BL00123G	26.01	1.000e-40	463-512	BL00123	Alkaline phosphatase proteins.
895	PR00113A	11.74	9.182e-25	77-97	PR00113	ALKALINE PHOSPHATASE SIGNATURE
895	PR00113B	14.32	9.526e-19	133-148	PR00113	ALKALINE PHOSPHATASE SIGNATURE
895	PR00113C	10.88	5.846e-25	180-200	PR00113	ALKALINE PHOSPHATASE SIGNATURE
895	PR00113D	6.87	6.063e-14	239-249	PR00113	ALKALINE PHOSPHATASE SIGNATURE
895	PR00113E	14.04	2.636e-35	330-360	PR00113	ALKALINE PHOSPHATASE SIGNATURE
898	BL00236D	25.66	6.860e-19	9-50	BL00236	Neurotransmitter-gated ion-channels proteins.
898	PR00253A	9.15	4.667e-15	25-45	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE
898	PR00253B	13.47	4.162e-18	51-72	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE
898	PR00253C	13.85	3.302e-16	85-106	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE
898	PR00253D	16.68	1.000e-18	228-248	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE
899	BL00048	6.39	1.000e-08	1924-1950	BL00048	Protamine P1 proteins.
899	BL00048	6.39	1.132e-12	1873-1899	BL00048	Protamine P1 proteins.
899	BL00048	6.39	1.500e-11	1859-1885	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.303e-10	1996-2022	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.421e-10	1870-1896	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.421e-10	1965-1991	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.421e-10	1972-1998	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.456e-12	1858-1884	BL00048	Protamine P1 proteins.
899	BL00048	6.39	2.721e-12	1988-2014	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.000e-11	1866-1892	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.132e-10	1850-1876	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.475e-09	1875-1901	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.487e-10	1857-1883	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
899	BL00048	6.39	3.605e-10	1935-1961	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.647e-12	1927-1953	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.813e-09	1855-1881	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.875e-11	1960-1986	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.875e-11	1967-1993	BL00048	Protamine P1 proteins.
899	BL00048	6.39	3.875e-11	1974-2000	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.044e-12	1871-1897	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.125e-11	1863-1889	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.323e-13	1860-1886	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.375e-09	1941-1967	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.713e-09	1961-1987	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.713e-09	1968-1994	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.713e-09	1975-2001	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.750e-11	1852-1878	BL00048	Protamine P1 proteins.
899	BL00048	6.39	4.838e-12	1861-1887	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.103e-12	1989-2015	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.125e-11	1958-1984	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.500e-10	1867-1893	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.500e-12	1874-1900	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.618e-10	1983-2009	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.632e-12	1981-2007	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.737e-10	2025-2051	BL00048	Protamine P1 proteins.
899	BL00048	6.39	5.855e-10	1932-1958	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.123e-13	1862-1888	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.125e-11	1869-1895	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.175e-09	1980-2006	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.294e-12	1853-1879	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.294e-12	1865-1891	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.329e-10	1856-1882	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.375e-11	1986-2012	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.500e-11	1979-2005	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.513e-09	1930-1956	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.566e-10	1951-1977	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.684e-10	2026-2052	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.738e-09	2002-2028	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
899	BL00048	6.39	6.850e-09	1993-2019	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.875e-11	1868-1894	BL00048	Protamine P1 proteins.
899	BL00048	6.39	6.963e-09	1854-1880	BL00048	Protamine P1 proteins.
899	BL00048	6.39	7.221e-12	1982-2008	BL00048	Protamine P1 proteins.
899	BL00048	6.39	7.231e-13	1926-1952	BL00048	Protamine P1 proteins.
899	BL00048	6.39	7.638e-09	1946-1972	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.200e-09	1950-1976	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.375e-11	1990-2016	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.477e-13	1864-1890	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.500e-11	1928-1954	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.544e-12	1872-1898	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.579e-10	1936-1962	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.625e-11	2021-2047	BL00048	Protamine P1 proteins.
899	BL00048	6.39	8.875e-09	2030-2056	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.100e-09	1959-1985	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.100e-09	1966-1992	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.100e-09	1973-1999	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.213e-09	1908-1934	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.289e-10	1848-1874	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.289e-10	1925-1951	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.526e-10	2024-2050	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.603e-12	1851-1877	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.625e-11	1953-1979	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.625e-11	1987-2013	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.763e-10	1849-1875	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.775e-09	1997-2023	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.888e-09	1964-1990	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.888e-09	1971-1997	BL00048	Protamine P1 proteins.
899	BL00048	6.39	9.888e-09	1978-2004	BL00048	Protamine P1 proteins.
899	BL00348F	23.19	8.169e-10	103-145	BL00348	p53 tumor antigen proteins.
899	BL00970B	10.09	6.736e-09	1952-1977	BL00970	Nuclear transition protein 2 proteins.
899	DM00215	19.43	4.706e-11	1151-1183	DM00215	PROLINE-RICH PROTEIN 3.
899	DM00215	19.43	6.644e-09	1150-1182	DM00215	PROLINE-RICH PROTEIN 3.
899	DM00215	19.43	8.780e-09	1154-1186	DM00215	PROLINE-RICH PROTEIN 3.
899	DM00892C	23.55	7.207e-28	2318-2351	DM00892	3 RETROVIRAL PROTEINASE.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
899	DM01206B	10.69	2.139e-09	1860-1879	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
900	BL00284A	15.64	2.565e-18	35-58	BL00284	Serpins proteins.
900	BL00284B	17.99	1.621e-13	173-193	BL00284	Serpins proteins.
900	BL00284C	28.56	2.038e-29	202-243	BL00284	Serpins proteins.
900	BL00284D	16.34	2.241e-17	315-341	BL00284	Serpins proteins.
900	BL00284E	19.15	7.158e-21	399-423	BL00284	Serpins proteins.
901	BL01160B	19.54	4.203e-09	982-1035	BL01160	Kinesin light chain repeat proteins.
901	BL01160B	19.54	8.932e-09	1480-1533	BL01160	Kinesin light chain repeat proteins.
901	PR00381A	9.55	1.321e-10	969-986	PR00381	KINESIN LIGHT CHAIN SIGNATURE
901	PR00820B	3.97	7.038e-09	1132-1146	PR00820	CBXX/CFQX PROTEIN SIGNATURE
902	PR00981A	11.62	4.240e-14	336-348	PR00981	SERYL-TRNA SYNTHETASE SIGNATURE
902	PR00981B	11.68	2.552e-15	348-361	PR00981	SERYL-TRNA SYNTHETASE SIGNATURE
902	PR00981C	15.34	3.919e-12	390-403	PR00981	SERYL-TRNA SYNTHETASE SIGNATURE
902	PR00981D	18.10	1.000e-15	407-423	PR00981	SERYL-TRNA SYNTHETASE SIGNATURE
902	PR00981E	13.40	6.667e-20	425-441	PR00981	SERYL-TRNA SYNTHETASE SIGNATURE
903	BL00509B	10.28	5.000e-09	234-244	BL00509	Ras GTPase-activating proteins.
903	BL01052C	18.51	7.204e-09	146-185	BL01052	Calponin family repeat proteins.
903	BL01159	13.85	5.959e-10	650-664	BL01159	WW/rsp5/WWP domain proteins.
903	PR00403B	12.19	3.593e-09	650-664	PR00403	WW DOMAIN SIGNATURE
904	BL00385A	11.67	6.727e-39	38-69	BL00385	Alpha-L-fucosidase proteins.
904	BL00385B	24.10	1.000e-40	79-130	BL00385	Alpha-L-fucosidase proteins.
904	BL00385C	13.73	1.000e-40	132-175	BL00385	Alpha-L-fucosidase proteins.
904	BL00385D	15.93	7.923e-29	176-199	BL00385	Alpha-L-fucosidase proteins.
904	BL00385E	16.21	1.000e-40	213-256	BL00385	Alpha-L-fucosidase proteins.
904	BL00385F	16.09	1.000e-40	257-302	BL00385	Alpha-L-fucosidase proteins.
904	BL00385G	15.69	2.800e-36	321-354	BL00385	Alpha-L-fucosidase proteins.
904	BL00385H	11.86	7.545e-28	355-378	BL00385	Alpha-L-fucosidase proteins.
904	BL00385I	16.17	1.000e-40	388-426	BL00385	Alpha-L-fucosidase proteins.
904	PR00741A	9.24	9.308e-20	93-108	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741B	14.23	1.409e-23	132-148	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741C	9.16	1.000e-25	151-169	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741D	16.11	1.621e-25	178-197	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741E	13.39	2.385e-21	218-234	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741F	14.66	8.000e-29	246-267	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
904	PR00741G	9.29	6.870e-26	321-342	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
904	PR00741H	10.32	1.409e-27	354-376	PR00741	GLYCOSYL HYDROLASE FAMILY 29 SIGNATURE
905	BL00319C	17.12	6.373e-11	371-404	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
905	BL00319C	17.12	9.171e-09	374-407	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
906	BL00266A	15.69	6.478e-12	41-67	BL00266	Somatotropin, prolactin and related hormones proteins.
907	BL00030A	14.39	5.714e-09	307-325	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
907	BL00048	6.39	1.225e-09	461-487	BL00048	Protamine P1 proteins.
907	BL00048	6.39	1.338e-09	452-478	BL00048	Protamine P1 proteins.
907	BL00048	6.39	1.829e-10	457-483	BL00048	Protamine P1 proteins.
907	BL00048	6.39	2.013e-09	552-578	BL00048	Protamine P1 proteins.
907	BL00048	6.39	2.125e-09	474-500	BL00048	Protamine P1 proteins.
907	BL00048	6.39	2.191e-12	454-480	BL00048	Protamine P1 proteins.
907	BL00048	6.39	2.575e-09	455-481	BL00048	Protamine P1 proteins.
907	BL00048	6.39	2.776e-10	450-476	BL00048	Protamine P1 proteins.
907	BL00048	6.39	3.842e-10	453-479	BL00048	Protamine P1 proteins.
907	BL00048	6.39	4.375e-11	456-482	BL00048	Protamine P1 proteins.
907	BL00048	6.39	4.488e-09	460-486	BL00048	Protamine P1 proteins.
907	BL00048	6.39	4.500e-11	440-466	BL00048	Protamine P1 proteins.
907	BL00048	6.39	4.825e-09	444-470	BL00048	Protamine P1 proteins.
907	BL00048	6.39	5.163e-09	555-581	BL00048	Protamine P1 proteins.
907	BL00048	6.39	5.382e-10	445-471	BL00048	Protamine P1 proteins.
907	BL00048	6.39	6.000e-11	447-473	BL00048	Protamine P1 proteins.
907	BL00048	6.39	6.447e-10	448-474	BL00048	Protamine P1 proteins.
907	BL00048	6.39	6.625e-09	449-475	BL00048	Protamine P1 proteins.
907	BL00048	6.39	6.625e-09	550-576	BL00048	Protamine P1 proteins.
907	BL00048	6.39	6.684e-10	458-484	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.300e-09	436-462	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.500e-11	442-468	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.525e-09	551-577	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.868e-10	451-477	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.975e-09	462-488	BL00048	Protamine P1 proteins.
907	BL00048	6.39	7.975e-09	476-502	BL00048	Protamine P1 proteins.
907	BL00048	6.39	8.000e-11	441-467	BL00048	Protamine P1 proteins.
907	BL00048	6.39	8.500e-	459-485	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			
907	BL00048	6.39	8.934e-10	438-464	BL00048	Protamine P1 proteins.
907	BL00048	6.39	9.053e-10	446-472	BL00048	Protamine P1 proteins.
907	BL00048	6.39	9.289e-10	443-469	BL00048	Protamine P1 proteins.
907	BL00048	6.39	9.408e-10	439-465	BL00048	Protamine P1 proteins.
907	PF01140D	15.54	6.625e-10	559-593	PF01140	Matrix protein (MA), p15.
907	PF01140D	15.54	6.860e-09	435-469	PF01140	Matrix protein (MA), p15.
909	BL00450D	21.14	9.534e-09	33-56	BL00450	Aconitase family proteins.
909	PR00764F	16.89	9.766e-09	51-71	PR00764	COMPLEMENT C9 SIGNATURE
910	BL00048	6.39	4.938e-09	47-73	BL00048	Protamine P1 proteins.
911	BL00292A	22.87	4.115e-25	105-138	BL00292	Cyclins proteins.
911	BL00292B	20.31	8.826e-19	148-178	BL00292	Cyclins proteins.
911	PD02331A	19.76	8.990e-11	121-167	PD02331	CYCLIN CELL CYCLE DIVISION PROTE.
912	BL00888B	14.79	1.310e-13	308-331	BL00888	Cyclic nucleotide-binding domain proteins.
912	BL00888B	14.79	7.600e-19	190-213	BL00888	Cyclic nucleotide-binding domain proteins.
912	DM01513B	6.81	2.833e-14	351-402	DM01513	CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN.
912	DM01513B	6.81	9.871e-34	227-278	DM01513	CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN.
912	PR00103A	9.59	3.483e-13	305-319	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103A	9.59	5.846e-16	187-201	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103B	13.39	5.950e-15	202-216	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103B	13.39	7.300e-11	320-334	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103C	15.68	2.800e-13	351-360	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103D	10.83	2.980e-09	239-250	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103D	10.83	3.700e-14	363-374	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
912	PR00103E	17.80	2.227e-15	384-396	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE
913	BL01154A	18.70	3.000e-22	57-77	BL01154	RNA polymerases L / 13 to 16 Kd subunits proteins.
913	BL01154B	24.55	5.500e-36	78-113	BL01154	RNA polymerases L / 13 to 16 Kd subunits proteins.
914	BL00048	6.39	9.100e-09	1321-1347	BL00048	Protamine P1 proteins.
914	BL00048	6.39	9.663e-09	1322-1348	BL00048	Protamine P1 proteins.
914	BL00291A	4.49	6.690e-09	894-928	BL00291	Prion protein.
914	BL00415C	7.09	3.182e-09	450-479	BL00415	Synapsins proteins.
914	BL00420A	20.42	2.938e-09	856-884	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
914	BL00420A	20.42	3.361e-10	763-791	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	3.400e-14	1482-1510	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	3.782e-11	617-645	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	4.246e-10	808-836	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	4.836e-10	1485-1513	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	5.500e-12	614-642	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	6.236e-11	679-707	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	6.400e-09	859-887	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	6.677e-09	802-830	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	7.709e-11	620-648	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	7.923e-09	641-669	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	8.672e-10	796-824	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	9.018e-11	644-672	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	9.031e-09	694-722	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	9.705e-10	938-966	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	9.827e-12	721-749	BL00420	Speract receptor repeat proteins domain proteins.
914	BL00420A	20.42	9.836e-11	697-725	BL00420	Speract receptor repeat proteins domain proteins.
914	BL01113A	17.99	1.000e-08	805-831	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.000e-13	802-828	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.173e-09	814-840	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.346e-09	1028-1054	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.383e-10	1244-1270	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.462e-12	1473-1499	BL01113	Clq domain proteins.
914	BL01113A	17.99	1.766e-10	685-711	BL01113	Clq domain proteins.
914	BL01113A	17.99	2.023e-11	617-643	BL01113	Clq domain proteins.
914	BL01113A	17.99	2.038e-09	817-843	BL01113	Clq domain proteins.
914	BL01113A	17.99	2.212e-	793-819	BL01113	Clq domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			
914	BL01113A	17.99	2.227e-11	947-973	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.385e-09	632-658	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.385e-12	1491-1517	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.432e-11	859-885	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.558e-09	620-646	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.731e-09	682-708	BL01113	C1q domain proteins.
914	BL01113A	17.99	2.731e-09	897-923	BL01113	C1q domain proteins.
914	BL01113A	17.99	3.489e-10	1488-1514	BL01113	C1q domain proteins.
914	BL01113A	17.99	3.769e-17	856-882	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.068e-11	941-967	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.288e-09	676-702	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.447e-10	862-888	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.462e-09	1213-1239	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.462e-09	989-1015	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.638e-10	811-837	BL01113	C1q domain proteins.
914	BL01113A	17.99	4.981e-09	748-774	BL01113	C1q domain proteins.
914	BL01113A	17.99	5.213e-10	697-723	BL01113	C1q domain proteins.
914	BL01113A	17.99	5.500e-09	611-637	BL01113	C1q domain proteins.
914	BL01113A	17.99	5.500e-11	727-753	BL01113	C1q domain proteins.
914	BL01113A	17.99	5.846e-09	826-852	BL01113	C1q domain proteins.
914	BL01113A	17.99	5.909e-11	944-970	BL01113	C1q domain proteins.
914	BL01113A	17.99	6.365e-09	1181-1207	BL01113	C1q domain proteins.
914	BL01113A	17.99	6.365e-09	614-640	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.128e-10	938-964	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.404e-09	820-846	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.404e-09	850-876	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.511e-10	1497-1523	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.577e-09	1253-1279	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.702e-10	799-825	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.818e-14	623-649	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.955e-11	1485-1511	BL01113	C1q domain proteins.
914	BL01113A	17.99	7.955e-11	796-822	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.096e-09	871-897	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.159e-11	808-834	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.364e-	626-652	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			
914	BL01113A	17.99	8.468e-10	865-891	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.541e-13	1247-1273	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.962e-09	1494-1520	BL01113	C1q domain proteins.
914	BL01113A	17.99	8.962e-09	691-717	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.308e-09	703-729	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.386e-11	1482-1508	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.426e-10	706-732	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.591e-11	853-879	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.617e-10	911-937	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.654e-09	736-762	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.727e-14	986-1012	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.757e-13	602-628	BL01113	C1q domain proteins.
914	BL01113A	17.99	9.809e-10	739-765	BL01113	C1q domain proteins.
914	PR00049D	0.00	6.339e-09	1490-1504	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
914	PR00049D	0.00	8.322e-09	856-870	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
914	PR00524F	5.36	3.394e-09	906-919	PR00524	CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE
914	PR00524F	5.36	5.552e-10	1497-1510	PR00524	CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE
916	BL00022B	7.54	1.000e-09	2640-2646	BL00022	EGF-like domain proteins.
916	BL00022B	7.54	1.000e-09	444-450	BL00022	EGF-like domain proteins.
916	BL00022B	7.54	1.900e-09	2129-2135	BL00022	EGF-like domain proteins.
916	BL00243H	17.53	4.682e-12	253-278	BL00243	Integrins beta chain cysteine-rich domain proteins.
916	BL01177C	17.39	3.000e-09	629-647	BL01177	Anaphylatoxin domain proteins.
916	BL01177D	17.50	3.000e-09	2097-2114	BL01177	Anaphylatoxin domain proteins.
916	BL01177D	17.50	9.333e-09	1321-1338	BL01177	Anaphylatoxin domain proteins.
916	BL01187A	9.98	2.125e-09	742-753	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	2.286e-10	1575-1586	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	2.286e-10	2059-2070	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	2.875e-09	375-386	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	2.895e-11	1367-1378	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	3.455e-14	936-947	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	3.571e-10	1492-1503	BL01187	Calcium-binding EGF-like domain proteins

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						pattern proteins.
916	BL01187A	9.98	4.000e-09	2142-2153	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	4.000e-10	1039-1050	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	4.316e-11	1937-1948	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	4.375e-12	619-630	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	4.750e-09	1451-1462	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	5.125e-09	1409-1420	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	5.286e-10	417-428	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	5.500e-09	1616-1627	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	5.714e-10	2335-2346	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	5.875e-09	1242-1253	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	6.250e-09	2020-2031	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	6.625e-09	659-670	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	7.000e-09	1284-1295	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	7.750e-09	1777-1788	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	8.125e-09	2295-2306	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	9.143e-10	1199-1210	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187A	9.98	9.250e-09	2614-2625	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	1.257e-10	1592-1607	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	1.300e-11	393-408	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	1.391e-13	435-450	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	1.450e-14	1511-1526	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	1.667e-12	1913-1928	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	2.000e-12	596-611	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
916	BL01187B	12.04	2.059e-15	2273-2288	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	2.059e-15	2631-2646	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	2.565e-13	1427-1442	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	2.957e-13	2160-2175	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	2.957e-13	2672-2687	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	3.077e-16	2590-2605	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	3.348e-13	912-927	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	3.700e-14	1633-1648	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.130e-13	1753-1768	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.150e-14	1955-1970	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.176e-15	2352-2367	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.300e-11	870-885	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.333e-12	759-774	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.522e-13	1343-1358	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	4.667e-12	1217-1232	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	5.050e-14	2438-2453	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	5.235e-15	635-650	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	5.667e-12	1794-1809	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.087e-13	1470-1485	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.100e-11	1057-1072	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.400e-14	2712-2727	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.667e-12	1996-2011	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.824e-15	2120-2135	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	6.870e-	2549-2564	BL01187	Calcium-binding EGF-

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			13			like domain proteins pattern proteins.
916	BL01187B	12.04	7.333e-12	2312-2327	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	7.686e-10	1385-1400	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	7.750e-14	2078-2093	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	7.750e-14	2794-2809	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.000e-12	1302-1317	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.500e-17	2753-2768	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.650e-14	677-692	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.667e-12	2396-2411	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.826e-13	1175-1190	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.826e-13	2036-2051	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	8.826e-13	718-733	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	9.550e-14	1260-1275	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	BL01187B	12.04	9.609e-13	1551-1566	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
916	DM00215	19.43	1.000e-09	530-562	DM00215	PROLINE-RICH PROTEIN 3.
916	DM00215	19.43	6.063e-12	545-577	DM00215	PROLINE-RICH PROTEIN 3.
916	DM00864B	11.34	4.896e-10	1960-1978	DM00864	EGF-LIKE DOMAIN.
916	DM00864B	11.34	6.577e-09	2799-2817	DM00864	EGF-LIKE DOMAIN.
916	DM00864B	11.34	7.179e-10	601-619	DM00864	EGF-LIKE DOMAIN.
916	DM00864B	11.34	8.732e-09	1556-1574	DM00864	EGF-LIKE DOMAIN.
916	PR00010A	11.79	4.115e-11	938-949	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	1.000e-10	640-650	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	1.214e-09	2443-2453	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	2.286e-09	2758-2768	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	2.667e-11	1348-1358	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	3.357e-09	1918-1928	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	3.455e-10	2125-2135	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	3.571e-09	2165-2175	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	4.429e-	2717-2727	PR00010	TYPE II EGF-LIKE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			SIGNATURE
916	PR00010C	11.16	4.818e-10	2357-2367	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	5.333e-11	917-927	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	5.364e-10	440-450	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	5.500e-09	2317-2327	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	6.182e-10	2677-2687	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	6.357e-09	1638-1648	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	7.000e-11	2636-2646	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	7.545e-10	2595-2605	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	9.143e-09	1265-1275	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	9.727e-10	2278-2288	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00010C	11.16	9.727e-10	2799-2809	PR00010	TYPE II EGF-LIKE SIGNATURE
916	PR00907B	11.29	1.000e-08	2790-2806	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907B	11.29	2.756e-09	2627-2643	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907B	11.29	5.957e-12	2708-2724	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907B	11.29	7.805e-09	2586-2602	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907D	5.59	8.609e-09	2278-2303	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	2.135e-09	1592-1618	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	3.189e-09	1633-1659	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	3.189e-09	2273-2299	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	3.673e-11	1260-1286	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	5.546e-12	2120-2146	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	6.514e-09	718-744	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	8.378e-09	1470-1496	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	9.321e-10	2396-2422	PR00907	THROMBOMODULIN SIGNATURE
916	PR00907G	11.63	9.406e-10	1343-1369	PR00907	THROMBOMODULIN SIGNATURE
917	BL00023	24.31	2.969e-28	332-368	BL00023	Type II fibronectin collagen-binding domain proteins.
917	BL00023	24.31	4.682e-35	390-426	BL00023	Type II fibronectin collagen-binding domain proteins.
917	BL00023	24.31	9.526e-24	274-310	BL00023	Type II fibronectin collagen-binding domain proteins.
917	BL00024A	11.49	2.800e-13	145-155	BL00024	Hemopexin domain proteins.
917	BL00024B	21.53	9.591e-33	166-199	BL00024	Hemopexin domain proteins.
917	BL00024C	22.98	1.000e-40	214-262	BL00024	Hemopexin domain proteins.
917	BL00024D	17.28	3.571e-35	442-473	BL00024	Hemopexin domain proteins.
917	BL00024E	7.58	6.625e-16	481-494	BL00024	Hemopexin domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
917	BL00024F	11.30	2.038e-22	523-543	BL00024	Hemopexin domain proteins.
917	BL00024G	13.31	7.158e-14	561-573	BL00024	Hemopexin domain proteins.
917	BL00024H	11.35	1.794e-11	581-592	BL00024	Hemopexin domain proteins.
917	BL00024H	11.35	4.600e-09	629-640	BL00024	Hemopexin domain proteins.
917	BL00142	8.38	6.000e-12	448-458	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
917	BL00546A	19.62	8.105e-30	125-154	BL00546	Matrixins cysteine switch.
917	BL00546B	20.11	1.000e-40	215-258	BL00546	Matrixins cysteine switch.
917	BL00546C	16.41	5.714e-35	442-473	BL00546	Matrixins cysteine switch.
917	BL00546D	10.34	4.000e-16	481-494	BL00546	Matrixins cysteine switch.
917	BL00546E	10.23	8.269e-23	523-543	BL00546	Matrixins cysteine switch.
917	BL00546F	12.40	7.955e-14	561-573	BL00546	Matrixins cysteine switch.
917	BL00546G	16.84	8.269e-17	582-601	BL00546	Matrixins cysteine switch.
917	BL00546H	10.76	1.257e-10	678-688	BL00546	Matrixins cysteine switch.
917	BL00546H	10.76	4.073e-09	629-639	BL00546	Matrixins cysteine switch.
917	PR00013A	12.26	5.333e-09	336-345	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013A	12.26	5.500e-13	394-403	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013A	12.26	7.833e-09	278-287	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013B	14.75	1.237e-11	405-417	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013B	14.75	4.000e-09	347-359	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013C	12.29	1.000e-20	422-437	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013C	12.29	3.571e-15	364-379	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00013C	12.29	7.800e-14	306-321	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
917	PR00138A	15.14	8.773e-16	145-158	PR00138	MATRIXIN SIGNATURE
917	PR00138B	15.82	5.500e-18	192-207	PR00138	MATRIXIN SIGNATURE
917	PR00138C	16.41	1.783e-32	215-243	PR00138	MATRIXIN SIGNATURE
917	PR00138D	16.56	8.920e-28	448-473	PR00138	MATRIXIN SIGNATURE
917	PR00138E	6.01	5.000e-16	481-494	PR00138	MATRIXIN SIGNATURE
917	PR00480B	15.41	2.286e-09	443-461	PR00480	ASTACIN FAMILY SIGNATURE
918	PF01130B	21.40	1.537e-15	223-268	PF01130	CD36 family.
918	PF01130C	22.91	1.851e-18	278-327	PF01130	CD36 family.
918	PF01130D	26.65	1.955e-23	360-413	PF01130	CD36 family.
920	BL01289A	12.18	8.200e-33	141-167	BL01289	TSC-22 / dip / bun family proteins.
920	BL01289B	10.45	8.071e-30	168-197	BL01289	TSC-22 / dip / bun family proteins.
920	DM00475B	12.12	5.891e-10	162-181	DM00475	w LOW TRANSPOSASE SAPA 12K.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
921	PD01719A	12.89	2.111e-09	416-443	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.
921	PR00711D	7.91	9.697e-09	255-272	PR00711	ATRIAL NATRIURETIC PEPTIDE SIGNATURE
923	BL00139A	10.29	6.478e-14	107-116	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
923	BL00139B	10.19	6.400e-10	152-160	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
923	BL00139D	9.24	9.182e-18	298-314	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
923	PR00705A	10.55	1.529e-16	107-122	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
923	PR00705B	10.22	4.115e-10	283-293	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
925	PF01140D	15.54	6.547e-09	176-210	PF01140	Matrix protein (MA), p15.
926	BL00755A	13.96	4.750e-14	50-68	BL00755	Protein secY proteins.
926	BL00755B	12.12	7.469e-18	87-106	BL00755	Protein secY proteins.
926	BL00755C	14.21	6.885e-13	203-218	BL00755	Protein secY proteins.
926	BL00755D	11.88	4.214e-17	291-309	BL00755	Protein secY proteins.
926	BL00755E	26.66	1.923e-26	385-425	BL00755	Protein secY proteins.
926	PR00303B	10.17	9.769e-09	86-106	PR00303	PREPROTEIN TRANSLOCASE SECY SUBUNIT SIGNATURE
928	BL01019A	13.20	1.000e-40	69-108	BL01019	ADP-ribosylation factors family proteins.
928	BL01019B	19.49	1.000e-40	113-167	BL01019	ADP-ribosylation factors family proteins.
928	BL01019C	12.52	3.842e-26	170-195	BL01019	ADP-ribosylation factors family proteins.
928	BL01020C	15.35	8.200e-15	97-147	BL01020	SAR1 family proteins.
928	PR00328A	10.62	5.213e-11	41-64	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE
928	PR00328C	13.16	2.444e-12	96-121	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE
930	BL00824A	13.78	8.650e-14	55-69	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
930	BL00824B	9.21	2.080e-21	132-151	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
930	BL00824C	14.58	1.000e-40	165-202	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
930	BL00824D	14.04	6.192e-39	203-237	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
930	BL00824E	12.49	3.333e-19	246-261	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
931	BL00291A	4.49	9.192e-11	140-174	BL00291	Prion protein.
931	PD01234B	15.53	5.179e-09	227-244	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.
931	PR00049D	0.00	7.504e-11	85-99	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
931	PR00049D	0.00	9.214e-	270-284	PR00049	WILM'S TUMOUR PROTEIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			SIGNATURE
931	PR00910A	2.51	9.571e-09	272-284	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE
933	BL00415O	3.44	3.368e-09	289-326	BL00415	Synapsins proteins.
933	BL01088A	7.26	4.000e-17	16-30	BL01088	CAP protein.
933	BL01088B	15.91	1.000e-40	150-191	BL01088	CAP protein.
933	BL01088C	9.97	6.684e-26	194-216	BL01088	CAP protein.
933	BL01088D	14.32	4.130e-36	264-296	BL01088	CAP protein.
933	BL01088E	15.83	1.375e-28	326-353	BL01088	CAP protein.
933	BL01088F	14.83	1.000e-40	358-403	BL01088	CAP protein.
933	BL01088G	12.70	1.000e-40	408-451	BL01088	CAP protein.
933	BL01088H	12.10	7.353e-24	453-472	BL01088	CAP protein.
933	PR00049D	0.00	6.143e-11	235-249	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
933	PR00049D	0.00	8.714e-11	236-250	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
933	PR00049D	0.00	8.714e-11	237-251	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
933	PR00049D	0.00	8.790e-11	238-252	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
934	BL00237A	27.68	8.875e-27	228-267	BL00237	G-protein coupled receptors proteins.
934	BL00237B	5.28	9.438e-11	339-350	BL00237	G-protein coupled receptors proteins.
934	BL00237C	13.19	3.172e-12	366-392	BL00237	G-protein coupled receptors proteins.
934	BL00237D	11.23	9.308e-11	423-439	BL00237	G-protein coupled receptors proteins.
934	PR00237A	11.48	8.714e-12	164-188	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237B	13.50	4.724e-11	197-218	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237C	15.69	8.800e-18	242-264	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237D	8.94	8.875e-10	278-299	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237E	13.03	7.000e-11	331-354	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237F	13.57	6.516e-11	371-395	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00237G	19.63	1.621e-13	413-439	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
934	PR00425C	13.23	3.036e-10	228-247	PR00425	BRADYKININ RECEPTOR SIGNATURE
934	PR00571E	19.50	2.333e-09	227-238	PR00571	ENDOTHELIN-B RECEPTOR SIGNATURE
934	PR00908A	7.78	5.909e-19	65-81	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908B	16.82	2.029e-20	148-164	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908C	9.93	1.310e-19	190-203	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908D	11.10	4.429e-19	269-283	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908E	3.45	1.000e-17	326-339	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908F	8.01	1.000e-23	355-373	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908G	13.24	5.865e-24	438-456	PR00908	THROMBIN RECEPTOR SIGNATURE
934	PR00908H	11.64	1.450e-	467-484	PR00908	THROMBIN RECEPTOR

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			23			SIGNATURE
935	BL00018	7.41	1.000e-09	79-91	BL00018	EF-hand calcium-binding domain proteins.
935	BL00018	7.41	3.400e-12	152-164	BL00018	EF-hand calcium-binding domain proteins.
935	BL00303B	26.15	6.344e-10	67-103	BL00303	S-100/ICaBP type calcium binding protein.
935	PR00450C	12.22	4.480e-10	111-132	PR00450	RECOVERIN FAMILY SIGNATURE
935	PR00450C	12.22	5.320e-10	38-59	PR00450	RECOVERIN FAMILY SIGNATURE
935	PR00450C	12.22	6.520e-10	74-95	PR00450	RECOVERIN FAMILY SIGNATURE
936	BL00030A	14.39	4.500e-10	107-125	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
936	BL00030B	7.03	1.474e-09	146-155	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
940	PR00401B	12.94	3.667e-09	129-139	PR00401	SH2 DOMAIN SIGNATURE
943	BL01052A	16.12	7.618e-32	35-66	BL01052	Calponin family repeat proteins.
943	BL01052B	15.31	8.031e-26	84-109	BL01052	Calponin family repeat proteins.
943	BL01052C	18.51	6.806e-40	119-158	BL01052	Calponin family repeat proteins.
943	BL01052D	10.26	1.000e-24	206-225	BL01052	Calponin family repeat proteins.
943	PR00888A	11.87	2.350e-16	35-49	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888B	13.72	2.350e-12	54-67	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888C	12.27	5.179e-18	84-99	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888D	16.09	4.273e-17	120-136	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888E	11.81	3.432e-16	136-151	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888F	7.44	4.825e-14	157-171	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888G	12.73	8.759e-14	194-207	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00888H	9.97	5.154e-20	207-222	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
943	PR00889E	12.18	2.726e-12	203-218	PR00889	CALPONIN SIGNATURE
943	PR00890A	8.61	9.775e-21	66-85	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
943	PR00890B	8.75	3.455e-17	94-109	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
943	PR00890C	8.22	1.000e-17	116-129	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
943	PR00890D	16.17	5.174e-13	150-159	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
943	PR00890E	14.34	3.813e-21	167-186	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
943	PR00890F	12.92	4.064e-	193-205	PR00890	SMOOTH MUSCLE PROTEIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			14			22-ALPHA (TRANSGELIN) SIGNATURE
947	BL00415N	4.29	2.248e-09	276-319	BL00415	Synapsins proteins.
950	BL01031C	17.68	6.400e-10	125-149	BL01031	Heat shock hsp20 proteins family profile.
950	PR00299D	8.56	6.318e-09	115-128	PR00299	ALPHA CRYSTALLIN SIGNATURE
950	PR00299F	13.20	2.139e-09	152-173	PR00299	ALPHA CRYSTALLIN SIGNATURE
951	BL00019A	12.56	4.789e-15	56-66	BL00019	Actinin-type actin-binding domain proteins.
951	BL00019B	13.34	9.250e-23	81-103	BL00019	Actinin-type actin-binding domain proteins.
951	BL00019C	14.66	7.300e-37	127-162	BL00019	Actinin-type actin-binding domain proteins.
951	BL00019D	15.33	7.000e-33	186-215	BL00019	Actinin-type actin-binding domain proteins.
951	BL00019E	15.91	4.000e-13	341-350	BL00019	Actinin-type actin-binding domain proteins.
951	BL00019F	19.68	6.464e-19	392-413	BL00019	Actinin-type actin-binding domain proteins.
951	BL00303B	26.15	8.172e-10	815-851	BL00303	S-100/ICaBP type calcium binding protein.
951	PF00435A	32.05	2.421e-19	243-271	PF00435	Spectrin repeat proteins.
951	PF00435B	13.41	2.174e-11	508-523	PF00435	Spectrin repeat proteins.
951	PF00435C	20.73	9.036e-09	526-545	PF00435	Spectrin repeat proteins.
952	PR00111A	11.49	4.150e-12	171-186	PR00111	ALPHA/BETA HYDROLASE FOLD SIGNATURE
952	PR00412A	13.23	6.400e-11	151-169	PR00412	EPOXIDE HYDROLASE SIGNATURE
952	PR00412B	12.59	2.929e-10	171-186	PR00412	EPOXIDE HYDROLASE SIGNATURE
954	BL01221A	17.26	7.750e-20	12-39	BL01221	PMP-22 / EMP / MP20 family proteins.
954	BL01221B	13.29	6.182e-12	46-59	BL01221	PMP-22 / EMP / MP20 family proteins.
954	BL01221C	26.20	8.159e-26	69-113	BL01221	PMP-22 / EMP / MP20 family proteins.
954	BL01221C	26.20	9.100e-28	72-116	BL01221	PMP-22 / EMP / MP20 family proteins.
955	PF00783A	11.91	4.214e-13	577-586	PF00783	Inositol polyphosphate phosphatase, catalytic domain proteins homologue.
955	PF00783B	10.54	2.552e-10	658-667	PF00783	Inositol polyphosphate phosphatase, catalytic domain proteins homologue.
955	PR00049D	0.00	3.071e-10	1019-1033	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
955	PR00049D	0.00	7.407e-09	1060-1074	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
956	BL00030B	7.03	3.368e-09	83-92	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
956	BL00048	6.39	1.415e-13	157-183	BL00048	Protamine P1 proteins.
956	BL00048	6.39	1.750e-11	151-177	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
956	BL00048	6.39	1.750e-11	240-266	BL00048	Protamine P1 proteins.
956	BL00048	6.39	2.184e-10	190-216	BL00048	Protamine P1 proteins.
956	BL00048	6.39	2.421e-10	198-224	BL00048	Protamine P1 proteins.
956	BL00048	6.39	2.588e-12	173-199	BL00048	Protamine P1 proteins.
956	BL00048	6.39	2.800e-09	188-214	BL00048	Protamine P1 proteins.
956	BL00048	6.39	2.895e-10	184-210	BL00048	Protamine P1 proteins.
956	BL00048	6.39	3.077e-13	160-186	BL00048	Protamine P1 proteins.
956	BL00048	6.39	3.813e-09	227-253	BL00048	Protamine P1 proteins.
956	BL00048	6.39	3.912e-12	175-201	BL00048	Protamine P1 proteins.
956	BL00048	6.39	3.925e-09	186-212	BL00048	Protamine P1 proteins.
956	BL00048	6.39	4.246e-14	166-192	BL00048	Protamine P1 proteins.
956	BL00048	6.39	4.316e-10	152-178	BL00048	Protamine P1 proteins.
956	BL00048	6.39	4.713e-09	153-179	BL00048	Protamine P1 proteins.
956	BL00048	6.39	5.375e-11	182-208	BL00048	Protamine P1 proteins.
956	BL00048	6.39	5.585e-17	163-189	BL00048	Protamine P1 proteins.
956	BL00048	6.39	5.708e-13	162-188	BL00048	Protamine P1 proteins.
956	BL00048	6.39	6.063e-09	176-202	BL00048	Protamine P1 proteins.
956	BL00048	6.39	6.143e-16	161-187	BL00048	Protamine P1 proteins.
956	BL00048	6.39	6.288e-09	189-215	BL00048	Protamine P1 proteins.
956	BL00048	6.39	6.311e-14	158-184	BL00048	Protamine P1 proteins.
956	BL00048	6.39	6.803e-10	223-249	BL00048	Protamine P1 proteins.
956	BL00048	6.39	7.188e-09	225-251	BL00048	Protamine P1 proteins.
956	BL00048	6.39	7.413e-09	183-209	BL00048	Protamine P1 proteins.
956	BL00048	6.39	7.618e-12	156-182	BL00048	Protamine P1 proteins.
956	BL00048	6.39	7.632e-10	180-206	BL00048	Protamine P1 proteins.
956	BL00048	6.39	7.639e-14	165-191	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.000e-11	164-190	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.000e-11	177-203	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.015e-12	167-193	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.088e-09	170-196	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.105e-10	154-180	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.302e-17	159-185	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.375e-11	169-195	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.377e-14	174-200	BL00048	Protamine P1 proteins.
956	BL00048	6.39	8.425e-09	168-194	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
956	BL00048	6.39	8.625e-11	181-207	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.100e-09	232-258	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.375e-11	194-220	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.625e-11	155-181	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.735e-12	172-198	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.875e-11	171-197	BL00048	Protamine P1 proteins.
956	BL00048	6.39	9.882e-10	192-218	BL00048	Protamine P1 proteins.
956	DM01206B	10.69	1.570e-09	169-188	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	DM01206B	10.69	4.452e-10	163-182	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	DM01206B	10.69	4.532e-09	157-176	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	DM01206B	10.69	4.532e-09	223-242	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	DM01206B	10.69	5.899e-09	155-174	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	DM01206B	10.69	7.411e-10	159-178	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
956	PD02784B	26.46	9.745e-09	79-121	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.
957	BL01160B	19.54	5.653e-09	253-306	BL01160	Kinesin light chain repeat proteins.
957	BL01160B	19.54	5.710e-11	260-313	BL01160	Kinesin light chain repeat proteins.
958	PR00049D	0.00	6.445e-11	430-444	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
959	BL00250A	21.24	7.000e-35	340-375	BL00250	TGF-beta family proteins.
959	BL00250B	27.37	8.071e-32	409-444	BL00250	TGF-beta family proteins.
959	PR00438A	13.54	7.300e-11	365-374	PR00438	GROWTH FACTOR CYSTINE KNOT SUPERFAMILY SIGNATURE
959	PR00669F	5.57	9.494e-09	357-374	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
959	PR00670A	11.24	1.750e-24	21-38	PR00670	INHIBIN BETA A CHAIN SIGNATURE
959	PR00670B	13.06	1.360e-28	38-59	PR00670	INHIBIN BETA A CHAIN SIGNATURE
959	PR00670C	11.98	3.250e-19	83-96	PR00670	INHIBIN BETA A CHAIN SIGNATURE
959	PR00670D	13.39	1.231e-22	123-139	PR00670	INHIBIN BETA A CHAIN SIGNATURE
959	PR00670E	3.63	1.333e-25	268-289	PR00670	INHIBIN BETA A CHAIN SIGNATURE
959	PR00670F	10.10	4.818e-13	298-308	PR00670	INHIBIN BETA A CHAIN SIGNATURE
960	BL00154C	12.38	6.580e-12	79-97	BL00154	E1-E2 ATPases phosphorylation site proteins.
960	BL00154E	20.37	9.820e-15	347-387	BL00154	E1-E2 ATPases phosphorylation site proteins.
960	BL00154F	8.23	8.859e-10	502-525	BL00154	E1-E2 ATPases phosphorylation site proteins.
960	BL00592E	12.53	9.100e-09	168-184	BL00592	Glycosyl hydrolases family 9 proteins.
960	BL01228D	17.44	7.150e-11	503-527	BL01228	Hypothetical cof family proteins.
960	PR00119B	13.94	6.694e-12	83-97	PR00119	P-TYPE CATION-TRANSPORTING ATPASE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SUPERFAMILY SIGNATURE
960	PR00119D	9.56	2.432e-09	363-373	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
960	PR00121D	16.72	4.621e-11	76-97	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
961	BL00030A	14.39	5.765e-11	14-32	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
961	BL00030A	14.39	6.571e-09	297-315	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
961	BL00030B	7.03	4.316e-09	334-343	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
961	BL00030B	7.03	6.400e-10	232-241	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
961	BL00030B	7.03	8.579e-09	139-148	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
961	PD02784A	21.09	4.583e-09	94-130	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.
961	PD02784B	26.46	4.651e-09	49-91	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.
961	PF00658A	19.88	1.000e-40	84-123	PF00658	Poly-adenylate binding protein, unique domain proteins.
961	PF00658B	28.57	1.000e-40	263-309	PF00658	Poly-adenylate binding protein, unique domain proteins.
961	PF00658C	16.33	8.500e-36	579-615	PF00658	Poly-adenylate binding protein, unique domain proteins.
962	BL00036	9.02	5.737e-11	682-694	BL00036	bZIP transcription factors basic domain proteins.
962	PF00624I	9.10	4.331e-09	507-536	PF00624	Flocculin repeat proteins.
962	PF00624I	9.10	5.125e-10	510-539	PF00624	Flocculin repeat proteins.
962	PF00624I	9.10	5.800e-10	511-540	PF00624	Flocculin repeat proteins.
962	PF00624I	9.10	6.457e-09	505-534	PF00624	Flocculin repeat proteins.
962	PF00624I	9.10	6.811e-09	502-531	PF00624	Flocculin repeat proteins.
962	PF00624I	9.10	8.441e-09	503-532	PF00624	Flocculin repeat proteins.
962	PR00043B	8.73	9.241e-11	682-698	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
963	BL01160B	19.54	9.676e-10	308-361	BL01160	Kinesin light chain repeat proteins.
964	BL00291A	4.49	1.000e-09	540-574	BL00291	Prion protein.
964	BL00415N	4.29	8.095e-09	347-390	BL00415	Synapsins proteins.
964	BL00420A	20.42	1.000e-12	345-373	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.148e-10	810-838	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.295e-10	873-901	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.590e-10	840-868	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.692e-09	438-466	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.738e-10	459-487	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
964	BL00420A	20.42	1.885e-10	207-235	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	1.969e-09	204-232	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.108e-09	198-226	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.108e-09	747-775	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.108e-09	867-895	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.246e-09	216-244	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.246e-09	669-697	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.523e-09	642-670	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.800e-09	219-247	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.800e-09	516-544	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	2.800e-09	564-592	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.066e-10	798-826	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.077e-09	687-715	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.213e-10	552-580	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.215e-09	330-358	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.354e-09	588-616	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.361e-10	627-655	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.492e-09	240-268	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.508e-10	327-355	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.618e-11	807-835	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.631e-09	106-134	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	3.631e-09	339-367	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.098e-10	366-394	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
964	BL00420A	20.42	4.098e-10	675-703	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.185e-09	348-376	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.185e-09	486-514	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.185e-09	756-784	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.306e-13	720-748	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.689e-10	480-508	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.689e-10	570-598	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.836e-10	195-223	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	4.927e-11	705-733	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.015e-09	189-217	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.091e-11	180-208	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.154e-09	861-889	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.426e-10	774-802	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.600e-14	408-436	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.708e-09	372-400	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.721e-10	651-679	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.776e-13	426-454	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.846e-09	300-328	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	5.869e-10	109-137	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.016e-10	537-565	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.073e-11	801-829	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.123e-09	546-574	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.123e-09	603-631	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.164e-	306-334	BL00420	Speract receptor repeat

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			proteins domain proteins.
964	BL00420A	20.42	6.164e-10	483-511	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.164e-10	549-577	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.164e-10	777-805	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.262e-09	183-211	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.262e-09	837-865	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.400e-09	741-769	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.400e-11	843-871	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.607e-10	186-214	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.754e-10	423-451	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	6.815e-09	753-781	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.049e-10	318-346	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.092e-09	789-817	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.231e-09	471-499	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.344e-10	390-418	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.923e-09	243-271	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.923e-09	261-289	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	7.923e-12	417-445	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.082e-10	813-841	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.200e-11	282-310	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.230e-10	771-799	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.338e-09	420-448	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.615e-09	513-541	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.754e-09	525-553	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
964	BL00420A	20.42	8.892e-09	681-709	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	8.898e-13	534-562	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.262e-10	249-277	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.262e-10	576-604	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.308e-09	201-229	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.446e-09	717-745	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.557e-10	297-325	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.585e-09	165-193	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.705e-10	684-712	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.723e-09	315-343	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.836e-11	498-526	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.852e-10	795-823	BL00420	Speract receptor repeat proteins domain proteins.
964	BL00420A	20.42	9.862e-09	118-146	BL00420	Speract receptor repeat proteins domain proteins.
964	BL01113A	17.99	1.000e-10	282-308	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.000e-10	669-695	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.000e-11	591-617	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.000e-12	813-839	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.000e-14	534-560	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.173e-09	357-383	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.191e-10	462-488	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.205e-11	798-824	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.243e-13	660-686	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.519e-09	621-647	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.692e-12	789-815	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.766e-10	339-365	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.766e-10	648-674	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.957e-10	822-848	BL01113	Clq domain proteins.
964	BL01113A	17.99	1.957e-10	879-905	BL01113	Clq domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
964	BL01113A	17.99	2.149e-10	831-857	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.154e-12	543-569	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.212e-09	231-257	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.212e-09	327-353	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.558e-09	372-398	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.703e-13	112-138	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.723e-10	189-215	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.723e-10	219-245	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.731e-09	555-581	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.742e-15	336-362	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.846e-12	109-135	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.904e-09	207-233	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.904e-09	306-332	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.904e-09	387-413	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.904e-09	564-590	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.915e-10	210-236	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.915e-10	840-866	BL01113	C1q domain proteins.
964	BL01113A	17.99	2.946e-13	846-872	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.077e-09	405-431	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.298e-10	756-782	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.423e-09	495-521	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.423e-09	720-746	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.455e-11	771-797	BL01113	C1q domain proteins.
964	BL01113A	17.99	3.613e-15	115-141	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.000e-14	738-764	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.064e-10	192-218	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.064e-10	345-371	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.064e-10	723-749	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.068e-11	540-566	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.194e-15	118-144	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.231e-12	456-482	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.255e-10	324-350	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.273e-11	195-221	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.288e-09	103-129	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.288e-09	127-153	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
964	BL01113A	17.99	4.462e-09	246-272	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.635e-09	204-230	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.638e-10	480-506	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.774e-15	297-323	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.808e-09	381-407	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.886e-11	249-275	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.923e-12	531-557	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.981e-09	375-401	BL01113	C1q domain proteins.
964	BL01113A	17.99	4.981e-09	837-863	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.021e-10	705-731	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.091e-11	645-671	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.091e-11	762-788	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.091e-14	807-833	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.385e-12	525-551	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.404e-10	291-317	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.404e-10	852-878	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.500e-11	573-599	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.615e-12	693-719	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.673e-09	447-473	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.673e-09	489-515	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.846e-12	546-572	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.909e-11	582-608	BL01113	C1q domain proteins.
964	BL01113A	17.99	5.979e-10	471-497	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.108e-13	237-263	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.114e-11	804-830	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.318e-11	216-242	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.362e-10	513-539	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.365e-09	333-359	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.365e-09	816-842	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.523e-11	708-734	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.538e-09	732-758	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.538e-12	171-197	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.712e-09	408-434	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.712e-09	603-629	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.745e-10	234-260	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
964	BL01113A	17.99	6.769e-12	636-662	BL01113	C1q domain proteins.
964	BL01113A	17.99	6.936e-10	777-803	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.128e-10	702-728	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.128e-10	867-893	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.136e-11	537-563	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.231e-09	561-587	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.231e-09	681-707	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.231e-09	855-881	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.273e-14	714-740	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.319e-10	876-902	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.324e-13	186-212	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.404e-09	528-554	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.511e-10	121-147	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.511e-10	657-683	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.545e-11	330-356	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.577e-09	711-737	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.692e-12	729-755	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.692e-12	747-773	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.702e-10	768-794	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.750e-09	684-710	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.750e-09	792-818	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.923e-09	402-428	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.923e-09	549-575	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.923e-09	627-653	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.923e-09	663-689	BL01113	C1q domain proteins.
964	BL01113A	17.99	7.923e-12	180-206	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.054e-13	567-593	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.085e-10	861-887	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.096e-09	315-341	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.096e-09	717-743	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.159e-11	600-626	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.277e-10	642-668	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.297e-13	240-266	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.385e-12	124-150	BL01113	C1q domain proteins.
964	BL01113A	17.99	8.442e-09	774-800	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
964	BL01113A	17.99	8.468e-10	873-899	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.548e-15	174-200	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.548e-15	672-698	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.636e-14	384-410	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.773e-11	522-548	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.773e-11	552-578	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.788e-09	252-278	BL01113	Clq domain proteins.
964	BL01113A	17.99	8.846e-12	177-203	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.043e-10	366-392	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.129e-15	183-209	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.135e-09	243-269	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.135e-09	465-491	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.182e-14	651-677	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.234e-10	501-527	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.308e-12	198-224	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.308e-12	516-542	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.386e-11	228-254	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.455e-14	426-452	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.538e-12	106-132	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.617e-10	606-632	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.654e-09	585-611	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.654e-09	843-869	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.757e-13	417-443	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.757e-13	435-461	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.809e-10	558-584	BL01113	Clq domain proteins.
964	BL01113A	17.99	9.809e-10	699-725	BL01113	Clq domain proteins.
964	BL01208B	15.83	1.900e-13	77-91	BL01208	VWFC domain proteins.
964	DM01418A	20.83	1.000e-40	955-1002	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
964	DM01418B	22.51	1.000e-40	1053-1094	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
964	DM01418C	20.48	1.000e-40	1124-1165	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
964	PR00049D	0.00	7.559e-09	176-190	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
964	PR00524F	5.36	8.468e-09	513-526	PR00524	CHOLECYSTOKININ TYPE A RECEPTOR SIGNATURE
965	BL00039A	18.44	4.600e-31	211-249	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
965	BL00039B	19.19	4.913e-17	269-294	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
965	BL00039C	15.63	8.000e-27	353-376	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
965	BL00039D	21.67	1.783e-40	506-551	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
965	BL00048	6.39	6.400e-09	612-638	BL00048	Protamine P1 proteins.
965	BL00291A	4.49	9.458e-10	630-664	BL00291	Prion protein.
965	PF00271	7.99	3.250e-09	537-544	PF00271	Helicases conserved C-terminal domain proteins.
966	PR00308C	3.83	2.169e-09	10-19	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
966	PR00456E	3.06	6.625e-10	12-26	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE
970	BL00460A	28.67	1.514e-24	57-91	BL00460	Glutathione peroxidases selenocysteine proteins.
970	BL00460B	9.73	4.600e-23	99-116	BL00460	Glutathione peroxidases selenocysteine proteins.
970	BL00460C	14.35	4.724e-21	137-159	BL00460	Glutathione peroxidases selenocysteine proteins.
970	BL00460D	16.89	1.818e-22	185-204	BL00460	Glutathione peroxidases selenocysteine proteins.
971	BL00262A	12.48	4.600e-15	124-141	BL00262	Insulin family proteins.
971	BL00262B	16.89	8.286e-17	160-179	BL00262	Insulin family proteins.
971	PR00276A	11.84	4.750e-13	161-170	PR00276	INSULIN A CHAIN SIGNATURE
971	PR00276B	8.02	7.828e-10	170-179	PR00276	INSULIN A CHAIN SIGNATURE
971	PR00277A	14.82	2.421e-13	121-134	PR00277	INSULIN B CHAIN SIGNATURE
971	PR00277B	12.79	2.350e-11	135-147	PR00277	INSULIN B CHAIN SIGNATURE
975	PF00023A	16.03	5.500e-10	132-147	PF00023	Ank repeat proteins.
975	PF00791B	28.49	1.818e-11	132-186	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
975	PF00791B	28.49	5.046e-09	165-219	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
975	PF00791B	28.49	6.942e-10	99-153	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
979	PF00777A	8.25	4.000e-10	52-63	PF00777	Sialyltransferase family.
979	PF00777B	29.69	1.500e-28	89-131	PF00777	Sialyltransferase family.
979	PF00777C	18.60	1.000e-40	158-212	PF00777	Sialyltransferase family.
979	PF00777D	22.05	9.325e-39	291-336	PF00777	Sialyltransferase family.
980	BL00171B	26.59	1.125e-16	69-119	BL00171	Triosephosphate isomerase proteins.
980	BL00171C	14.53	6.294e-36	163-195	BL00171	Triosephosphate isomerase proteins.
980	BL00171D	15.75	1.563e-37	211-245	BL00171	Triosephosphate isomerase proteins.
981	BL00061A	9.41	4.600e-13	139-149	BL00061	Short-chain dehydrogenases/reductases family proteins.
981	BL00061B	25.79	9.250e-	187-224	BL00061	Short-chain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			27			dehydrogenases/reductases family proteins.
981	BL00061C	7.86	1.563e-10	231-240	BL00061	Short-chain dehydrogenases/reductases family proteins.
981	PR00080A	9.32	3.143e-12	139-150	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
981	PR00080C	17.16	4.429e-13	207-226	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
981	PR00081A	10.53	4.333e-14	63-80	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
981	PR00081B	10.38	8.800e-14	139-150	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
981	PR00081D	15.80	5.800e-12	207-226	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
981	PR00081E	17.54	9.250e-12	230-247	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
982	BL01073	24.30	1.000e-40	51-100	BL01073	Ribosomal protein L24e proteins.
985	BL00223A	15.59	2.253e-11	298-331	BL00223	Annexins repeat proteins domain proteins.
985	BL00223A	15.59	8.250e-27	138-171	BL00223	Annexins repeat proteins domain proteins.
985	BL00223A	15.59	8.750e-27	66-99	BL00223	Annexins repeat proteins domain proteins.
985	BL00223B	28.47	3.032e-37	208-257	BL00223	Annexins repeat proteins domain proteins.
985	BL00223C	24.79	1.000e-40	285-339	BL00223	Annexins repeat proteins domain proteins.
985	BL00223C	24.79	2.735e-15	125-179	BL00223	Annexins repeat proteins domain proteins.
985	BL00223C	24.79	9.438e-16	53-107	BL00223	Annexins repeat proteins domain proteins.
985	PR00196A	11.16	4.676e-10	147-169	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196A	11.16	8.773e-23	75-97	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196B	10.68	5.050e-17	115-131	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196C	10.36	1.443e-13	70-91	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196C	10.36	7.968e-21	142-163	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196C	10.36	9.609e-11	302-323	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196D	21.86	1.818e-23	226-252	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196E	9.19	1.900e-09	74-94	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196E	9.19	9.100e-22	306-326	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196E	9.19	9.763e-10	146-166	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196F	13.89	1.720e-14	334-349	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00196G	11.72	9.333e-14	350-363	PR00196	ANNEXIN FAMILY SIGNATURE
985	PR00197B	7.56	9.786e-12	75-97	PR00197	ANNEXIN TYPE I SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
985	PR00197D	7.50	6.242e-10	302-323	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00197D	7.50	7.207e-11	70-91	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00197D	7.50	8.500e-15	142-163	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00197E	11.89	3.415e-14	226-252	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00197F	9.03	5.757e-17	306-326	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00197F	9.03	9.724e-09	146-166	PR00197	ANNEXIN TYPE I SIGNATURE
985	PR00198B	8.71	5.400e-12	75-97	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198D	7.65	2.113e-10	302-323	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198D	7.65	4.812e-13	142-163	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198D	7.65	6.155e-09	70-91	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198E	14.67	7.698e-14	226-252	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198G	8.09	9.407e-10	146-166	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198G	8.09	9.486e-16	306-326	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00198H	12.05	3.025e-09	350-363	PR00198	ANNEXIN TYPE II SIGNATURE
985	PR00199B	6.86	9.316e-17	75-97	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199B	6.86	9.518e-09	147-169	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199C	13.84	5.680e-11	115-131	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199D	5.65	6.013e-12	142-163	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199D	5.65	9.609e-09	302-323	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199D	5.65	9.750e-14	70-91	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199F	16.19	5.565e-15	226-252	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199G	9.09	5.821e-14	307-332	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00199H	12.62	5.632e-09	350-363	PR00199	ANNEXIN TYPE III SIGNATURE
985	PR00200B	7.39	1.429e-10	147-169	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200B	7.39	9.372e-15	75-97	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200D	10.01	8.012e-13	115-131	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200E	10.00	4.522e-11	70-91	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200E	10.00	6.157e-12	302-323	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200E	10.00	7.446e-17	142-163	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200F	13.72	1.228e-17	226-252	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200G	9.43	3.473e-16	306-332	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200G	9.43	6.218e-09	146-172	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00200H	13.68	9.775e-10	350-363	PR00200	ANNEXIN TYPE IV SIGNATURE
985	PR00201A	6.05	4.623e-15	75-97	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201A	6.05	8.958e-10	147-169	PR00201	ANNEXIN TYPE V SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
985	PR00201C	11.13	1.947e-17	115-131	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201D	10.49	5.330e-09	302-323	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201D	10.49	6.764e-13	142-163	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201E	12.37	9.780e-17	226-252	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201G	11.02	5.375e-21	306-332	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00201H	12.04	9.859e-12	350-363	PR00201	ANNEXIN TYPE V SIGNATURE
985	PR00202B	11.44	8.590e-15	74-97	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202C	13.34	5.438e-16	115-131	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202D	5.58	8.813e-13	142-163	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202E	13.00	6.663e-14	226-252	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202G	8.01	5.703e-10	146-172	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202G	8.01	6.357e-18	306-332	PR00202	ANNEXIN TYPE VI SIGNATURE
985	PR00202H	9.20	3.588e-10	350-363	PR00202	ANNEXIN TYPE VI SIGNATURE
990	BL01159	13.85	5.776e-10	166-180	BL01159	WW/xsp5/WWP domain proteins.
990	PR00403A	16.82	9.561e-09	151-164	PR00403	WW DOMAIN SIGNATURE
990	PR00403B	12.19	1.184e-11	166-180	PR00403	WW DOMAIN SIGNATURE
991	BL01182F	10.07	4.162e-16	9-23	BL01182	Glycosyl hydrolases family 35 proteins.
991	PR00742I	13.54	6.455e-18	9-25	PR00742	GLYCOSYL HYDROLASE FAMILY 35 SIGNATURE
994	BL00563A	16.73	7.097e-40	26-64	BL00563	Stathmin family proteins.
994	BL00563B	6.08	1.000e-32	65-91	BL00563	Stathmin family proteins.
994	BL00563C	12.83	2.174e-37	95-124	BL00563	Stathmin family proteins.
994	BL00563D	11.38	1.000e-40	125-160	BL00563	Stathmin family proteins.
994	BL00563D	11.38	9.609e-09	74-109	BL00563	Stathmin family proteins.
994	PR00345A	13.46	4.316e-22	30-48	PR00345	STATHMIN FAMILY SIGNATURE
994	PR00345B	7.12	7.750e-35	59-87	PR00345	STATHMIN FAMILY SIGNATURE
994	PR00345C	4.54	5.714e-29	88-111	PR00345	STATHMIN FAMILY SIGNATURE
994	PR00345D	10.97	6.850e-31	112-135	PR00345	STATHMIN FAMILY SIGNATURE
994	PR00345E	8.54	3.571e-29	136-160	PR00345	STATHMIN FAMILY SIGNATURE
998	PF00846A	11.74	5.537e-09	108-154	PF00846	Hantavirus nucleocapsid protein.
999	BL00142	8.38	9.438e-10	528-538	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
999	PR00756A	12.90	6.500e-18	367-382	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE
999	PR00756B	14.06	4.000e-14	415-430	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE
999	PR00756C	11.60	6.087e-13	492-502	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SIGNATURE
999	PR00756D	10.58	8.412e-21	528-543	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE
999	PR00756E	11.91	4.375e-16	547-559	PR00756	MEMBRANE ALANYL DIPEPTIDASE (M1) FAMILY SIGNATURE
1000	BL00139A	10.29	8.457e-11	277-286	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1000	BL00139C	9.23	3.769e-12	429-438	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1000	BL00139D	9.24	3.769e-21	447-463	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1000	PR00705A	10.55	6.000e-13	277-292	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1000	PR00705B	10.22	6.143e-12	430-440	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1000	PR00705C	11.87	6.824e-09	447-453	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1001	PF01008A	20.14	9.333e-14	144-164	PF01008	Initiation factor 2 subunit.
1001	PF01008B	25.59	1.964e-32	192-234	PF01008	Initiation factor 2 subunit.
1001	PF01008C	12.25	9.667e-18	273-292	PF01008	Initiation factor 2 subunit.
1002	BL01164A	19.74	6.063e-23	324-353	BL01164	Copper amine oxidase topaquinone proteins.
1002	BL01164B	19.21	1.818e-21	364-390	BL01164	Copper amine oxidase topaquinone proteins.
1002	BL01164C	17.88	1.563e-23	391-419	BL01164	Copper amine oxidase topaquinone proteins.
1002	BL01164D	19.79	1.333e-33	470-504	BL01164	Copper amine oxidase topaquinone proteins.
1002	BL01164E	13.77	6.000e-18	530-547	BL01164	Copper amine oxidase topaquinone proteins.
1002	BL01164F	19.03	5.091e-28	677-706	BL01164	Copper amine oxidase topaquinone proteins.
1002	PR00766A	16.19	5.500e-23	86-105	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766B	10.58	4.706e-25	115-134	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766C	15.50	4.130e-23	204-224	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766D	9.15	1.000e-26	227-247	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766E	9.59	2.421e-27	361-382	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766F	15.10	4.522e-28	439-462	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1002	PR00766G	11.62	1.643e-27	678-698	PR00766	AMILORIDE-SENSITIVE AMINE OXIDASE SIGNATURE
1004	PF00642	11.59	3.700e-16	166-176	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).
1004	PF00642	11.59	7.900e-12	128-138	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).
1007	BL00142	8.38	4.857e-09	582-592	BL00142	Neutral zinc metalloproteases, zinc-binding region proteins.
1007	PR00786A	11.12	4.857e-13	536-548	PR00786	NEPRILYSIN METALLOPROTEASE (M13) FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1007	PR00786B	9.59	8.000e-17	554-566	PR00786	NEPRILYSIN METALLOPROTEASE (M13) FAMILY SIGNATURE
1007	PR00786C	9.76	2.000e-22	575-591	PR00786	NEPRILYSIN METALLOPROTEASE (M13) FAMILY SIGNATURE
1007	PR00786D	9.78	5.500e-14	648-659	PR00786	NEPRILYSIN METALLOPROTEASE (M13) FAMILY SIGNATURE
1008	BL00232A	27.72	3.739e-26	82-114	BL00232	Cadherins extracellular repeat proteins domain proteins.
1008	BL00232B	32.79	5.125e-40	174-221	BL00232	Cadherins extracellular repeat proteins domain proteins.
1008	BL00232B	32.79	9.286e-19	281-328	BL00232	Cadherins extracellular repeat proteins domain proteins.
1008	BL00232C	10.65	6.143e-16	279-296	BL00232	Cadherins extracellular repeat proteins domain proteins.
1008	BL00232D	16.25	3.842e-13	796-810	BL00232	Cadherins extracellular repeat proteins domain proteins.
1008	PR00205A	14.73	4.000e-12	206-221	PR00205	CADHERIN SIGNATURE
1008	PR00205B	11.39	2.241e-16	279-296	PR00205	CADHERIN SIGNATURE
1008	PR00205C	13.65	2.688e-10	540-554	PR00205	CADHERIN SIGNATURE
1009	BL00262A	12.48	3.829e-09	57-74	BL00262	Insulin family proteins.
1009	BL00262B	16.89	4.977e-11	146-165	BL00262	Insulin family proteins.
1010	PF00013	5.78	4.150e-09	127-138	PF00013	KH domain proteins family of RNA binding proteins.
1011	BL00719A	16.66	7.488e-09	88-101	BL00719	Glycosyl hydrolases family 2 proteins.
1013	BL00412D	16.54	6.969e-09	75-125	BL00412	Neuromodulin (GAP-43) proteins.
1014	PR00449D	10.79	8.364e-12	55-68	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1014	PR00449E	13.50	4.706e-11	90-112	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1015	PD02870B	18.83	3.872e-09	345-377	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1016	BL00022B	7.54	1.000e-08	328-334	BL00022	EGF-like domain proteins.
1016	BL01177C	17.39	3.286e-09	394-412	BL01177	Anaphylatoxin domain proteins.
1016	BL01177C	17.39	5.119e-10	352-370	BL01177	Anaphylatoxin domain proteins.
1016	BL01187A	9.98	2.286e-13	343-354	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1016	BL01187A	9.98	4.750e-09	383-394	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1016	BL01187B	12.04	1.900e-09	276-291	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1016	BL01187B	12.04	3.667e-12	358-373	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1016	BL01187B	12.04	8.200e-14	443-458	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1016	BL01187B	12.04	8.826e-13	400-415	BL01187	Calcium-binding EGF-like domain proteins

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						pattern proteins.
1016	PD00919A	11.53	5.227e-09	306-317	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.
1016	PR00255E	15.23	9.882e-09	586-608	PR00255	NATRIURETIC PEPTIDE RECEPTOR SIGNATURE
1016	PR00352B	13.51	6.400e-09	240-250	PR00352	3FE-4S FERREDOXIN SIGNATURE
1016	PR00907G	11.63	1.243e-09	400-426	PR00907	THROMBOMODULIN SIGNATURE
1020	BL00222B	11.09	1.878e-12	114-129	BL00222	Insulin-like growth factor binding proteins.
1020	BL00222B	11.09	3.250e-16	100-115	BL00222	Insulin-like growth factor binding proteins.
1020	BL00222C	22.97	7.900e-25	158-185	BL00222	Insulin-like growth factor binding proteins.
1020	BL01185A	8.11	6.318e-16	100-111	BL01185	C-terminal cystine knot proteins.
1020	BL01185B	21.14	1.000e-40	151-199	BL01185	C-terminal cystine knot proteins.
1020	BL01185C	15.86	2.038e-37	247-285	BL01185	C-terminal cystine knot proteins.
1020	BL01185D	23.45	1.000e-40	321-373	BL01185	C-terminal cystine knot proteins.
1020	BL01208B	15.83	5.500e-12	247-261	BL01208	VWFC domain proteins.
1020	BL01208C	14.16	6.400e-11	280-290	BL01208	VWFC domain proteins.
1021	BL00030A	14.39	9.571e-09	9-27	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1021	BL00030B	7.03	1.000e-12	40-49	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1021	BL00048	6.39	1.000e-12	294-320	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	2.059e-12	293-319	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	2.324e-12	295-321	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	2.913e-09	308-334	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	2.938e-13	296-322	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.125e-11	284-310	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.250e-11	291-317	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.625e-11	282-308	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.700e-09	275-301	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.724e-10	306-332	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	3.750e-11	298-324	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	4.046e-13	283-309	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	4.176e-12	304-330	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	4.671e-10	292-318	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	5.015e-13	281-307	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	5.125e-11	302-328	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	5.145e-10	337-363	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	5.500e-10	278-304	BL00048	Protamine P1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1021	BL00048	6.39	5.846e-13	285-311	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	5.974e-10	276-302	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	6.092e-10	305-331	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	6.329e-10	273-299	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	6.400e-09	303-329	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	7.492e-14	289-315	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	7.500e-11	301-327	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	7.785e-13	279-305	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.377e-14	297-323	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.538e-09	339-365	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.627e-15	277-303	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.672e-14	287-313	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.816e-10	280-306	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	8.941e-12	286-312	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	9.000e-11	299-325	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	9.100e-09	312-338	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	9.308e-13	300-326	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	9.723e-13	290-316	BL00048	Protamine P1 proteins.
1021	BL00048	6.39	9.735e-12	288-314	BL00048	Protamine P1 proteins.
1021	DM01206B	10.69	1.000e-08	291-310	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	1.134e-11	287-306	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	3.284e-11	285-304	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	3.734e-09	310-329	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	4.714e-12	289-308	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	5.433e-11	283-302	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	5.438e-10	281-300	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	5.671e-09	346-365	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	5.970e-11	304-323	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	6.918e-10	306-325	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	7.714e-12	279-298	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	7.835e-09	293-312	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	7.949e-09	302-321	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	8.105e-13	308-327	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	8.105e-13	312-331	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.
1021	DM01206B	10.69	8.291e-09	277-296	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1022	BL00345A	13.96	3.903e-14	406-424	BL00345	Ets-domain proteins.
1022	BL00345B	21.28	1.000e-40	439-489	BL00345	Ets-domain proteins.
1022	PD01234B	15.53	3.893e-09	507-524	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.
1022	PR00454A	13.64	6.625e-13	410-423	PR00454	ETS DOMAIN SIGNATURE
1022	PR00454B	20.78	3.625e-18	434-452	PR00454	ETS DOMAIN SIGNATURE
1022	PR00454C	11.24	5.065e-22	453-471	PR00454	ETS DOMAIN SIGNATURE
1022	PR00454D	10.89	5.950e-19	472-490	PR00454	ETS DOMAIN SIGNATURE
1023	BL00511	18.40	1.429e-31	193-224	BL00511	Corticotropin-releasing factor family proteins.
1027	BL00456A	22.59	8.527e-09	87-141	BL00456	Sodium:solute symporter family proteins.
1027	BL00456C	24.55	4.000e-22	223-277	BL00456	Sodium:solute symporter family proteins.
1029	BL00360A	16.97	6.478e-23	19-45	BL00360	Ribosomal protein S9 proteins.
1029	BL00360B	20.22	5.286e-29	62-97	BL00360	Ribosomal protein S9 proteins.
1029	BL00360C	17.65	8.105e-27	125-151	BL00360	Ribosomal protein S9 proteins.
1031	BL00406A	9.95	1.000e-40	31-65	BL00406	Actins proteins.
1031	BL00406B	5.47	1.000e-40	107-161	BL00406	Actins proteins.
1031	BL00406C	6.75	1.000e-40	166-220	BL00406	Actins proteins.
1031	BL00406D	12.58	1.000e-40	293-347	BL00406	Actins proteins.
1031	BL00406E	8.44	1.000e-40	350-399	BL00406	Actins proteins.
1031	PR00190A	7.24	1.375e-13	50-59	PR00190	ACTIN SIGNATURE
1031	PR00190B	9.98	1.000e-15	73-84	PR00190	ACTIN SIGNATURE
1031	PR00190C	11.49	1.474e-30	85-107	PR00190	ACTIN SIGNATURE
1031	PR00190D	19.23	1.450e-26	108-126	PR00190	ACTIN SIGNATURE
1031	PR00190E	7.16	1.450e-19	139-152	PR00190	ACTIN SIGNATURE
1031	PR00190F	7.80	2.286e-24	164-183	PR00190	ACTIN SIGNATURE
1031	PR00190G	12.62	1.600e-21	260-276	PR00190	ACTIN SIGNATURE
1032	BL00180A	13.20	5.065e-14	199-211	BL00180	Glutamine synthetase proteins.
1032	BL00180B	18.03	4.971e-14	235-253	BL00180	Glutamine synthetase proteins.
1032	BL00180C	12.14	4.600e-14	269-278	BL00180	Glutamine synthetase proteins.
1032	BL00180D	13.26	2.174e-24	286-307	BL00180	Glutamine synthetase proteins.
1032	BL00180E	17.60	1.000e-40	321-372	BL00180	Glutamine synthetase proteins.
1032	BL00180F	10.05	6.211e-17	385-397	BL00180	Glutamine synthetase proteins.
1032	BL00180G	10.20	8.435e-17	474-488	BL00180	Glutamine synthetase proteins.
1034	BL00021B	13.33	8.984e-12	545-562	BL00021	Kringle domain proteins.
1034	BL00134A	11.96	5.781e-15	545-561	BL00134	Serine proteases, trypsin family, histidine proteins.
1034	BL00134B	15.99	4.194e-	727-750	BL00134	Serine proteases,

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			14			trypsin family, histidine proteins.
1034	BL00495N	11.04	9.735e-11	719-753	BL00495	Apple domain proteins.
1034	BL01253G	11.34	5.348e-09	726-739	BL01253	Type I fibronectin domain proteins.
1034	PR00453A	12.79	5.345e-14	303-320	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE
1034	PR00453B	14.65	4.682e-10	342-356	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE
1034	PR00722A	12.27	9.129e-13	546-561	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1034	PR00722B	12.51	4.000e-09	606-620	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1034	PR00722C	10.87	4.273e-11	726-738	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1036	BL00018	7.41	7.300e-10	219-231	BL00018	EF-hand calcium-binding domain proteins.
1037	BL00036	9.02	6.786e-13	86-98	BL00036	bZIP transcription factors basic domain proteins.
1037	PR00041C	16.23	8.875e-16	36-47	PR00041	CAMP RESPONSE ELEMENT BINDING (CREB) PROTEIN SIGNATURE
1037	PR00041D	7.95	4.750e-21	74-90	PR00041	CAMP RESPONSE ELEMENT BINDING (CREB) PROTEIN SIGNATURE
1037	PR00041E	7.20	1.243e-27	92-112	PR00041	CAMP RESPONSE ELEMENT BINDING (CREB) PROTEIN SIGNATURE
1037	PR00041F	8.53	2.125e-22	112-129	PR00041	CAMP RESPONSE ELEMENT BINDING (CREB) PROTEIN SIGNATURE
1038	PD00210	15.25	7.231e-16	47-62	PD00210	PROTEIN ANTIOXIDANT PEROXIDASE RED.
1039	BL00028	16.07	6.143e-09	440-456	BL00028	Zinc finger, C2H2 type, domain proteins.
1039	BL00028	16.07	8.826e-12	382-398	BL00028	Zinc finger, C2H2 type, domain proteins.
1039	PD00066	13.92	6.870e-11	398-410	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.
1039	PR00048A	10.52	9.280e-09	379-392	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE
1039	PR00308C	3.83	8.714e-09	66-75	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
1039	PR00558C	6.54	5.846e-09	37-56	PR00558	ALPHA-2A ADRENERGIC RECEPTOR SIGNATURE
1040	BL00142	8.38	2.688e-10	351-361	BL00142	Neutral zinc metalloproteases, zinc-binding region proteins.
1040	BL00427	13.93	8.375e-25	454-508	BL00427	Disintegrins proteins.
1040	PR00289A	13.62	7.525e-18	468-487	PR00289	DISINTEGRIN SIGNATURE
1040	PR00289B	11.79	5.245e-10	497-509	PR00289	DISINTEGRIN SIGNATURE
1040	PR00451A	6.49	5.696e-10	466-474	PR00451	CHITIN-BINDING DOMAIN SIGNATURE
1041	BL01271A	8.06	5.333e-21	147-166	BL01271	Sodium:sulfate symporter family proteins.
1041	BL01271A	8.06	8.986e-09	487-506	BL01271	Sodium:sulfate symporter family proteins.
1041	BL01271B	12.02	4.375e-19	246-270	BL01271	Sodium:sulfate symporter family

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1041	BL01271C	13.62	8.714e-20	438-459	BL01271	Sodium:sulfate symporter family proteins.
1041	BL01271D	25.26	2.532e-32	511-565	BL01271	Sodium:sulfate symporter family proteins.
1042	PR00371E	14.06	1.000e-10	66-75	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE
1042	PR00371F	10.12	5.135e-09	79-90	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE
1043	BL00021B	13.33	1.265e-20	120-137	BL00021	Kringle domain proteins.
1043	BL00021C	22.21	9.250e-10	203-224	BL00021	Kringle domain proteins.
1043	BL00021D	24.56	9.813e-25	290-331	BL00021	Kringle domain proteins.
1043	BL00134A	11.96	5.737e-19	120-136	BL00134	Serine proteases, trypsin family, histidine proteins.
1043	BL00134B	15.99	7.231e-16	282-305	BL00134	Serine proteases, trypsin family, histidine proteins.
1043	BL00134C	13.45	1.692e-11	318-331	BL00134	Serine proteases, trypsin family, histidine proteins.
1043	BL00495K	12.58	8.600e-12	122-154	BL00495	Apple domain proteins.
1043	BL00495L	11.94	6.757e-10	155-193	BL00495	Apple domain proteins.
1043	BL00495M	8.50	4.058e-10	194-228	BL00495	Apple domain proteins.
1043	BL00495N	11.04	1.409e-27	274-308	BL00495	Apple domain proteins.
1043	BL00495O	13.75	7.459e-13	309-337	BL00495	Apple domain proteins.
1043	BL01253D	4.84	5.500e-12	120-133	BL01253	Type I fibronectin domain proteins.
1043	BL01253E	16.01	8.579e-15	192-228	BL01253	Type I fibronectin domain proteins.
1043	BL01253G	11.34	1.000e-15	281-294	BL01253	Type I fibronectin domain proteins.
1043	BL01253H	13.15	5.500e-20	300-334	BL01253	Type I fibronectin domain proteins.
1043	PR00722A	12.27	8.941e-18	121-136	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1043	PR00722B	12.51	4.000e-09	180-194	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1043	PR00722C	10.87	5.235e-13	281-293	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1045	BL00022B	7.54	8.200e-09	865-871	BL00022	EGF-like domain proteins.
1045	BL00279E	37.11	9.241e-10	66-113	BL00279	Membrane attack complex components / perforin proteins.
1045	BL01187A	9.98	1.000e-08	715-726	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187A	9.98	2.875e-09	921-932	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187A	9.98	7.000e-09	592-603	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187A	9.98	7.857e-	756-767	BL01187	Calcium-binding EGF-

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			like domain proteins pattern proteins.
1045	BL01187A	9.98	9.526e-11	675-686	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	1.257e-10	1161-1176	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	1.391e-13	321-336	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	2.350e-14	856-871	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	4.130e-13	897-912	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	4.600e-11	939-954	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	4.913e-13	773-788	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	5.500e-14	814-829	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	7.000e-17	1360-1375	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	9.229e-10	1315-1330	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	9.609e-13	610-625	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	BL01187B	12.04	9.667e-12	732-747	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1045	PD00919B	9.47	7.485e-10	697-711	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.
1045	PR00009C	14.11	9.118e-09	736-747	PR00009	TYPE I EGF SIGNATURE
1045	PR00010C	11.16	1.857e-09	615-625	PR00010	TYPE II EGF-LIKE SIGNATURE
1045	PR00010C	11.16	4.857e-09	1365-1375	PR00010	TYPE II EGF-LIKE SIGNATURE
1045	PR00010C	11.16	7.545e-10	1320-1330	PR00010	TYPE II EGF-LIKE SIGNATURE
1045	PR00010C	11.16	7.667e-11	861-871	PR00010	TYPE II EGF-LIKE SIGNATURE
1045	PR00011D	14.03	2.696e-09	92-110	PR00011	TYPE III EGF-LIKE SIGNATURE
1045	PR00907G	11.63	7.973e-09	568-594	PR00907	THROMBOMODULIN SIGNATURE
1048	BL00352A	12.19	7.000e-14	377-391	BL00352	'Cold-shock' DNA-binding domain proteins.
1048	BL00352B	23.66	2.000e-20	737-775	BL00352	'Cold-shock' DNA-binding domain proteins.
1050	BL00326A	14.01	6.128e-09	1284-1317	BL00326	Tropomyosins proteins.
1050	BL00447C	13.79	9.813e-09	198-212	BL00447	DNA polymerase family A proteins.
1050	DM00215	19.43	7.712e-09	1026-1058	DM00215	PROLINE-RICH PROTEIN 3.
1050	PD00301B	5.49	6.885e-09	1095-1105	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1050	PF00992A	16.67	1.355e-09	1297-1331	PF00992	Troponin.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1050	PF00992A	16.67	4.434e-09	1289-1323	PF00992	Troponin.
1050	PF00992A	16.67	7.513e-09	1298-1332	PF00992	Troponin.
1050	PF01140D	15.54	1.628e-09	1073-1107	PF01140	Matrix protein (MA), p15.
1050	PF01140D	15.54	4.872e-09	1295-1329	PF01140	Matrix protein (MA), p15.
1051	BL00310A	14.05	7.000e-15	61-75	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	BL00310B	22.33	5.034e-32	113-148	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	BL00310C	26.35	3.400e-39	166-212	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	BL00310D	14.97	7.818e-28	238-264	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	BL00310E	19.92	2.250e-24	339-363	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	BL00310F	23.26	1.000e-40	374-428	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1051	PR00336A	12.86	9.727e-24	241-265	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1051	PR00336B	15.42	4.000e-16	351-365	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1051	PR00336C	14.47	9.333e-12	388-400	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1051	PR00336D	9.96	4.150e-24	402-424	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1051	PR00336E	11.59	3.382e-13	425-437	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1052	PF00550B	10.27	2.588e-10	129-142	PF00550	Phosphopantetheine attachment site proteins.
1055	BL00690A	6.87	3.455e-12	424-433	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1055	BL00690B	13.38	6.571e-16	453-470	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1055	BL00690C	7.51	7.429e-10	519-528	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1056	PR00704A	14.68	7.375e-22	60-83	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704B	17.94	6.276e-23	105-127	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704C	11.88	6.625e-20	129-145	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704D	11.05	5.065e-29	165-190	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1056	PR00704E	12.55	8.875e-28	195-218	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704F	13.61	7.632e-30	220-247	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704G	13.87	1.391e-25	350-371	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704H	13.38	9.217e-22	400-417	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1056	PR00704I	9.52	1.000e-30	508-536	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1057	BL01108A	20.33	2.241e-22	135-167	BL01108	Ribosomal protein L24 proteins.
1057	BL01108B	11.40	8.457e-10	182-192	BL01108	Ribosomal protein L24 proteins.
1058	BL00250A	21.24	4.130e-27	263-298	BL00250	TGF-beta family proteins.
1058	BL00250B	27.37	3.000e-20	331-366	BL00250	TGF-beta family proteins.
1058	PR00669A	12.84	4.414e-31	110-134	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669B	8.27	6.927e-20	188-204	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669C	14.90	1.220e-21	206-223	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669D	7.36	5.974e-25	241-260	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669E	16.28	3.152e-23	263-280	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669F	5.57	6.077e-25	280-297	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669G	7.46	8.650e-26	324-343	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00669H	19.13	3.893e-29	345-366	PR00669	INHIBIN ALPHA CHAIN SIGNATURE
1058	PR00712A	6.07	7.722e-10	4-20	PR00712	BRAIN NATRIURETIC PEPTIDE SIGNATURE
1059	PR00854B	7.30	2.519e-10	5-22	PR00854	PROSTAGLANDIN D RECEPTOR SIGNATURE
1063	PR00846A	15.43	1.818e-13	49-61	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1063	PR00846B	13.97	7.750e-17	109-123	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1063	PR00846C	12.18	5.696e-23	141-158	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1063	PR00846D	17.96	4.130e-29	199-224	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1063	PR00846E	12.07	3.700e-17	248-262	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1063	PR00846F	14.27	5.875e-13	353-366	PR00846	GLYCOSYL HYDROLASE FAMILY 56 SIGNATURE
1064	BL00226A	12.77	2.543e-12	97-111	BL00226	Intermediate filaments proteins.
1064	BL00226B	23.86	1.000e-31	197-244	BL00226	Intermediate filaments proteins.
1064	BL00226B	23.86	7.600e-11	148-195	BL00226	Intermediate filaments proteins.
1064	BL00226C	13.23	1.000e-22	263-293	BL00226	Intermediate filaments proteins.
1064	BL00226D	19.10	1.000e-40	364-410	BL00226	Intermediate filaments proteins.
1064	PR00042D	8.97	5.793e-09	325-346	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1066	BL00610B	23.65	9.265e-09	38-87	BL00610	Sodium:neurotransmitter symporter family proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1067	BL00965B	17.77	9.735e-11	146-172	BL00965	Phosphomannose isomerase type I proteins.
1067	BL00965C	23.78	1.225e-14	341-389	BL00965	Phosphomannose isomerase type I proteins.
1067	PF00801B	23.63	6.344e-11	289-316	PF00801	PKD domain proteins.
1067	PR00049D	0.00	5.689e-11	319-333	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1067	PR00049D	0.00	6.643e-10	321-335	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1067	PR00049D	0.00	9.786e-10	323-337	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1067	PR00910A	2.51	8.393e-09	323-335	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE
1069	BL01019A	13.20	9.520e-13	58-97	BL01019	ADP-ribosylation factors family proteins.
1069	BL01115A	10.22	5.075e-11	24-67	BL01115	GTP-binding nuclear protein ran proteins.
1069	PR00449A	13.20	5.846e-21	24-45	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1069	PR00449B	14.34	5.500e-13	47-63	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1069	PR00449C	17.27	3.700e-24	65-87	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1069	PR00449D	10.79	4.273e-12	127-140	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1069	PR00449E	13.50	7.000e-19	162-184	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1070	BL00415B	9.91	9.404e-09	731-766	BL00415	Synapsins proteins.
1070	BL00415N	4.29	7.832e-09	1057-1100	BL00415	Synapsins proteins.
1070	BL00904A	8.30	6.489e-09	496-545	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.
1070	DM00215	19.43	3.746e-09	1043-1075	DM00215	PROLINE-RICH PROTEIN 3.
1070	PR00049D	0.00	2.831e-09	1299-1313	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1070	PR00049D	0.00	8.169e-09	1301-1315	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1070	PR00628A	14.81	8.134e-19	233-252	PR00628	INSULIN RECEPTOR SUBSTRATE-1 PTB DOMAIN SIGNATURE
1070	PR00628B	14.71	2.556e-15	254-274	PR00628	INSULIN RECEPTOR SUBSTRATE-1 PTB DOMAIN SIGNATURE
1070	PR00628C	16.37	9.289e-16	276-292	PR00628	INSULIN RECEPTOR SUBSTRATE-1 PTB DOMAIN SIGNATURE
1070	PR00628D	15.47	4.000e-15	293-305	PR00628	INSULIN RECEPTOR SUBSTRATE-1 PTB DOMAIN SIGNATURE
1070	PR00628F	16.74	8.116e-18	317-341	PR00628	INSULIN RECEPTOR SUBSTRATE-1 PTB DOMAIN SIGNATURE
1071	BL00143A	20.91	4.808e-22	116-142	BL00143	Insulinase family, zinc-binding region proteins.
1071	BL00143B	14.41	3.077e-13	162-176	BL00143	Insulinase family, zinc-binding region proteins.
1071	BL00143C	14.16	7.000e-11	264-276	BL00143	Insulinase family, zinc-binding region proteins.
1072	PF00686C	12.33	8.740e-	320-340	PF00686	Starch binding domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			proteins.
1074	DM00215	19.43	2.220e-09	41-73	DM00215	PROLINE-RICH PROTEIN 3.
1074	DM00215	19.43	3.593e-09	77-109	DM00215	PROLINE-RICH PROTEIN 3.
1074	DM00215	19.43	8.780e-09	84-116	DM00215	PROLINE-RICH PROTEIN 3.
1074	DM00215	19.43	9.847e-09	81-113	DM00215	PROLINE-RICH PROTEIN 3.
1074	PR00049D	0.00	4.966e-09	77-91	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1074	PR00049D	0.00	9.237e-09	101-115	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1076	BL00022B	7.54	6.400e-09	672-678	BL00022	EGF-like domain proteins.
1076	BL00243H	17.53	9.526e-09	570-595	BL00243	Integrins beta chain cysteine-rich domain proteins.
1076	BL00243I	31.77	4.549e-09	2113-2155	BL00243	Integrins beta chain cysteine-rich domain proteins.
1076	BL00790E	29.58	7.964e-11	548-595	BL00790	Receptor tyrosine kinase class V proteins.
1076	BL01248	11.02	1.000e-11	346-358	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	2.895e-16	1905-1917	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	3.377e-09	539-551	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	5.415e-09	629-641	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	6.625e-10	2016-2028	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	7.000e-14	418-430	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	8.132e-09	2112-2124	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	8.302e-09	2146-2158	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	8.302e-09	575-587	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	BL01248	11.02	9.491e-09	1574-1586	BL01248	Laminin-type EGF-like (LE) domain proteins.
1076	PD00320A	14.49	7.750e-09	352-365	PD00320	LAMININ CHAIN EGF-LIKE DOMAIN P.
1076	PD00320A	14.49	9.357e-09	827-840	PD00320	LAMININ CHAIN EGF-LIKE DOMAIN P.
1076	PR00011A	14.06	1.196e-17	1611-1629	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	1.391e-10	575-593	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	2.452e-12	462-480	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	2.875e-16	711-729	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	3.625e-16	1565-1583	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	5.271e-13	863-881	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	5.313e-16	812-830	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	6.081e-12	2103-2121	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	7.873e-14	1513-1531	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	9.660e-15	1472-1490	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	9.673e-14	2055-2073	PR00011	TYPE III EGF-LIKE SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1076	PR00011A	14.06	9.710e-12	530-548	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011A	14.06	9.830e-15	2146-2164	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.458e-13	1611-1629	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.610e-13	812-830	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.614e-17	2055-2073	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.692e-15	575-593	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.740e-09	530-548	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	1.833e-14	2103-2121	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	3.177e-12	462-480	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	3.942e-15	1565-1583	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	4.500e-14	2146-2164	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	5.875e-16	711-729	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	8.017e-13	1472-1490	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	9.217e-10	1513-1531	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011B	13.08	9.862e-11	863-881	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011C	24.25	1.450e-10	1618-1646	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011C	24.25	4.571e-09	766-794	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011C	24.25	5.143e-09	2122-2150	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011C	24.25	8.714e-09	546-574	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	1.551e-14	462-480	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	2.328e-11	1472-1490	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	2.653e-14	2103-2121	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	3.361e-11	530-548	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	3.800e-15	1611-1629	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	3.803e-11	863-881	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	4.375e-16	2055-2073	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	4.836e-11	812-830	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	5.224e-14	575-593	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	5.500e-17	1565-1583	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	5.826e-09	1513-1531	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	6.815e-10	665-683	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	7.344e-11	620-638	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	7.975e-16	711-729	PR00011	TYPE III EGF-LIKE SIGNATURE
1076	PR00011D	14.03	9.000e-15	2146-2164	PR00011	TYPE III EGF-LIKE SIGNATURE
1077	BL01107A	12.03	1.000e-40	10-52	BL01107	Ribosomal protein L27e proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1077	BL01107B	16.28	1.000e-40	53-96	BL01107	Ribosomal protein L27e proteins.
1077	BL01107C	9.88	6.344e-26	122-143	BL01107	Ribosomal protein L27e proteins.
1077	BL01170A	12.34	9.124e-10	7-42	BL01170	Ribosomal protein L6e proteins.
1078	BL01019A	13.20	8.694e-18	107-146	BL01019	ADP-ribosylation factors family proteins.
1078	BL01019B	19.49	8.603e-21	151-205	BL01019	ADP-ribosylation factors family proteins.
1078	BL01020C	15.35	7.722e-20	135-185	BL01020	SAR1 family proteins.
1078	BL01115A	10.22	9.151e-11	77-120	BL01115	GTP-binding nuclear protein ran proteins.
1078	PR00328C	13.16	2.111e-12	134-159	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE
1078	PR00328D	12.56	8.071e-11	179-200	PR00328	GTP-BINDING SAR1 PROTEIN SIGNATURE
1080	BL01243C	14.19	5.111e-13	165-199	BL01243	Uncharacterized protein family UPF0005 proteins.
1080	BL01243D	21.15	9.581e-11	247-281	BL01243	Uncharacterized protein family UPF0005 proteins.
1081	BL00292A	22.87	6.786e-24	111-144	BL00292	Cyclins proteins.
1081	BL00292B	20.31	3.739e-19	154-184	BL00292	Cyclins proteins.
1082	BL01013A	25.14	1.000e-34	489-524	BL01013	Oxysterol-binding protein family proteins.
1082	BL01013B	11.33	3.813e-14	554-564	BL01013	Oxysterol-binding protein family proteins.
1082	BL01013C	9.97	6.211e-14	577-586	BL01013	Oxysterol-binding protein family proteins.
1082	BL01013D	26.81	1.000e-37	775-818	BL01013	Oxysterol-binding protein family proteins.
1083	PF00075D	10.71	8.929e-10	305-315	PF00075	RNase H.
1085	PR00237B	13.50	6.000e-09	68-89	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE
1090	BL00218B	21.44	1.621e-10	103-134	BL00218	Amino acid permeases proteins.
1090	BL00218D	21.49	3.797e-11	271-315	BL00218	Amino acid permeases proteins.
1090	BL00218E	23.30	3.520e-10	352-391	BL00218	Amino acid permeases proteins.
1092	BL00061A	9.41	8.435e-09	107-117	BL00061	Short-chain dehydrogenases/reductases family proteins.
1092	BL00061B	25.79	5.605e-09	171-208	BL00061	Short-chain dehydrogenases/reductases family proteins.
1092	BL00061C	7.86	8.941e-09	213-222	BL00061	Short-chain dehydrogenases/reductases family proteins.
1092	PF00426W	7.96	2.765e-09	25-51	PF00426	Outer Capsid protein VP4 (Hemagglutinin).
1092	PR00080A	9.32	6.226e-10	107-118	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
1092	PR00081A	10.53	3.106e-10	31-48	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1092	PR00081B	10.38	6.727e-11	107-118	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SIGNATURE
1092	PR00081E	17.54	3.935e-10	212-229	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1093	BL00115Z	3.12	9.074e-09	157-205	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1093	PR00910A	2.51	8.889e-10	203-215	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE
1094	BL00492A	11.53	4.724e-18	16-32	BL00492	Clusterin proteins.
1094	BL00492B	10.36	9.053e-28	40-62	BL00492	Clusterin proteins.
1094	BL00492C	8.35	1.000e-38	66-99	BL00492	Clusterin proteins.
1094	BL00492D	13.23	1.000e-40	100-136	BL00492	Clusterin proteins.
1094	BL00492E	12.52	1.000e-40	142-190	BL00492	Clusterin proteins.
1094	BL00492F	16.61	1.000e-40	232-273	BL00492	Clusterin proteins.
1094	BL00492G	13.20	1.000e-40	299-348	BL00492	Clusterin proteins.
1094	BL00492H	16.50	6.870e-40	427-463	BL00492	Clusterin proteins.
1096	BL00420A	20.42	1.000e-08	248-276	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.000e-09	779-807	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.000e-10	1043-1071	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.138e-09	824-852	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.148e-10	377-405	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.164e-11	329-357	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.295e-10	608-636	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.491e-11	1145-1173	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.738e-10	887-915	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.831e-09	1040-1068	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	1.969e-09	530-558	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.108e-09	461-489	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.108e-09	842-870	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.108e-09	932-960	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.108e-09	956-984	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1096	BL00420A	20.42	2.246e-09	401-429	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.309e-11	347-375	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.309e-11	803-831	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.385e-09	833-861	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.473e-11	500-528	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.523e-09	1142-1170	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.662e-09	130-158	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	2.770e-10	674-702	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.077e-09	395-423	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.215e-09	133-161	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.215e-09	467-495	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.455e-11	551-579	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.618e-11	908-936	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.631e-09	1073-1101	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.631e-09	497-525	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.656e-10	539-567	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.803e-10	209-237	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.908e-09	515-543	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.908e-09	584-612	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	3.951e-10	881-909	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.046e-09	191-219	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.046e-09	341-369	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.246e-10	1013-1041	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1096	BL00420A	20.42	4.273e-11	299-327	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.323e-09	1046-1074	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.323e-09	242-270	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.490e-13	566-594	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.738e-09	440-468	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.738e-09	641-669	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.927e-11	1103-1131	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.984e-10	707-735	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	4.984e-10	878-906	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.154e-09	1166-1194	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.154e-09	443-471	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.154e-09	647-675	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.292e-09	710-738	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.292e-09	935-963	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.426e-10	869-897	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.569e-09	127-155	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.869e-10	872-900	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	5.909e-11	968-996	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.123e-09	1124-1152	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.123e-09	488-516	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.123e-09	590-618	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.143e-13	653-681	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.262e-09	791-819	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.400e-	371-399	BL00420	Speract receptor repeat

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			proteins domain proteins.
1096	BL00420A	20.42	6.400e-11	572-600	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.459e-10	263-291	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.538e-09	359-387	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	6.815e-09	521-549	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.092e-09	1160-1188	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.092e-09	731-759	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.092e-09	890-918	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.197e-10	317-345	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.197e-10	425-453	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.231e-09	836-864	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.369e-09	218-246	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.508e-09	1148-1176	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.508e-09	992-1020	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.646e-09	227-255	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.646e-09	491-519	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	7.787e-10	185-213	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.036e-11	722-750	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.071e-15	410-438	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.082e-10	206-234	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.230e-10	518-546	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.338e-09	812-840	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.347e-13	944-972	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.377e-10	284-312	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1096	BL00420A	20.42	8.377e-10	587-615	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.477e-09	542-570	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.477e-09	635-663	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.525e-10	773-801	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.531e-13	485-513	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.615e-12	605-633	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.754e-09	758-786	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.892e-09	230-258	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.892e-09	506-534	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	8.892e-09	911-939	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.031e-09	398-426	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.031e-09	677-705	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.031e-09	860-888	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.115e-10	947-975	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.135e-12	800-828	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.169e-09	1121-1149	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.182e-11	629-657	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.262e-10	136-164	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.345e-11	197-225	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.585e-09	407-435	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.585e-09	971-999	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL00420A	20.42	9.852e-10	719-747	BL00420	Speract receptor repeat proteins domain proteins.
1096	BL01113A	17.99	1.000e-08	1022-1048	BL01113	Clq domain proteins.
1096	BL01113A	17.99	1.000e-	593-619	BL01113	Clq domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			
1096	BL01113A	17.99	1.173e-09	1145-1171	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.346e-09	461-487	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.519e-09	524-550	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.614e-11	139-165	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.614e-11	584-610	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.692e-09	209-235	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.692e-09	410-436	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.692e-09	644-670	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.818e-11	896-922	BL01113	C1q domain proteins.
1096	BL01113A	17.99	1.957e-10	815-841	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.038e-09	233-259	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.154e-12	515-541	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.227e-11	191-217	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.241e-16	130-156	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.532e-10	419-445	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.558e-09	566-592	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.731e-09	1040-1066	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.731e-09	365-391	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.846e-12	716-742	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.846e-12	806-832	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.904e-09	521-547	BL01113	C1q domain proteins.
1096	BL01113A	17.99	2.915e-10	965-991	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.045e-11	218-244	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.077e-09	995-1021	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.106e-10	491-517	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.250e-09	338-364	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.250e-11	482-508	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.298e-10	473-499	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.298e-10	560-586	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.298e-10	929-955	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.489e-10	284-310	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.489e-10	377-403	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.489e-10	638-664	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.596e-09	989-1015	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.659e-	911-937	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			
1096	BL01113A	17.99	3.681e-10	242-268	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.769e-09	124-150	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.769e-09	467-493	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.769e-09	917-943	BL01113	C1q domain proteins.
1096	BL01113A	17.99	3.769e-12	197-223	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.064e-10	773-799	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.068e-11	569-595	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.115e-09	878-904	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.162e-13	548-574	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.288e-09	1031-1057	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.447e-10	653-679	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.447e-10	710-736	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.462e-09	662-688	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.477e-11	926-952	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.635e-09	422-448	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.638e-10	452-478	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.682e-11	133-159	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.682e-11	920-946	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.692e-12	809-835	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.774e-15	428-454	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.808e-09	374-400	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.808e-09	890-916	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.808e-17	136-162	BL01113	C1q domain proteins.
1096	BL01113A	17.99	4.892e-13	887-913	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.154e-12	404-430	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.295e-11	1181-1207	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.327e-09	497-523	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.327e-09	674-700	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.500e-09	821-847	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.500e-09	944-970	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.500e-11	1166-1192	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.596e-10	386-412	BL01113	C1q domain proteins.
1096	BL01113A	17.99	5.787e-10	335-361	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.019e-09	263-289	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.019e-	914-940	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			
1096	BL01113A	17.99	6.077e-12	188-214	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.077e-12	290-316	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.114e-11	224-250	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.170e-10	791-817	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.192e-09	380-406	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.308e-12	557-583	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.308e-12	731-757	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.362e-10	221-247	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.362e-10	872-898	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.455e-14	842-868	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.538e-09	293-319	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.553e-10	1142-1168	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.745e-10	575-601	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.769e-12	1046-1072	BL01113	C1q domain proteins.
1096	BL01113A	17.99	6.936e-10	947-973	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.058e-09	608-634	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.128e-10	248-274	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.128e-10	938-964	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.231e-12	121-147	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.319e-10	182-208	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.319e-10	563-589	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.341e-11	974-1000	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.404e-09	539-565	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.511e-10	1001-1027	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.511e-10	206-232	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.511e-10	851-877	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.545e-14	239-265	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.545e-14	299-325	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.577e-09	1175-1201	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.702e-10	656-682	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.750e-09	1127-1153	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.750e-09	203-229	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.750e-09	332-358	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.923e-09	485-511	BL01113	C1q domain proteins.
1096	BL01113A	17.99	7.955e-	1010-1036	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			
1096	BL01113A	17.99	8.085e-10	551-577	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.096e-09	998-1024	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.159e-11	1151-1177	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.277e-10	506-532	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.385e-12	1118-1144	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.442e-09	145-171	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.442e-09	254-280	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.442e-09	941-967	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.468e-10	1160-1186	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.568e-11	695-721	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.615e-09	215-241	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.615e-09	650-676	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.615e-12	647-673	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.660e-10	683-709	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.660e-10	758-784	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.773e-11	1121-1147	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.788e-09	281-307	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.851e-10	413-439	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.962e-09	641-667	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.962e-09	818-844	BL01113	C1q domain proteins.
1096	BL01113A	17.99	8.962e-09	956-982	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.043e-10	1157-1183	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.043e-10	308-334	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.043e-10	623-649	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.077e-12	185-211	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.135e-09	389-415	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.135e-09	488-514	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.182e-11	740-766	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.308e-09	443-469	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.426e-10	1025-1051	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.426e-10	536-562	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.455e-14	800-826	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.481e-09	704-730	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.514e-13	1043-1069	BL01113	C1q domain proteins.
1096	BL01113A	17.99	9.591e-	476-502	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			
1096	BL01113A	17.99	9.617e-10	194-220	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.617e-10	395-421	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.617e-10	770-796	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.654e-09	200-226	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.654e-09	230-256	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.757e-13	127-153	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.757e-13	142-168	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.809e-10	722-748	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.827e-09	545-571	BL01113	Clq domain proteins.
1096	BL01113A	17.99	9.827e-09	692-718	BL01113	Clq domain proteins.
1096	BL01208B	15.83	5.950e-13	84-98	BL01208	VWFC domain proteins.
1096	DM01418A	20.83	1.000e-40	1255-1302	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1096	DM01418B	22.51	1.000e-40	1354-1395	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1096	DM01418C	20.48	5.500e-40	1425-1466	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1096	PR00049D	0.00	5.271e-09	1181-1195	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1096	PR00049D	0.00	5.424e-09	1180-1194	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1096	PR00049D	0.00	6.186e-09	142-156	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1096	PR00049D	0.00	8.571e-10	1177-1191	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1100	BL01019A	13.20	4.156e-12	234-273	BL01019	ADP-ribosylation factors family proteins.
1100	PR00318A	7.84	1.600e-19	88-103	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1100	PR00318B	14.79	9.000e-28	221-243	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1100	PR00318C	12.09	3.571e-24	250-267	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1100	PR00318D	16.28	1.563e-30	272-300	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1100	PR00318E	7.23	2.125e-13	318-327	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1100	PR00440A	9.18	5.645e-15	88-103	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1100	PR00440B	13.27	6.260e-13	221-243	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1100	PR00440C	9.54	6.885e-18	250-267	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1100	PR00440D	8.15	1.303e-15	272-300	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1100	PR00440E	11.16	3.880e-10	319-327	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1100	PR00441A	10.69	1.375e-19	88-103	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00441B	16.16	4.000e-29	221-243	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00441C	14.17	1.409e-24	250-267	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00441D	14.44	9.250e-36	272-300	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00441E	8.35	1.214e-11	319-327	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1100	PR00441F	11.65	6.850e-14	331-341	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00441G	11.67	2.543e-13	347-361	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1100	PR00442A	6.46	2.385e-14	88-103	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1100	PR00442B	7.17	1.794e-18	221-244	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1100	PR00442C	17.61	9.654e-20	250-267	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1100	PR00442D	9.29	8.071e-18	272-300	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1100	PR00442E	7.23	1.106e-11	319-327	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1100	PR00443A	15.16	8.313e-18	88-103	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1100	PR00443C	14.35	7.446e-16	221-243	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1100	PR00443D	13.15	3.361e-17	250-267	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1100	PR00443E	11.98	7.513e-17	272-300	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1100	PR00443F	12.68	5.909e-10	319-327	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1100	PR00449A	13.20	1.000e-08	87-108	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1101	BL00166C	18.93	4.600e-13	453-479	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1101	BL00166D	22.87	5.600e-16	504-539	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1101	BL00598	14.45	6.625e-16	92-113	BL00598	Chromo domain proteins.
1101	PR00504B	9.12	4.600e-13	86-100	PR00504	CHROMODOMAIN SIGNATURE
1101	PR00504C	11.19	5.592e-09	101-113	PR00504	CHROMODOMAIN SIGNATURE
1101	PR00584E	4.20	8.000e-09	126-133	PR00584	PROSTANOID EP3 RECEPTOR TYPE 2 SIGNATURE
1102	BL00383A	13.34	4.150e-14	926-940	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383B	7.61	5.000e-09	951-959	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383C	10.10	5.091e-12	981-991	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383D	11.92	1.000e-14	1055-1067	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383D	11.92	5.500e-09	1293-1305	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383E	10.35	1.789e-09	1387-1397	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383E	10.35	7.300e-14	1093-1103	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383F	15.51	1.439e-09	1425-1440	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00383F	15.51	4.913e-14	1131-1146	BL00383	Tyrosine specific protein phosphatases proteins.
1102	BL00740A	13.87	8.667e-13	36-48	BL00740	MAM domain proteins.
1102	BL00740B	19.76	5.500e-	167-187	BL00740	MAM domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			16			
1102	BL00740C	15.93	9.000e-11	681-691	BL00740	MAM domain proteins.
1102	BL00790H	13.42	3.769e-09	498-523	BL00790	Receptor tyrosine kinase class V proteins.
1102	BL00790I	20.01	2.607e-09	552-582	BL00790	Receptor tyrosine kinase class V proteins.
1102	PR00014C	15.44	4.913e-09	331-349	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1102	PR00014C	15.44	9.000e-11	541-559	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1102	PR00014D	12.04	9.400e-11	559-573	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1102	PR00020A	18.17	1.000e-17	34-52	PR00020	MAM DOMAIN SIGNATURE
1102	PR00020B	15.52	4.971e-14	68-84	PR00020	MAM DOMAIN SIGNATURE
1102	PR00020C	13.66	3.483e-13	95-106	PR00020	MAM DOMAIN SIGNATURE
1102	PR00020D	12.70	2.543e-15	147-161	PR00020	MAM DOMAIN SIGNATURE
1102	PR00020E	8.64	6.586e-13	165-178	PR00020	MAM DOMAIN SIGNATURE
1102	PR00700B	16.80	4.162e-16	1257-1277	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700B	16.80	6.400e-23	968-988	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700C	13.17	3.077e-19	1051-1068	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700D	12.47	7.136e-13	1384-1402	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700D	12.47	7.158e-20	1090-1108	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700E	17.57	9.550e-13	1121-1136	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1102	PR00700F	11.18	6.824e-13	1137-1147	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1104	PF00855	13.75	1.000e-20	119-135	PF00855	PWWP domain proteins.
1105	BL50062B	12.92	1.290e-12	280-290	BL50062	BCL2-like apoptosis inhibitors (spans part of BH3, BH1 and BH).
1105	BL50062C	6.66	8.676e-09	325-333	BL50062	BCL2-like apoptosis inhibitors (spans part of BH3, BH1 and BH).
1106	BL00216B	27.64	5.765e-35	123-172	BL00216	Sugar transport proteins.
1106	PR00171A	10.00	8.615e-13	24-34	PR00171	SUGAR TRANSPORTER SIGNATURE
1106	PR00171B	14.73	4.789e-17	124-143	PR00171	SUGAR TRANSPORTER SIGNATURE
1106	PR00171C	10.97	3.143e-13	283-293	PR00171	SUGAR TRANSPORTER SIGNATURE
1106	PR00171D	12.76	5.500e-19	370-391	PR00171	SUGAR TRANSPORTER SIGNATURE
1106	PR00171E	14.87	8.500e-13	393-405	PR00171	SUGAR TRANSPORTER SIGNATURE
1106	PR00172A	9.82	9.182e-26	273-294	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1106	PR00172B	8.42	1.000e-23	308-329	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1106	PR00172C	9.51	7.828e-19	339-359	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1106	PR00172D	9.13	1.000e-25	370-393	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1106	PR00172E	8.29	2.895e-21	403-421	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1106	PR00172F	8.47	7.188e-	433-453	PR00172	GLUCOSE TRANSPORTER

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			20			SIGNATURE
1107	PR00704A	14.68	9.069e-20	14-37	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704B	17.94	2.636e-22	54-76	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704C	11.88	4.000e-16	78-94	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704D	11.05	2.000e-30	120-145	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704E	12.55	5.886e-25	150-173	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704F	13.61	8.364e-25	175-202	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704G	13.87	7.667e-24	322-343	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704H	13.38	3.676e-19	373-390	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1107	PR00704I	9.52	8.941e-26	464-492	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1108	BL00383E	10.35	9.780e-12	402-412	BL00383	Tyrosine specific protein phosphatases proteins.
1108	BL00383F	15.51	9.341e-09	239-254	BL00383	Tyrosine specific protein phosphatases proteins.
1108	PR00716C	17.65	5.011e-09	147-167	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE
1112	BL00657A	19.39	8.091e-30	109-150	BL00657	Fork head domain proteins.
1112	BL00657B	22.27	7.750e-26	157-199	BL00657	Fork head domain proteins.
1112	PR00053A	8.86	8.050e-09	109-122	PR00053	FORK HEAD DOMAIN SIGNATURE
1112	PR00053B	13.70	7.698e-13	130-147	PR00053	FORK HEAD DOMAIN SIGNATURE
1112	PR00053C	12.80	2.125e-19	158-175	PR00053	FORK HEAD DOMAIN SIGNATURE
1113	BL00484B	9.04	3.400e-12	189-202	BL00484	Thyroglobulin type-1 repeat proteins proteins.
1113	BL00484C	17.01	9.206e-12	208-222	BL00484	Thyroglobulin type-1 repeat proteins proteins.
1117	BL00222A	11.34	5.125e-09	92-102	BL00222	Insulin-like growth factor binding proteins.
1117	BL00222B	11.09	1.375e-16	111-126	BL00222	Insulin-like growth factor binding proteins.
1117	BL00222C	22.97	1.667e-26	261-288	BL00222	Insulin-like growth factor binding proteins.
1117	BL00484B	9.04	3.118e-17	262-275	BL00484	Thyroglobulin type-1 repeat proteins proteins.
1117	BL00484C	17.01	4.536e-13	286-300	BL00484	Thyroglobulin type-1 repeat proteins proteins.
1119	BL00022B	7.54	7.750e-10	203-209	BL00022	EGF-like domain proteins.
1119	BL01187A	9.98	2.714e-	175-186	BL01187	Calcium-binding EGF-

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			like domain proteins pattern proteins.
1119	BL01187A	9.98	4.750e-09	216-227	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	BL01187A	9.98	4.750e-09	46-57	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	BL01187B	12.04	3.000e-12	272-287	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	BL01187B	12.04	5.304e-13	194-209	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	BL01187B	12.04	5.500e-14	232-247	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	BL01187B	12.04	9.400e-11	313-328	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1119	PD02283C	17.54	8.988e-09	58-85	PD02283	PROTEIN SPORULATION REPEAT PRECU.
1119	PR00010C	11.16	1.273e-10	237-247	PR00010	TYPE II EGF-LIKE SIGNATURE
1119	PR00010C	11.16	4.667e-11	199-209	PR00010	TYPE II EGF-LIKE SIGNATURE
1119	PR00907B	11.29	6.260e-10	309-325	PR00907	THROMBOMODULIN SIGNATURE
1119	PR00907G	11.63	3.676e-09	194-220	PR00907	THROMBOMODULIN SIGNATURE
1119	PR00907G	11.63	7.368e-10	232-258	PR00907	THROMBOMODULIN SIGNATURE
1120	BL50017B	17.60	5.263e-11	4112-4127	BL50017	Death domain proteins profile.
1120	DM00784B	17.87	6.311e-09	3961-3985	DM00784	APILOMAVIRUS E4 PROTEIN.
1120	DM00784B	17.87	7.197e-09	3964-3988	DM00784	APILOMAVIRUS E4 PROTEIN.
1120	DM00784B	17.87	9.705e-09	3968-3992	DM00784	APILOMAVIRUS E4 PROTEIN.
1120	PD00078B	13.14	6.478e-09	701-713	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.
1120	PD01364B	13.94	2.421e-09	3974-3989	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.
1120	PD01364B	13.94	3.368e-09	3969-3984	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.
1120	PD01364B	13.94	6.684e-09	3967-3982	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.
1120	PD01364B	13.94	8.364e-10	3970-3985	PD01364	MUCIN GLYCOPROTEIN PRECURSOR MEM.
1120	PF00023A	16.03	1.000e-09	118-133	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	2.875e-10	85-100	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	3.000e-12	477-492	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	4.214e-09	576-591	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	4.375e-10	444-459	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	6.143e-09	279-294	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	7.000e-10	378-393	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	7.000e-11	675-690	PF00023	Ank repeat proteins.
1120	PF00023A	16.03	9.679e-09	312-327	PF00023	Ank repeat proteins.
1120	PF00023B	14.20	5.000e-10	704-713	PF00023	Ank repeat proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1120	PF00023B	14.20	5.500e-09	572-581	PF00023	Ank repeat proteins.
1120	PF00023B	14.20	8.500e-10	407-416	PF00023	Ank repeat proteins.
1120	PF00023B	14.20	8.773e-09	605-614	PF00023	Ank repeat proteins.
1120	PF00023B	14.20	9.000e-10	242-251	PF00023	Ank repeat proteins.
1120	PF00023B	14.20	9.182e-09	770-779	PF00023	Ank repeat proteins.
1120	PF00791A	27.85	1.000e-40	168-222	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	1.000e-40	279-333	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	1.205e-14	118-172	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	1.692e-13	151-205	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	2.367e-17	411-465	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	3.368e-12	85-139	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	4.221e-12	213-267	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	4.462e-13	609-663	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	4.987e-17	477-531	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	5.500e-14	543-597	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	5.500e-16	246-300	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	6.637e-13	345-399	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	6.874e-12	708-762	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	6.927e-16	741-795	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	6.932e-14	642-696	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	7.136e-14	378-432	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	7.442e-12	444-498	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	7.459e-15	312-366	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	7.835e-17	510-564	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791B	28.49	8.354e-16	675-729	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1120	PF00791B	28.49	8.364e-14	576-630	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	1.000e-10	132-170	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	1.000e-10	326-364	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	1.818e-12	557-595	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	1.882e-09	99-137	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	2.432e-12	392-430	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	3.311e-16	623-661	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	3.961e-15	227-265	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	5.147e-09	491-529	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	6.318e-12	689-727	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	6.747e-13	260-298	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	6.778e-14	722-760	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	7.163e-11	293-331	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	7.216e-10	359-397	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	7.239e-12	755-793	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	7.265e-09	165-203	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	7.706e-26	590-628	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	8.826e-11	524-562	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791C	20.98	9.536e-10	425-463	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791D	20.37	1.675e-36	1110-1152	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791E	25.76	1.000e-40	1178-1230	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791F	18.25	2.313e-19	1399-1423	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1120	PF00791G	12.16	2.887e-11	1436-1451	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.
1121	BL00107A	18.39	4.938e-	459-489	BL00107	Protein kinases ATP-

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			21			binding region proteins.
1121	BL00239B	25.15	8.967e-19	394-441	BL00239	Receptor tyrosine kinase class II proteins.
1121	BL00239C	18.75	9.169e-11	446-468	BL00239	Receptor tyrosine kinase class II proteins.
1121	BL00239E	17.14	1.802e-10	516-565	BL00239	Receptor tyrosine kinase class II proteins.
1121	BL00239F	28.15	6.082e-09	571-615	BL00239	Receptor tyrosine kinase class II proteins.
1121	BL00240E	11.56	3.813e-11	445-482	BL00240	Receptor tyrosine kinase class III proteins.
1121	BL00240F	17.74	3.172e-09	515-562	BL00240	Receptor tyrosine kinase class III proteins.
1121	BL00478B	14.79	1.643e-13	51-65	BL00478	LIM domain proteins.
1121	BL00478B	14.79	7.800e-11	109-123	BL00478	LIM domain proteins.
1121	BL00790M	8.74	5.382e-13	450-471	BL00790	Receptor tyrosine kinase class V proteins.
1121	BL50001B	17.40	1.000e-08	456-476	BL50001	Src homology 2 (SH2) domain proteins profile.
1121	PD00289	9.97	8.200e-11	219-232	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.
1121	PF00595	13.40	3.000e-11	216-226	PF00595	PDZ domain proteins (Also known as DHR or GLGF).
1121	PR00109A	15.00	8.839e-10	423-436	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1121	PR00109B	12.27	7.511e-13	459-477	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1121	PR00109E	14.41	7.894e-10	590-612	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1123	BL00280	24.61	3.172e-33	36-79	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1123	PR00759A	14.51	3.880e-10	26-40	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1123	PR00759B	11.26	6.400e-13	54-64	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1123	PR00759C	14.15	2.364e-12	64-79	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1125	PR00790I	14.97	1.818e-32	77-100	PR00790	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE SIGNATURE
1126	DM00406	7.73	2.000e-09	637-649	DM00406	GLIADIN.
1126	PD01234A	11.06	1.450e-09	638-648	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.
1126	PF00806B	11.32	4.176e-12	980-989	PF00806	Pumilio-family RNA binding domain proteins (aka PUM-HD, Pumilio homol.
1126	PF00806C	7.81	2.452e-10	1131-1139	PF00806	Pumilio-family RNA binding domain proteins (aka PUM-HD, Pumilio

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						homol.
1126	PF00806C	7.81	5.263e-11	1052-1060	PF00806	Pumilio-family RNA binding domain proteins (aka PUM-HD, Pumilio homol.
1126	PF00806C	7.81	7.632e-09	908-916	PF00806	Pumilio-family RNA binding domain proteins (aka PUM-HD, Pumilio homol.
1126	PR00308C	3.83	9.649e-09	490-499	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
1130	PD00301B	5.49	5.154e-09	137-147	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1130	PR00796I	8.96	1.517e-09	98-123	PR00796	VIRAL SPIKE GLYCOPROTEIN PRECURSOR SIGNATURE
1132	BL00018	7.41	8.435e-09	28-40	BL00018	EF-hand calcium-binding domain proteins.
1133	BL00203	13.94	7.415e-10	2460-2505	BL00203	Vertebrate metallothioneins proteins.
1133	BL01185C	15.86	4.506e-10	2043-2081	BL01185	C-terminal cystine knot proteins.
1133	BL01185C	15.86	9.065e-10	960-998	BL01185	C-terminal cystine knot proteins.
1133	BL01185D	23.45	8.800e-16	2860-2912	BL01185	C-terminal cystine knot proteins.
1133	BL01208B	15.83	4.938e-10	775-789	BL01208	VWFC domain proteins.
1133	PD02576A	27.60	1.000e-40	932-980	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.
1133	PD02576A	27.60	4.857e-27	453-501	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.
1133	PD02576A	27.60	7.882e-10	2534-2582	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.
1133	PD02576B	25.43	1.667e-22	1495-1522	PD02576	PRECURSOR GLYCOPROTEIN SIGNAL CELL.
1133	PF00094A	11.09	4.333e-13	476-485	PF00094	von Willebrand factor type D domain proteins.
1133	PF00094B	10.43	3.647e-23	624-641	PF00094	von Willebrand factor type D domain proteins.
1133	PF00094B	10.43	8.440e-11	1096-1113	PF00094	von Willebrand factor type D domain proteins.
1133	PF00094B	10.43	9.571e-14	262-279	PF00094	von Willebrand factor type D domain proteins.
1133	PF00094C	12.88	5.500e-15	835-844	PF00094	von Willebrand factor type D domain proteins.
1133	PR00453A	12.79	4.656e-13	1382-1399	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE
1133	PR00453A	12.79	5.696e-10	1603-1620	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE
1133	PR00453B	14.65	5.135e-11	1642-1656	PR00453	VON WILLEBRAND FACTOR TYPE A DOMAIN SIGNATURE
1134	PR00421B	11.40	7.600e-09	94-103	PR00421	THIOREDOXIN FAMILY SIGNATURE
1135	DM00215	19.43	5.729e-09	37-69	DM00215	PROLINE-RICH PROTEIN 3.
1137	BL00107A	18.39	1.000e-20	197-227	BL00107	Protein kinases ATP-binding region proteins.
1137	BL00107B	13.31	2.286e-10	268-283	BL00107	Protein kinases ATP-binding region proteins.
1137	BL00239B	25.15	4.097e-09	124-171	BL00239	Receptor tyrosine kinase class II proteins.
1137	BL00240E	11.56	5.371e-09	183-220	BL00240	Receptor tyrosine kinase class III proteins.
1137	BL00479C	12.01	3.500e-	246-258	BL00479	Phorbol esters /

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			diacylglycerol binding domain proteins.
1137	PR00109B	12.27	3.471e-12	197-215	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1137	PR00109D	17.04	3.441e-10	269-291	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1138	BL00297A	17.58	2.895e-35	86-122	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297B	22.91	1.000e-40	126-174	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297C	9.51	1.000e-40	211-262	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297D	11.95	3.813e-40	270-309	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297E	18.56	6.478e-32	371-414	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297F	11.84	4.750e-25	434-461	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297G	21.87	1.000e-40	464-518	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00297H	15.46	1.000e-40	527-580	BL00297	Heat shock hsp70 proteins family proteins.
1138	BL00933A	17.50	7.857e-09	84-107	BL00933	FGGY family of carbohydrate kinases proteins.
1138	PR00301A	14.84	3.455e-15	84-97	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301B	15.36	7.000e-15	112-124	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301C	8.62	3.903e-09	135-143	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301D	15.51	5.500e-27	219-239	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301E	8.11	1.900e-11	278-288	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301F	13.98	4.240e-18	410-426	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301G	13.78	9.609e-22	441-461	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301H	8.81	2.688e-22	464-483	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1138	PR00301I	12.76	7.500e-21	545-561	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1139	BL00960A	10.98	5.304e-12	64-75	BL00960	BTG1 family proteins.
1139	BL00960B	24.47	1.000e-40	84-128	BL00960	BTG1 family proteins.
1139	BL00960C	12.68	3.647e-26	148-169	BL00960	BTG1 family proteins.
1139	PD01234B	15.53	9.679e-09	36-53	PD01234	PROTEIN NUCLEAR BROMODOMAIN TRANS.
1139	PR00310A	11.17	7.000e-27	66-90	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE
1139	PR00310B	10.59	4.000e-39	91-120	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE
1139	PR00310C	12.74	5.286e-35	121-150	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1139	PR00310D	9.10	1.540e-37	151-180	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE
1139	PR00310E	13.58	6.914e-24	197-216	PR00310	ANTI-PROLIFERATIVE PROTEIN BTG1 FAMILY SIGNATURE
1141	BL00547A	19.15	7.900e-22	89-115	BL00547	Transglutaminases proteins.
1141	BL00547B	29.05	1.000e-40	209-259	BL00547	Transglutaminases proteins.
1141	BL00547C	20.72	2.029e-29	281-318	BL00547	Transglutaminases proteins.
1141	BL00547D	20.72	1.000e-40	338-382	BL00547	Transglutaminases proteins.
1141	BL00547E	17.36	4.667e-37	396-430	BL00547	Transglutaminases proteins.
1141	BL00547F	20.84	9.700e-28	440-471	BL00547	Transglutaminases proteins.
1141	BL00547G	17.29	4.971e-31	489-526	BL00547	Transglutaminases proteins.
1141	BL00547H	14.36	9.471e-16	681-701	BL00547	Transglutaminases proteins.
1141	PR00445A	9.20	6.824e-09	356-363	PR00445	HUPF/HYPC HYDROGENASE EXPRESSION/SYNTHESIS FAMILY SIGNATURE
1143	BL00224B	16.94	9.673e-09	589-641	BL00224	Clathrin light chain proteins.
1143	BL00686	13.91	6.581e-09	820-868	BL00686	CBF-B/NF-YA subunit proteins.
1143	PF00992A	16.67	1.474e-09	819-853	PF00992	Troponin.
1143	PF00992A	16.67	2.184e-09	798-832	PF00992	Troponin.
1143	PF00992A	16.67	9.463e-11	812-846	PF00992	Troponin.
1143	PF00992A	16.67	9.463e-11	853-887	PF00992	Troponin.
1143	PF01140D	15.54	4.035e-09	797-831	PF01140	Matrix protein (MA), p15.
1143	PF01140D	15.54	6.850e-10	811-845	PF01140	Matrix protein (MA), p15.
1145	BL00211A	12.23	2.350e-09	122-133	BL00211	ABC transporters family proteins.
1145	BL00617A	25.53	7.000e-10	105-147	BL00617	RecF protein.
1146	BL00710	12.98	3.880e-16	182-196	BL00710	Phosphoglucosyltransferase and phosphomannosyltransferase phosphoserine signa.
1146	PR00509A	14.01	1.964e-17	181-195	PR00509	PHOSPHOGLUCOMUTASE/PHOSPHOMANNOMUTASE FAMILY SIGNATURE
1146	PR00509B	15.05	7.353e-19	288-307	PR00509	PHOSPHOGLUCOMUTASE/PHOSPHOMANNOMUTASE FAMILY SIGNATURE
1146	PR00509C	9.78	8.875e-16	324-337	PR00509	PHOSPHOGLUCOMUTASE/PHOSPHOMANNOMUTASE FAMILY SIGNATURE
1146	PR00509D	9.21	3.000e-19	352-367	PR00509	PHOSPHOGLUCOMUTASE/PHOSPHOMANNOMUTASE FAMILY SIGNATURE
1147	BL00415B	9.91	9.206e-09	5-40	BL00415	Synapsins proteins.
1150	PR00676D	10.15	9.536e-09	47-62	PR00676	MASPIN SIGNATURE
1152	BL01123D	9.68	6.651e-11	217-232	BL01123	Thermonuclease family proteins.
1154	BL00226A	12.77	6.500e-16	133-147	BL00226	Intermediate filaments proteins.
1154	BL00226B	23.86	1.000e-40	229-276	BL00226	Intermediate filaments proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1154	BL00226B	23.86	3.160e-11	180-227	BL00226	Intermediate filaments proteins.
1154	BL00226C	13.23	3.700e-25	294-324	BL00226	Intermediate filaments proteins.
1154	BL00226D	19.10	1.000e-40	395-441	BL00226	Intermediate filaments proteins.
1154	BL01160B	19.54	1.763e-09	180-233	BL01160	Kinesin light chain repeat proteins.
1154	BL01312I	22.76	1.758e-09	162-210	BL01312	Protein secA proteins.
1155	BL00022B	7.54	1.000e-09	1154-1160	BL00022	EGF-like domain proteins.
1155	BL00022B	7.54	3.250e-10	1558-1564	BL00022	EGF-like domain proteins.
1155	BL00240B	24.70	8.660e-09	3622-3645	BL00240	Receptor tyrosine kinase class III proteins.
1155	BL00243H	17.53	9.645e-09	4180-4205	BL00243	Integrins beta chain cysteine-rich domain proteins.
1155	BL00562	16.21	5.814e-09	4127-4157	BL00562	Cellulose-binding domain proteins fungal type.
1155	BL01209	9.31	2.174e-11	370-382	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1155	BL01209	9.31	4.808e-10	414-426	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1155	BL01209	9.31	6.304e-09	245-257	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1155	BL01209	9.31	9.053e-15	330-342	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1155	BL01248	11.02	3.829e-12	1206-1218	BL01248	Laminin-type EGF-like (LE) domain proteins.
1155	BL01248	11.02	4.724e-13	811-823	BL01248	Laminin-type EGF-like (LE) domain proteins.
1155	BL01248	11.02	8.650e-11	1610-1622	BL01248	Laminin-type EGF-like (LE) domain proteins.
1155	DM00060	6.92	3.700e-10	1687-1696	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.
1155	DM00060	6.92	7.000e-11	888-897	DM00060	338 kw NEUREXIN ALPHA III CYSTEINE.
1155	DM00179	13.97	2.421e-10	3386-3395	DM00179	w KINASE ALPHA ADHESION T-CELL.
1155	PD00320A	14.49	3.455e-11	1586-1599	PD00320	LAMININ CHAIN EGF-LIKE DOMAIN P.
1155	PD00919B	9.47	8.015e-10	1662-1676	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.
1155	PD01270A	17.22	3.903e-09	431-470	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.
1155	PD02870B	18.83	3.968e-09	2516-2548	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	6.300e-10	1853-1885	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	6.400e-10	3198-3230	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	6.553e-09	2130-2162	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	6.649e-09	2420-2452	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	7.798e-09	1759-1791	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	9.000e-10	2613-2645	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870B	18.83	9.809e-09	2709-2741	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1155	PD02870D	15.74	1.383e-	1853-1887	PD02870	RECEPTOR INTERLEUKIN-1

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			PRECURSOR.
1155	PR00010A	11.79	1.000e-08	4132-4143	PR00010	TYPE II EGF-LIKE SIGNATURE
1155	PR00010C	11.16	9.333e-11	3893-3903	PR00010	TYPE II EGF-LIKE SIGNATURE
1155	PR00011A	14.06	9.384e-09	1314-1332	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00011B	13.08	6.055e-09	1314-1332	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00011C	24.25	8.000e-09	920-948	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00011C	24.25	9.518e-11	1321-1349	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00011D	14.03	1.000e-11	1314-1332	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00011D	14.03	9.169e-10	4185-4203	PR00011	TYPE III EGF-LIKE SIGNATURE
1155	PR00261A	11.02	4.296e-12	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261A	11.02	5.895e-17	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261A	11.02	8.676e-13	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261A	11.02	8.984e-15	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261B	14.12	2.356e-12	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261B	14.12	2.588e-14	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261B	14.12	5.500e-17	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261B	14.12	7.662e-11	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261C	11.37	2.826e-13	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261C	11.37	6.373e-14	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261C	11.37	8.500e-20	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261C	11.37	9.014e-12	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261D	12.47	1.305e-16	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261D	12.47	5.000e-15	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261D	12.47	8.734e-14	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261D	12.47	9.859e-14	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261E	11.08	3.727e-12	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261E	11.08	6.906e-13	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SIGNATURE
1155	PR00261E	11.08	7.171e-11	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261E	11.08	7.545e-12	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261F	11.57	5.355e-14	236-257	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261F	11.57	6.280e-10	361-382	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261F	11.57	7.589e-16	321-342	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00261F	11.57	9.603e-12	405-426	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1155	PR00764B	13.56	5.091e-10	356-376	PR00764	COMPLEMENT C9 SIGNATURE
1155	PR00764B	13.56	5.388e-09	316-336	PR00764	COMPLEMENT C9 SIGNATURE
1158	BL00107A	18.39	1.750e-26	324-354	BL00107	Protein kinases ATP-binding region proteins.
1158	BL00107B	13.31	5.500e-11	389-404	BL00107	Protein kinases ATP-binding region proteins.
1158	BL00479C	12.01	3.571e-11	368-380	BL00479	Phorbol esters / diacylglycerol binding domain proteins.
1158	PF00564B	24.74	8.329e-13	275-325	PF00564	Octicosapeptide repeat proteins.
1158	PR00109B	12.27	1.882e-12	324-342	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1163	PD00247C	22.11	2.125e-09	70-97	PD00247	POLYPROTEIN COAT PROTEIN TRANSMEMBRANE PRECURSOR.
1163	PR00049D	0.00	2.786e-10	41-55	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1163	PR00049D	0.00	4.356e-09	42-56	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1163	PR00221H	12.82	7.614e-09	372-385	PR00221	CAULIMOVIRUS COAT PROTEIN SIGNATURE
1164	BL00649B	20.68	2.966e-10	484-529	BL00649	G-protein coupled receptors family 2 proteins.
1164	BL00649C	17.82	5.255e-13	542-567	BL00649	G-protein coupled receptors family 2 proteins.
1164	BL00649E	15.34	1.000e-08	624-653	BL00649	G-protein coupled receptors family 2 proteins.
1164	BL00649G	13.52	5.208e-09	706-731	BL00649	G-protein coupled receptors family 2 proteins.
1164	BL01187A	9.98	1.000e-10	137-148	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1164	BL01187B	12.04	1.529e-15	105-120	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1164	BL01187B	12.04	6.250e-17	156-171	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1164	PR00010C	11.16	7.214e-09	110-120	PR00010	TYPE II EGF-LIKE SIGNATURE
1164	PR00249C	17.08	5.708e-	544-567	PR00249	SECRETIN-LIKE GPCR

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			SUPERFAMILY SIGNATURE
1164	PR00249D	13.09	7.429e-09	582-607	PR00249	SECRETIN-LIKE GPCR SUPERFAMILY SIGNATURE
1165	BL00216B	27.64	5.000e-34	147-196	BL00216	Sugar transport proteins.
1165	PR00171A	10.00	1.429e-11	48-58	PR00171	SUGAR TRANSPORTER SIGNATURE
1165	PR00171B	14.73	3.813e-18	148-167	PR00171	SUGAR TRANSPORTER SIGNATURE
1165	PR00171C	10.97	3.143e-13	307-317	PR00171	SUGAR TRANSPORTER SIGNATURE
1165	PR00171D	12.76	7.750e-20	394-415	PR00171	SUGAR TRANSPORTER SIGNATURE
1165	PR00171E	14.87	2.800e-11	417-429	PR00171	SUGAR TRANSPORTER SIGNATURE
1165	PR00172A	9.82	5.091e-26	297-318	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1165	PR00172B	8.42	9.500e-24	332-353	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1165	PR00172C	9.51	5.000e-22	363-383	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1165	PR00172D	9.13	6.824e-28	394-417	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1165	PR00172E	8.29	2.500e-23	427-445	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1165	PR00172F	8.47	7.750e-24	457-477	PR00172	GLUCOSE TRANSPORTER SIGNATURE
1167	PD00301A	10.24	1.000e-08	277-287	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1168	BL00218D	21.49	7.324e-11	274-318	BL00218	Amino acid permeases proteins.
1168	BL00218E	23.30	3.475e-09	355-394	BL00218	Amino acid permeases proteins.
1170	PD00301A	10.24	6.400e-09	73-83	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1170	PR00049D	0.00	8.627e-09	175-189	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1172	BL00453A	15.57	1.000e-16	56-70	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.
1172	BL00453B	23.86	7.231e-26	81-114	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.
1172	BL00453C	9.72	4.214e-13	122-134	BL00453	FKBP-type peptidyl-prolyl cis-trans isomerase proteins.
1176	BL00136A	14.35	1.720e-11	177-189	BL00136	Serine proteases, subtilase family, aspartic acid proteins.
1176	BL00136B	9.63	2.500e-12	218-230	BL00136	Serine proteases, subtilase family, aspartic acid proteins.
1176	BL00136C	8.52	9.609e-11	392-402	BL00136	Serine proteases, subtilase family, aspartic acid proteins.
1176	PR00723A	13.37	5.200e-17	170-189	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE
1176	PR00723B	11.22	5.050e-13	216-229	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE
1176	PR00723C	10.64	2.929e-13	391-407	PR00723	SUBTILISIN SERINE PROTEASE FAMILY (S8) SIGNATURE
1182	BL00420A	20.42	1.138e-09	505-533	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.148e-10	1129-1157	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1182	BL00420A	20.42	1.173e-12	1564-1592	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.554e-09	1069-1097	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.554e-09	928-956	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.692e-09	1507-1535	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.692e-09	1558-1586	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.738e-10	1087-1115	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.918e-13	1378-1406	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	1.969e-09	1423-1451	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.328e-10	1252-1280	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.328e-10	1297-1325	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.385e-09	655-683	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.385e-12	1294-1322	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.475e-10	1486-1514	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.523e-09	1126-1154	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.623e-10	1057-1085	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.662e-09	673-701	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	2.918e-10	754-782	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.213e-10	1420-1448	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.492e-09	1009-1037	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.631e-09	670-698	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.769e-09	1459-1487	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.945e-11	922-950	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	3.951e-10	1579-1607	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.046e-	1339-1367	BL00420	Speract receptor repeat

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			proteins domain proteins.
1182	BL00420A	20.42	4.246e-10	1555-1583	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.635e-12	787-815	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.689e-10	871-899	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.836e-10	820-848	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.984e-10	1489-1517	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	4.984e-10	796-824	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.154e-12	817-845	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.292e-09	838-866	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.431e-09	1183-1211	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.569e-09	1093-1121	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.574e-10	724-752	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.574e-10	751-779	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.721e-10	1567-1595	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.745e-11	994-1022	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.846e-12	991-1019	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.869e-10	1372-1400	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	5.985e-09	1012-1040	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.459e-10	1045-1073	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.607e-10	805-833	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.677e-09	958-986	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.815e-09	1369-1397	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.815e-09	1471-1499	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.815e-09	895-923	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1182	BL00420A	20.42	6.885e-12	1321-1349	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	6.954e-09	1483-1511	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.049e-10	1180-1208	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.049e-10	847-875	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.055e-11	1504-1532	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.218e-11	1315-1343	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.231e-09	1285-1313	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.231e-09	850-878	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.245e-13	1099-1127	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.369e-09	1162-1190	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.369e-09	634-662	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.429e-13	1249-1277	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.492e-10	721-749	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.785e-09	1048-1076	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.785e-09	748-776	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	7.934e-10	904-932	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.062e-09	1171-1199	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.338e-09	1522-1550	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.377e-10	1132-1160	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.615e-09	1117-1145	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.615e-09	1306-1334	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.672e-10	1270-1298	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.691e-11	1375-1403	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1182	BL00420A	20.42	8.754e-09	529-557	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	8.967e-10	1492-1520	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.031e-09	1156-1184	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.031e-09	931-959	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.115e-10	781-809	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.115e-10	910-938	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.169e-09	925-953	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.182e-11	1414-1442	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.262e-10	1411-1439	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.446e-09	1402-1430	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.449e-13	1318-1346	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.585e-09	1123-1151	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.585e-09	637-665	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.705e-10	919-947	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.723e-09	1477-1505	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.852e-10	526-554	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00420A	20.42	9.862e-09	649-677	BL00420	Speract receptor repeat proteins domain proteins.
1182	BL00604F	5.96	7.020e-09	1433-1477	BL00604	Synaptophysin / synaptoporin proteins.
1182	BL01113A	17.99	1.000e-09	1123-1149	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.000e-09	1405-1431	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.000e-10	1396-1422	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.000e-10	514-540	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.191e-10	730-756	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.231e-12	1492-1518	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.243e-13	1177-1203	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.519e-09	886-912	BL01113	Clq domain proteins.
1182	BL01113A	17.99	1.545e-	1138-1164	BL01113	Clq domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			14			
1182	BL01113A	17.99	1.614e-11	640-666	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.614e-11	805-831	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.614e-11	985-1011	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.818e-11	751-777	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.865e-09	523-549	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.865e-09	979-1005	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.923e-12	1387-1413	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.957e-10	535-561	BL01113	C1q domain proteins.
1182	BL01113A	17.99	1.957e-10	655-681	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.023e-11	715-741	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.038e-09	718-744	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.216e-13	1372-1398	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.385e-09	1450-1476	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.452e-15	673-699	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.459e-13	1225-1251	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.532e-10	1084-1110	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.532e-10	1468-1494	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.532e-10	754-780	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.558e-09	712-738	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.558e-09	811-837	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.636e-11	1048-1074	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.723e-10	1561-1587	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.731e-09	1108-1134	BL01113	C1q domain proteins.
1182	BL01113A	17.99	2.915e-10	1081-1107	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.045e-11	727-753	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.298e-10	1585-1611	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.298e-10	1594-1620	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.432e-13	787-813	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.455e-11	922-948	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.455e-14	1555-1581	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.489e-10	688-714	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.596e-09	1411-1437	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.596e-09	685-711	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.596e-09	739-765	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.769e-	1117-1143	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			
1182	BL01113A	17.99	3.769e-09	517-543	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.769e-09	736-762	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.872e-10	724-750	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.942e-09	1384-1410	BL01113	C1q domain proteins.
1182	BL01113A	17.99	3.942e-09	1414-1440	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.064e-10	1051-1077	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.068e-11	931-957	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.255e-10	1375-1401	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.288e-09	625-651	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.447e-10	1480-1506	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.447e-10	1570-1596	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.462e-12	1000-1026	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.462e-12	1249-1275	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.462e-12	895-921	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.477e-11	1318-1344	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.635e-09	1027-1053	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.635e-09	1255-1281	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.635e-09	601-627	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.808e-09	1279-1305	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.830e-10	1057-1083	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.830e-10	1312-1338	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.830e-10	595-621	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.830e-10	742-768	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.886e-11	1267-1293	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.892e-13	796-822	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.923e-12	814-840	BL01113	C1q domain proteins.
1182	BL01113A	17.99	4.981e-09	1213-1239	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.021e-10	907-933	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.091e-11	1489-1515	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.154e-09	1321-1347	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.154e-09	1429-1455	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.295e-11	1045-1071	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.295e-11	1369-1395	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.295e-11	1558-1584	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.378e-	1303-1329	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			13			
1182	BL01113A	17.99	5.378e-13	1357-1383	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.385e-12	1354-1380	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.385e-12	529-555	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.404e-10	1063-1089	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.500e-09	1135-1161	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.500e-09	898-924	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.615e-12	1477-1503	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.622e-13	766-792	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.636e-14	1564-1590	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.705e-11	781-807	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.787e-10	604-630	BL01113	C1q domain proteins.
1182	BL01113A	17.99	5.846e-09	1285-1311	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.019e-09	823-849	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.114e-11	1348-1374	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.182e-14	1495-1521	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.192e-09	1402-1428	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.365e-09	904-930	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.455e-14	994-1020	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.538e-09	1186-1212	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.538e-09	772-798	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.553e-10	1453-1479	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.553e-10	709-735	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.595e-13	721-747	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.712e-09	1501-1527	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.727e-11	508-534	BL01113	C1q domain proteins.
1182	BL01113A	17.99	6.769e-12	790-816	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.000e-12	1129-1155	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.058e-09	1519-1545	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.058e-09	901-927	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.058e-09	910-936	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.081e-13	682-708	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.128e-10	1327-1353	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.136e-11	1423-1449	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.231e-09	619-645	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.231e-	703-729	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			
1182	BL01113A	17.99	7.273e-14	1297-1323	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.341e-11	1258-1284	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.341e-11	610-636	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.387e-15	1363-1389	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.511e-10	1054-1080	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.511e-10	1075-1101	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.545e-11	1420-1446	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.545e-11	1459-1485	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.545e-11	784-810	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.545e-14	1114-1140	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.568e-13	1381-1407	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.577e-09	1210-1236	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.577e-09	1336-1362	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.577e-09	631-657	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.750e-09	1183-1209	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.750e-09	1252-1278	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.923e-09	1102-1128	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.923e-09	1513-1539	BL01113	C1q domain proteins.
1182	BL01113A	17.99	7.923e-12	880-906	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.085e-10	1465-1491	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.096e-09	1306-1332	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.138e-16	1486-1512	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.154e-12	1147-1173	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.269e-09	958-984	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.277e-10	1417-1443	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.364e-11	1567-1593	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.468e-10	532-558	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.615e-12	1132-1158	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.636e-14	1288-1314	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.660e-10	889-915	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.788e-09	691-717	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.788e-09	760-786	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.846e-12	1099-1125	BL01113	C1q domain proteins.
1182	BL01113A	17.99	8.977e-11	1072-1098	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.043e-	1573-1599	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			
1182	BL01113A	17.99	9.129e-15	1378-1404	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.135e-09	1462-1488	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.135e-09	859-885	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.234e-10	1216-1242	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.270e-13	775-801	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.270e-13	991-1017	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.426e-10	1066-1092	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.426e-10	799-825	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.769e-12	1003-1029	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.769e-12	505-531	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.827e-09	1180-1206	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.827e-09	1588-1614	BL01113	C1q domain proteins.
1182	BL01113A	17.99	9.827e-09	955-981	BL01113	C1q domain proteins.
1182	DM01418A	20.83	1.000e-40	1668-1715	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1182	DM01418B	22.51	5.821e-39	1763-1804	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1182	DM01418C	20.48	1.000e-34	1831-1872	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1185	BL00514C	17.41	9.082e-28	264-300	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1185	BL00514D	15.35	3.118e-11	305-317	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1185	BL00514G	15.98	1.000e-14	391-420	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1185	BL00514H	14.95	7.545e-13	426-450	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1187	BL50002A	14.19	4.750e-12	339-357	BL50002	Src homology 3 (SH3) domain proteins profile.
1187	PR00452B	11.65	5.500e-09	349-364	PR00452	SH3 DOMAIN SIGNATURE
1188	BL00663A	11.51	8.364e-22	44-64	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663B	27.86	1.000e-40	69-122	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663C	22.59	1.000e-40	131-185	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663D	24.77	1.000e-40	206-252	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663E	21.19	2.200e-33	254-291	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663F	20.78	7.000e-40	321-361	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663G	24.17	1.000e-40	393-442	BL00663	Vinculin family talin-binding region

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1188	BL00663H	27.09	1.000e-40	465-517	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663I	27.27	1.000e-40	543-596	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663J	18.16	1.000e-40	725-761	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663K	21.52	1.000e-40	770-824	BL00663	Vinculin family talin-binding region proteins.
1188	BL00663L	20.67	9.053e-38	837-872	BL00663	Vinculin family talin-binding region proteins.
1188	PR00805A	11.15	1.692e-31	36-60	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805B	14.82	1.409e-25	134-152	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805C	8.43	1.300e-23	153-171	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805D	7.82	1.257e-31	329-353	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805E	10.38	1.375e-27	397-417	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805F	11.72	1.375e-31	518-542	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805G	11.78	1.000e-31	633-657	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805H	14.97	1.161e-31	735-757	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805I	12.05	1.188e-32	799-823	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00805J	7.44	2.800e-25	879-897	PR00805	ALPHA-CATENIN SIGNATURE
1188	PR00806C	11.07	2.258e-09	734-751	PR00806	VINCULIN SIGNATURE
1188	PR00929C	5.26	9.069e-09	71-81	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE
1189	BL00223A	15.59	1.911e-11	78-111	BL00223	Annexins repeat proteins domain proteins.
1189	BL00223C	24.79	5.725e-40	65-119	BL00223	Annexins repeat proteins domain proteins.
1189	PR00196C	10.36	6.311e-13	82-103	PR00196	ANNEXIN FAMILY SIGNATURE
1189	PR00196D	21.86	6.400e-09	6-32	PR00196	ANNEXIN FAMILY SIGNATURE
1189	PR00196E	9.19	7.128e-18	86-106	PR00196	ANNEXIN FAMILY SIGNATURE
1189	PR00196F	13.89	1.000e-14	114-129	PR00196	ANNEXIN FAMILY SIGNATURE
1189	PR00196G	11.72	1.439e-11	130-143	PR00196	ANNEXIN FAMILY SIGNATURE
1189	PR00197D	7.50	1.297e-10	82-103	PR00197	ANNEXIN TYPE I SIGNATURE
1189	PR00197F	9.03	3.314e-17	86-106	PR00197	ANNEXIN TYPE I SIGNATURE
1189	PR00198D	7.65	1.175e-09	82-103	PR00198	ANNEXIN TYPE II SIGNATURE
1189	PR00198G	8.09	3.132e-14	86-106	PR00198	ANNEXIN TYPE II SIGNATURE
1189	PR00198H	12.05	9.663e-09	130-143	PR00198	ANNEXIN TYPE II SIGNATURE
1189	PR00199D	5.65	8.699e-11	82-103	PR00199	ANNEXIN TYPE III SIGNATURE
1189	PR00199G	9.09	2.588e-20	87-112	PR00199	ANNEXIN TYPE III SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1189	PR00199H	12.62	3.000e-15	130-143	PR00199	ANNEXIN TYPE III SIGNATURE
1189	PR00200E	10.00	1.489e-11	82-103	PR00200	ANNEXIN TYPE IV SIGNATURE
1189	PR00200G	9.43	1.000e-18	86-112	PR00200	ANNEXIN TYPE IV SIGNATURE
1189	PR00200H	13.68	2.987e-11	130-143	PR00200	ANNEXIN TYPE IV SIGNATURE
1189	PR00201D	10.49	8.981e-09	82-103	PR00201	ANNEXIN TYPE V SIGNATURE
1189	PR00201G	11.02	1.625e-21	86-112	PR00201	ANNEXIN TYPE V SIGNATURE
1189	PR00201H	12.04	8.024e-11	130-143	PR00201	ANNEXIN TYPE V SIGNATURE
1189	PR00202G	8.01	9.538e-21	86-112	PR00202	ANNEXIN TYPE VI SIGNATURE
1189	PR00202H	9.20	2.800e-10	130-143	PR00202	ANNEXIN TYPE VI SIGNATURE
1190	BL00593A	13.25	6.700e-30	38-63	BL00593	Heme oxygenase proteins.
1190	BL00593B	13.38	1.000e-40	72-115	BL00593	Heme oxygenase proteins.
1190	BL00593C	10.02	1.000e-40	144-188	BL00593	Heme oxygenase proteins.
1190	BL00593D	19.91	1.000e-40	192-244	BL00593	Heme oxygenase proteins.
1190	BL00593E	13.32	4.000e-24	292-314	BL00593	Heme oxygenase proteins.
1190	PR00088A	13.37	1.237e-29	38-63	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088B	14.55	5.615e-29	73-98	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088C	13.00	7.395e-30	99-124	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088D	16.75	1.000e-27	152-173	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088E	11.90	4.900e-25	174-195	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088F	12.62	3.025e-24	196-217	PR00088	HAEM OXYGENASE SIGNATURE
1190	PR00088G	10.67	7.429e-21	228-246	PR00088	HAEM OXYGENASE SIGNATURE
1193	BL00388A	23.14	1.257e-33	15-60	BL00388	Proteasome A-type subunits proteins.
1193	BL00388B	31.38	7.429e-28	74-115	BL00388	Proteasome A-type subunits proteins.
1193	BL00388C	18.79	9.710e-17	129-150	BL00388	Proteasome A-type subunits proteins.
1193	BL00388D	20.71	3.382e-20	157-187	BL00388	Proteasome A-type subunits proteins.
1193	PF00227	14.68	5.950e-09	22-33	PF00227	Proteasome A-type and B-type.
1194	BL00061B	25.79	2.636e-17	219-256	BL00061	Short-chain dehydrogenases/reductases family proteins.
1194	PR00080C	17.16	8.714e-13	239-258	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
1194	PR00081A	10.53	5.979e-10	91-108	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1194	PR00081C	15.13	9.654e-11	213-229	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1194	PR00081D	15.80	1.231e-10	239-258	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1195	BL00326A	14.01	9.686e-09	34-67	BL00326	Tropomyosins proteins.
1197	PF00651	15.00	7.857e-10	345-357	PF00651	BTB (also known as BR-C/Ttk) domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1199	PR00001A	12.78	9.379e-15	38-51	PR00001	COAGULATION FACTOR GLA DOMAIN SIGNATURE
1199	PR00001B	10.75	6.932e-13	52-65	PR00001	COAGULATION FACTOR GLA DOMAIN SIGNATURE
1199	PR00001C	16.60	2.459e-11	66-80	PR00001	COAGULATION FACTOR GLA DOMAIN SIGNATURE
1200	PD00289	9.97	4.103e-09	160-173	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYN.
1201	BL00107A	18.39	3.118e-20	733-763	BL00107	Protein kinases ATP-binding region proteins.
1201	BL00107B	13.31	8.615e-12	803-818	BL00107	Protein kinases ATP-binding region proteins.
1201	BL00239B	25.15	9.224e-21	667-714	BL00239	Receptor tyrosine kinase class II proteins.
1201	BL00239C	18.75	7.474e-13	720-742	BL00239	Receptor tyrosine kinase class II proteins.
1201	BL00239D	16.81	2.373e-11	745-770	BL00239	Receptor tyrosine kinase class II proteins.
1201	BL00239E	17.14	4.682e-24	775-824	BL00239	Receptor tyrosine kinase class II proteins.
1201	BL00239F	28.15	2.929e-20	829-873	BL00239	Receptor tyrosine kinase class II proteins.
1201	BL00240E	11.56	7.808e-17	719-756	BL00240	Receptor tyrosine kinase class III proteins.
1201	BL00240F	17.74	9.241e-19	774-821	BL00240	Receptor tyrosine kinase class III proteins.
1201	BL00240G	28.45	2.611e-11	821-873	BL00240	Receptor tyrosine kinase class III proteins.
1201	BL00790A	19.74	5.371e-17	20-41	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790B	21.59	1.000e-40	53-104	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790C	16.65	1.000e-40	161-214	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790D	12.41	2.703e-22	238-262	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790E	29.58	6.400e-39	271-318	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790F	15.90	7.250e-22	337-363	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790G	22.06	2.846e-34	373-416	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790H	13.42	1.771e-23	452-477	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790I	20.01	8.941e-27	499-529	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790J	14.21	1.000e-40	588-627	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790K	9.30	1.000e-40	640-693	BL00790	Receptor tyrosine kinase class V

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1201	BL00790L	11.16	3.423e-24	704-723	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790M	8.74	4.977e-26	724-745	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790N	13.25	8.071e-31	746-772	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790O	7.68	1.000e-40	782-814	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790P	12.33	1.281e-30	815-839	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790Q	15.61	1.000e-40	840-888	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL00790R	16.20	4.000e-39	931-974	BL00790	Receptor tyrosine kinase class V proteins.
1201	BL50001B	17.40	3.647e-13	730-750	BL50001	Src homology 2 (SH2) domain proteins profile.
1201	BL50001C	10.17	1.000e-09	784-794	BL50001	Src homology 2 (SH2) domain proteins profile.
1201	PR00014D	12.04	3.077e-12	506-520	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1201	PR00109A	15.00	1.409e-12	696-709	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1201	PR00109B	12.27	1.000e-19	733-751	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1201	PR00109C	12.85	5.235e-12	785-795	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1201	PR00109D	17.04	2.038e-20	804-826	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1201	PR00109E	14.41	8.500e-18	848-870	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1203	DM00215	19.43	9.390e-09	157-189	DM00215	PROLINE-RICH PROTEIN 3.
1203	PR00049D	0.00	7.254e-09	175-189	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1204	BL00225A	13.82	3.127e-09	1133-1153	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225A	13.82	5.829e-12	1417-1437	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225B	18.06	2.575e-19	1270-1304	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225B	18.06	4.808e-14	970-1004	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225B	18.06	5.500e-14	1451-1485	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225B	18.06	7.517e-24	1179-1213	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1204	BL00225B	18.06	8.200e-19	1072-1106	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1204	BL00225B	18.06	8.297e-20	1361-1395	BL00225	Crystallins beta and gamma 'Greek key' motif proteins.
1205	BL00266B	24.48	8.457e-21	19-56	BL00266	Somatotropin, prolactin and related hormones proteins.
1205	PR00836A	14.40	2.800e-13	19-32	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1205	PR00836B	16.59	5.814e-10	41-59	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1205	PR00836C	11.95	1.000e-12	119-135	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1206	BL00046	12.95	1.000e-40	59-113	BL00046	Histone H2A proteins.
1206	PR00620A	11.03	2.636e-27	40-62	PR00620	HISTONE H2A SIGNATURE
1206	PR00620B	8.47	1.750e-20	69-84	PR00620	HISTONE H2A SIGNATURE
1206	PR00620C	10.19	2.125e-17	84-97	PR00620	HISTONE H2A SIGNATURE
1206	PR00620D	11.39	1.692e-19	98-112	PR00620	HISTONE H2A SIGNATURE
1206	PR00620E	8.91	2.500e-16	112-124	PR00620	HISTONE H2A SIGNATURE
1206	PR00620F	7.29	7.750e-22	126-144	PR00620	HISTONE H2A SIGNATURE
1208	BL00309A	19.16	7.545e-20	75-99	BL00309	Vertebrate galactoside-binding lectin proteins.
1208	BL00309B	12.11	6.000e-16	101-115	BL00309	Vertebrate galactoside-binding lectin proteins.
1208	BL00309C	18.65	5.000e-24	123-147	BL00309	Vertebrate galactoside-binding lectin proteins.
1209	PF00075B	12.56	4.073e-10	260-270	PF00075	RNase H.
1209	PF00075C	11.58	9.786e-11	295-306	PF00075	RNase H.
1209	PF00075D	10.71	7.000e-11	327-337	PF00075	RNase H.
1209	PF00075F	12.87	4.750e-11	685-695	PF00075	RNase H.
1209	PF00075J	15.78	8.350e-11	980-997	PF00075	RNase H.
1209	PF00429	31.08	3.492e-17	1105-1154	PF00429	ENV polyprotein (coat polyprotein).
1210	BL00272C	8.27	8.326e-09	95-106	BL00272	Snake toxins proteins.
1210	BL00983C	12.69	4.981e-09	91-106	BL00983	Ly-6 / u-PAR domain proteins.
1211	BL00139A	10.29	7.261e-14	320-329	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1211	BL00139C	9.23	1.000e-11	461-470	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1211	BL00139D	9.24	5.125e-17	477-493	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1211	PR00705A	10.55	6.294e-16	320-335	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1211	PR00705B	10.22	1.844e-09	462-472	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1214	BL00282	16.88	6.294e-11	12-34	BL00282	Kazal serine protease inhibitors family proteins.
1216	BL01177C	17.39	2.875e-	109-127	BL01177	Anaphylatoxin domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			20			proteins.
1216	BL01187A	9.98	1.000e-12	100-111	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1216	BL01187A	9.98	6.625e-09	58-69	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1216	BL01187B	12.04	3.250e-14	76-91	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1216	BL01187B	12.04	6.478e-13	115-130	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1216	PR00010A	11.79	9.308e-09	102-113	PR00010	TYPE II EGF-LIKE SIGNATURE
1216	PR00010C	11.16	5.714e-09	81-91	PR00010	TYPE II EGF-LIKE SIGNATURE
1218	BL00226D	19.10	1.000e-40	31-77	BL00226	Intermediate filaments proteins.
1219	BL00107A	18.39	6.192e-12	211-241	BL00107	Protein kinases ATP-binding region proteins.
1219	BL00239B	25.15	8.909e-17	146-193	BL00239	Receptor tyrosine kinase class II proteins.
1219	BL00240D	23.07	3.483e-09	135-189	BL00240	Receptor tyrosine kinase class III proteins.
1219	BL00240E	11.56	6.185e-12	197-234	BL00240	Receptor tyrosine kinase class III proteins.
1219	BL00479C	12.01	2.000e-09	263-275	BL00479	Phorbol esters / diacylglycerol binding domain proteins.
1219	BL00790M	8.74	3.571e-09	202-223	BL00790	Receptor tyrosine kinase class V proteins.
1219	PR00109A	15.00	1.486e-09	175-188	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1219	PR00109B	12.27	5.596e-13	211-229	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1221	BL00421E	20.97	5.125e-16	41-70	BL00421	Transmembrane 4 family proteins.
1221	PR00259D	13.50	2.241e-21	44-70	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1222	BL00540B	18.82	1.000e-40	50-104	BL00540	Ferritin iron-binding regions proteins.
1222	BL00540C	13.00	7.750e-14	115-126	BL00540	Ferritin iron-binding regions proteins.
1223	BL00824B	9.21	7.750e-22	89-108	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1224	BL00266A	15.69	9.000e-19	30-56	BL00266	Somatotropin, prolactin and related hormones proteins.
1224	BL00266B	24.48	7.261e-16	74-111	BL00266	Somatotropin, prolactin and related hormones proteins.
1224	PR00836A	14.40	9.379e-11	74-87	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1225	PF00084C	11.25	3.571e-10	34-43	PF00084	Sushi domain proteins (SCR repeat proteins.
1227	BL00475C	13.06	3.700e-17	57-73	BL00475	Ribosomal protein L15 proteins.
1228	PR00702G	9.63	2.625e-09	22-45	PR00702	ACRIFLAVIN RESISTANCE PROTEIN FAMILY SIGNATURE
1231	PD02269B	18.48	2.667e-	74-100	PD02269	CYTIDINE DEAMINASE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			27			HYDROLASE ZINC AMINOHY.
1231	PD02269C	16.36	7.882e-17	119-131	PD02269	CYTIDINE DEAMINASE HYDROLASE ZINC AMINOHY.
1232	BL00061A	9.41	4.600e-13	105-115	BL00061	Short-chain dehydrogenases/reductases family proteins.
1232	PR00080A	9.32	3.143e-12	105-116	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
1232	PR00081B	10.38	8.800e-14	105-116	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1233	BL00064A	21.16	1.000e-33	48-85	BL00064	L-lactate dehydrogenase proteins.
1233	BL00957A	8.31	9.609e-09	48-63	BL00957	NAD-dependent glycerol-3-phosphate dehydrogenase proteins.
1233	PR00086A	16.12	4.000e-26	48-72	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE
1233	PR00086B	13.67	4.462e-24	73-97	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE
1234	BL00353B	11.47	1.000e-40	65-114	BL00353	HMG1/2 proteins.
1234	BL00353C	14.83	5.680e-24	115-161	BL00353	HMG1/2 proteins.
1234	BL00353C	14.83	7.254e-09	31-77	BL00353	HMG1/2 proteins.
1234	PR00886A	10.08	2.929e-30	27-49	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1234	PR00886B	9.88	6.625e-27	50-70	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1234	PR00886C	11.84	1.500e-22	97-115	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1234	PR00886D	15.72	4.830e-14	115-134	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1234	PR00886E	8.85	9.316e-09	50-70	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1235	BL00740A	13.87	7.200e-10	64-76	BL00740	MAM domain proteins.
1235	PR00020A	18.17	6.684e-10	62-80	PR00020	MAM DOMAIN SIGNATURE
1236	BL01187A	9.98	3.250e-09	68-79	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1236	BL01187A	9.98	3.571e-10	27-38	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1236	BL01187B	12.04	1.391e-13	46-61	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1236	BL01187B	12.04	2.000e-12	5-20	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1236	BL01187B	12.04	4.375e-09	86-101	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1236	PR00010C	11.16	7.000e-09	51-61	PR00010	TYPE II EGF-LIKE SIGNATURE
1236	PR00907G	11.63	6.514e-09	46-72	PR00907	THROMBOMODULIN SIGNATURE
1236	PR00907G	11.63	8.622e-09	5-31	PR00907	THROMBOMODULIN SIGNATURE
1237	BL00287	17.35	1.947e-20	25-48	BL00287	Cysteine proteases inhibitors proteins.
1245	DM00303A	13.20	3.382e-11	52-101	DM00303	6 LEA 11-MER REPEAT REPEAT.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description.
1246	BL00064C	17.28	1.000e-40	18-62	BL00064	L-lactate dehydrogenase proteins.
1246	BL00064D	14.19	8.875e-32	63-92	BL00064	L-lactate dehydrogenase proteins.
1246	BL00068C	29.08	3.089e-17	14-60	BL00068	Malate dehydrogenase proteins.
1246	PR00086C	16.22	6.400e-25	15-35	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE
1246	PR00086D	15.53	4.600e-24	39-57	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE
1246	PR00086E	11.21	8.364e-18	69-82	PR00086	L-LACTATE DEHYDROGENASE SIGNATURE
1251	BL00142	8.38	4.429e-09	430-440	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
1251	PD01719A	12.89	3.429e-14	594-621	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.
1251	PD01719A	12.89	9.408e-10	943-970	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.
1254	BL00319C	17.12	1.592e-09	43-76	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	2.625e-10	106-139	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	3.013e-09	100-133	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	3.857e-12	101-134	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	4.671e-09	107-140	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	4.875e-10	97-130	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	5.836e-11	44-77	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	7.625e-10	104-137	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	8.105e-09	98-131	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	8.800e-13	102-135	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	8.857e-12	105-138	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	9.289e-09	39-72	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1254	BL00319C	17.12	9.289e-09	96-129	BL00319	Amyloidogenic glycoprotein extracellular domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1254	BL00412D	16.54	3.935e-10	66-116	BL00412	Neuromodulin (GAP-43) proteins.
1254	BL00412D	16.54	6.283e-10	93-143	BL00412	Neuromodulin (GAP-43) proteins.
1254	BL00412D	16.54	6.420e-11	68-118	BL00412	Neuromodulin (GAP-43) proteins.
1254	BL00824B	9.21	2.216e-09	107-126	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1254	BL00824B	9.21	2.338e-09	106-125	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1254	BL00824B	9.21	4.770e-09	105-124	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1254	BL00824B	9.21	5.257e-09	45-64	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1254	BL00824B	9.21	8.435e-10	102-121	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1254	BL00884B	12.47	9.664e-09	76-119	BL00884	Osteopontin proteins.
1254	BL01115D	14.49	6.924e-09	14-45	BL01115	GTP-binding nuclear protein ran proteins.
1254	PD00301A	10.24	1.900e-09	116-126	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1254	PD00919F	11.63	5.107e-09	33-61	PD00919	CALCIUM-BINDING PRECURSOR SIGNAL R.
1254	PF00922A	19.17	4.951e-10	92-125	PF00922	Vesiculovirus phosphoprotein.
1254	PF00922A	19.17	5.966e-09	94-127	PF00922	Vesiculovirus phosphoprotein.
1254	PF00922A	19.17	6.690e-09	91-124	PF00922	Vesiculovirus phosphoprotein.
1254	PF00922A	19.17	9.561e-10	93-126	PF00922	Vesiculovirus phosphoprotein.
1255	PR00121B	7.83	9.250e-09	87-107	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1256	BL00406B	5.47	1.000e-40	72-126	BL00406	Actins proteins.
1256	PR00190A	7.24	1.375e-13	15-24	PR00190	ACTIN SIGNATURE
1256	PR00190B	9.98	1.000e-15	38-49	PR00190	ACTIN SIGNATURE
1256	PR00190C	11.49	1.474e-30	50-72	PR00190	ACTIN SIGNATURE
1256	PR00190D	19.23	1.450e-26	73-91	PR00190	ACTIN SIGNATURE
1256	PR00190E	7.16	1.450e-19	104-117	PR00190	ACTIN SIGNATURE
1258	BL00389A	11.02	7.188e-10	37-49	BL00389	ATP synthase delta (OSCP) subunit proteins.
1258	BL00389B	17.02	6.211e-13	107-128	BL00389	ATP synthase delta (OSCP) subunit proteins.
1258	BL00389C	20.13	6.760e-25	168-205	BL00389	ATP synthase delta (OSCP) subunit proteins.
1258	PR00125A	16.03	8.364e-15	37-56	PR00125	ATP SYNTHASE DELTA SUBUNIT SIGNATURE
1258	PR00125B	12.78	8.125e-10	106-117	PR00125	ATP SYNTHASE DELTA SUBUNIT SIGNATURE
1258	PR00125D	11.00	5.345e-11	169-184	PR00125	ATP SYNTHASE DELTA SUBUNIT SIGNATURE
1258	PR00125E	13.56	9.250e-16	184-202	PR00125	ATP SYNTHASE DELTA SUBUNIT SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1260	BL00678	9.67	1.947e-09	194-204	BL00678	Trp-Asp (WD) repeat proteins proteins.
1260	BL00678	9.67	9.053e-09	290-300	BL00678	Trp-Asp (WD) repeat proteins proteins.
1260	PR00320A	16.74	2.862e-11	288-302	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320A	16.74	2.976e-09	332-346	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320A	16.74	5.714e-13	192-206	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320B	12.19	1.783e-13	288-302	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320B	12.19	5.114e-10	192-206	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320C	13.01	1.783e-11	332-346	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320C	13.01	3.400e-09	192-206	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1260	PR00320C	13.01	9.640e-10	288-302	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1261	BL00678	9.67	7.158e-09	69-79	BL00678	Trp-Asp (WD) repeat proteins proteins.
1261	PR00320A	16.74	6.707e-09	203-217	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1261	PR00320A	16.74	9.122e-09	67-81	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1261	PR00320B	12.19	1.514e-10	67-81	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1261	PR00320C	13.01	2.500e-09	67-81	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1261	PR00320C	13.01	4.960e-10	203-217	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1262	BL00019A	12.56	3.475e-13	73-83	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019B	13.34	4.288e-10	2002-2024	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019B	13.34	9.135e-10	98-120	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019C	14.66	4.800e-30	146-181	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019D	15.33	2.623e-13	2465-2494	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019D	15.33	8.105e-09	210-239	BL00019	Actinin-type actin-binding domain proteins.
1262	BL00019F	19.68	6.609e-09	182-203	BL00019	Actinin-type actin-binding domain proteins.
1264	BL00514C	17.41	4.000e-29	59-95	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1264	BL00514D	15.35	7.511e-12	100-112	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1264	BL00514E	14.28	3.951e-10	119-135	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1264	BL00514G	15.98	2.268e-16	184-213	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1264	BL00514H	14.95	7.245e-15	217-241	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1265	BL00038B	16.97	4.273e-11	112-132	BL00038	Myc-type, 'helix-loop-helix' dimerization

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						domain proteins.
1266	BL00421A	11.79	3.864e-20	8-26	BL00421	Transmembrane 4 family proteins.
1266	BL00421B	17.62	5.737e-39	62-100	BL00421	Transmembrane 4 family proteins.
1266	BL00421C	12.89	3.667e-11	146-157	BL00421	Transmembrane 4 family proteins.
1266	BL00421E	20.97	4.115e-26	192-221	BL00421	Transmembrane 4 family proteins.
1266	BL00456C	24.55	7.223e-09	52-106	BL00456	Sodium:solute symporter family proteins.
1266	PD02680A	23.51	9.341e-10	60-110	PD02680	TRANSPORT GLUCONATE TRANSMEMBRANE PROTEIN PERMEA.
1266	PR00259A	9.27	2.241e-22	12-35	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1266	PR00259B	14.81	8.071e-28	56-82	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1266	PR00259C	16.40	2.688e-30	83-111	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1266	PR00259D	13.50	4.316e-26	195-221	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1268	BL00223A	15.59	4.783e-14	252-285	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223A	15.59	5.500e-21	93-126	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223A	15.59	5.500e-32	21-54	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223B	28.47	1.000e-40	162-211	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223C	24.79	1.000e-40	239-293	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223C	24.79	1.424e-14	80-134	BL00223	Annexins repeat proteins domain proteins.
1268	BL00223C	24.79	2.515e-10	8-62	BL00223	Annexins repeat proteins domain proteins.
1268	PR00196A	11.16	6.704e-10	102-124	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196A	11.16	9.100e-21	30-52	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196B	10.68	3.700e-17	70-86	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196C	10.36	2.174e-23	97-118	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196C	10.36	5.167e-15	25-46	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196C	10.36	7.344e-13	256-277	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196D	21.86	3.032e-24	180-206	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196E	9.19	1.118e-10	101-121	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196E	9.19	8.333e-23	260-280	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196F	13.89	2.714e-15	288-303	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196F	13.89	4.188e-09	129-144	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196G	11.72	3.000e-14	304-317	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00196G	11.72	9.217e-10	229-242	PR00196	ANNEXIN FAMILY SIGNATURE
1268	PR00197B	7.56	2.206e-	30-52	PR00197	ANNEXIN TYPE I

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			SIGNATURE
1268	PR00197D	7.50	1.250e-15	25-46	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00197D	7.50	1.542e-12	256-277	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00197D	7.50	1.844e-18	97-118	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00197E	11.89	8.463e-14	180-206	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00197F	9.03	5.250e-16	260-280	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00197F	9.03	7.894e-10	101-121	PR00197	ANNEXIN TYPE I SIGNATURE
1268	PR00198B	8.71	9.357e-10	30-52	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198C	14.32	6.718e-10	70-86	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198D	7.65	2.271e-13	256-277	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198D	7.65	8.333e-15	97-118	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198D	7.65	9.894e-13	25-46	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198E	14.67	6.381e-11	180-206	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198G	8.09	4.656e-09	101-121	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198G	8.09	7.943e-16	260-280	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00198H	12.05	1.462e-10	304-317	PR00198	ANNEXIN TYPE II SIGNATURE
1268	PR00199B	6.86	1.574e-13	30-52	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199B	6.86	8.313e-09	102-124	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199C	13.84	1.857e-09	70-86	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199D	5.65	3.443e-15	97-118	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199D	5.65	5.375e-14	25-46	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199D	5.65	7.987e-13	256-277	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199F	16.19	5.636e-16	180-206	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199G	9.09	6.365e-09	102-127	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199G	9.09	8.364e-21	261-286	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00199H	12.62	5.339e-12	304-317	PR00199	ANNEXIN TYPE III SIGNATURE
1268	PR00200A	4.93	2.125e-14	5-15	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200B	7.39	1.643e-29	30-52	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200C	8.76	1.500e-12	54-62	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200D	10.01	2.286e-22	70-86	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200E	10.00	1.110e-27	97-118	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200E	10.00	2.111e-14	25-46	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200E	10.00	2.859e-11	256-277	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200F	13.72	1.118e-35	180-206	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200G	9.43	1.000e-34	260-286	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200G	9.43	1.983e-	101-127	PR00200	ANNEXIN TYPE IV

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			SIGNATURE
1268	PR00200G	9.43	5.294e-11	29-55	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00200H	13.68	1.766e-18	304-317	PR00200	ANNEXIN TYPE IV SIGNATURE
1268	PR00201A	6.05	4.770e-16	30-52	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201C	11.13	9.316e-12	70-86	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201D	10.49	1.456e-15	97-118	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201D	10.49	6.179e-09	25-46	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201E	12.37	4.103e-15	180-206	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201G	11.02	8.402e-10	29-55	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201G	11.02	9.419e-26	260-286	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201G	11.02	9.912e-11	101-127	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00201H	12.04	4.375e-14	304-317	PR00201	ANNEXIN TYPE V SIGNATURE
1268	PR00202B	11.44	2.763e-11	29-52	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202C	13.34	3.800e-11	70-86	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202D	5.58	1.908e-09	25-46	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202D	5.58	3.224e-15	97-118	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202E	13.00	4.643e-16	180-206	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202G	8.01	4.833e-28	260-286	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202G	8.01	5.881e-09	101-127	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202G	8.01	9.237e-09	29-55	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00202H	9.20	4.740e-11	304-317	PR00202	ANNEXIN TYPE VI SIGNATURE
1268	PR00301D	15.51	7.395e-09	38-58	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1269	BL01179A	12.63	1.429e-11	209-220	BL01179	Phosphotyrosine interaction domain proteins (PID) profile.
1269	BL01179B	15.18	9.679e-11	400-414	BL01179	Phosphotyrosine interaction domain proteins (PID) profile.
1270	BL01033A	16.94	7.923e-18	25-46	BL01033	Globins profile.
1270	BL01033B	13.81	1.000e-15	93-104	BL01033	Globins profile.
1270	PR00612D	9.76	3.415e-10	80-93	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
1270	PR00814A	12.94	5.500e-22	30-46	PR00814	BETA HAEMOGLOBIN SIGNATURE
1270	PR00814B	9.18	3.250e-17	48-63	PR00814	BETA HAEMOGLOBIN SIGNATURE
1270	PR00814C	9.20	4.273e-16	72-89	PR00814	BETA HAEMOGLOBIN SIGNATURE
1270	PR00814D	15.25	2.286e-09	94-99	PR00814	BETA HAEMOGLOBIN SIGNATURE
1270	PR00814E	10.17	8.071e-19	128-144	PR00814	BETA HAEMOGLOBIN SIGNATURE
1273	BL00407A	18.57	8.500e-35	11-47	BL00407	Connexins proteins.
1273	BL00407B	14.23	1.000e-35	48-78	BL00407	Connexins proteins.
1273	BL00407C	14.61	6.850e-	79-106	BL00407	Connexins proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			31			
1273	BL00407D	17.61	5.091e-28	157-186	BL00407	Connexins proteins.
1273	BL00407E	22.17	1.000e-40	195-239	BL00407	Connexins proteins.
1273	PR00206A	11.35	9.053e-27	29-53	PR00206	CONNEXIN SIGNATURE
1273	PR00206B	13.75	7.882e-30	60-82	PR00206	CONNEXIN SIGNATURE
1273	PR00206C	15.16	3.842e-23	85-105	PR00206	CONNEXIN SIGNATURE
1273	PR00206D	16.57	4.429e-26	159-185	PR00206	CONNEXIN SIGNATURE
1273	PR00206E	15.09	1.857e-25	195-215	PR00206	CONNEXIN SIGNATURE
1273	PR00206F	16.77	6.571e-23	216-239	PR00206	CONNEXIN SIGNATURE
1274	BL00021B	13.33	3.786e-18	34-51	BL00021	Kringle domain proteins.
1274	BL00021D	24.56	4.759e-11	190-231	BL00021	Kringle domain proteins.
1274	BL00134A	11.96	9.609e-18	34-50	BL00134	Serine proteases, trypsin family, histidine proteins.
1274	BL00134B	15.99	5.714e-19	185-208	BL00134	Serine proteases, trypsin family, histidine proteins.
1274	BL00134C	13.45	4.750e-12	218-231	BL00134	Serine proteases, trypsin family, histidine proteins.
1274	BL00495K	12.58	3.796e-09	36-68	BL00495	Apple domain proteins.
1274	BL01253D	4.84	9.855e-12	34-47	BL01253	Type I fibronectin domain proteins.
1274	BL01253G	11.34	7.972e-14	184-197	BL01253	Type I fibronectin domain proteins.
1274	BL01253H	13.15	7.680e-12	200-234	BL01253	Type I fibronectin domain proteins.
1274	PR00722A	12.27	6.087e-16	35-50	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1274	PR00722C	10.87	5.500e-15	184-196	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1276	PD01876C	21.73	8.529e-11	461-513	PD01876	ANTIGEN MELANOMA-ASSOCIATED MULTIGENE FAMILY TUM.
1276	PR00411A	15.95	4.724e-09	749-771	PR00411	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-I SIGNATURE
1279	BL01310	14.74	1.321e-36	28-63	BL01310	ATP1G1 / PLM / MAT8 family proteins.
1281	BL00296B	15.98	6.625e-09	83-136	BL00296	Chaperonins cpn60 proteins.
1281	BL00750A	20.07	1.310e-30	32-74	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750B	16.17	7.517e-37	76-125	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750C	25.65	2.909e-15	157-188	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750D	16.16	9.719e-11	206-224	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750E	24.59	2.406e-21	296-332	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750F	18.40	4.938e-25	371-411	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750G	20.12	2.324e-28	432-471	BL00750	Chaperonins TCP-1 proteins.
1281	BL00750H	21.44	2.875e-25	491-525	BL00750	Chaperonins TCP-1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1281	PR00304A	9.20	5.737e-15	41-57	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1281	PR00304B	11.60	9.700e-18	63-81	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1281	PR00304C	8.69	2.575e-17	93-112	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1281	PR00304D	11.04	4.405e-17	374-396	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1281	PR00304E	7.79	9.217e-13	408-420	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1282	BL00194	12.16	3.813e-15	47-59	BL00194	Thioredoxin family proteins.
1282	BL00194	12.16	4.857e-16	182-194	BL00194	Thioredoxin family proteins.
1282	PR00421A	10.15	4.000e-10	46-54	PR00421	THIOREDOXIN FAMILY SIGNATURE
1282	PR00421A	10.15	4.857e-10	181-189	PR00421	THIOREDOXIN FAMILY SIGNATURE
1282	PR00421B	11.40	3.348e-12	189-198	PR00421	THIOREDOXIN FAMILY SIGNATURE
1282	PR00421B	11.40	9.379e-11	54-63	PR00421	THIOREDOXIN FAMILY SIGNATURE
1282	PR00421C	13.60	5.714e-10	233-244	PR00421	THIOREDOXIN FAMILY SIGNATURE
1283	BL00142	8.38	6.625e-10	559-569	BL00142	Neutral zinc metallopeptidases, zinc-binding region proteins.
1283	PF00084B	9.45	5.500e-09	1370-1381	PF00084	Sushi domain proteins (SCR repeat proteins.
1283	PR00014A	8.22	8.773e-09	687-696	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1283	PR00480B	15.41	2.286e-09	554-572	PR00480	ASTACIN FAMILY SIGNATURE
1284	BL00299	28.84	4.188e-19	92-143	BL00299	Ubiquitin domain proteins.
1285	BL00036	9.02	4.214e-13	197-209	BL00036	bZIP transcription factors basic domain proteins.
1285	PR00042A	10.04	2.500e-22	113-130	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1285	PR00042B	10.70	1.191e-21	181-197	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1285	PR00042C	8.29	1.273e-22	198-214	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1285	PR00042D	8.97	2.500e-27	216-237	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1285	PR00042E	9.69	8.200e-29	237-260	PR00042	FOS TRANSFORMING PROTEIN SIGNATURE
1285	PR00043B	8.73	5.652e-09	197-213	PR00043	JUN TRANSCRIPTION FACTOR SIGNATURE
1286	BL00297A	17.58	4.375e-37	31-67	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297B	22.91	4.316e-38	71-119	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297C	9.51	1.000e-40	160-211	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297D	11.95	1.000e-40	220-259	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297E	18.56	6.400e-35	316-359	BL00297	Heat shock hsp70 proteins family

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1286	BL00297F	11.84	1.692e-30	380-407	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297G	21.87	1.000e-40	412-466	BL00297	Heat shock hsp70 proteins family proteins.
1286	BL00297H	15.46	1.000e-40	475-528	BL00297	Heat shock hsp70 proteins family proteins.
1286	PR00301A	14.84	5.846e-17	29-42	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301B	15.36	3.118e-16	57-69	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301D	15.51	2.227e-26	168-188	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301E	8.11	4.789e-13	228-238	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301F	13.98	1.857e-19	355-371	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301G	13.78	1.000e-25	387-407	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301H	8.81	5.909e-20	412-431	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1286	PR00301I	12.76	5.500e-18	493-509	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1287	BL00194	12.16	3.813e-15	398-410	BL00194	Thioredoxin family proteins.
1287	BL00194	12.16	5.091e-17	49-61	BL00194	Thioredoxin family proteins.
1287	PR00421A	10.15	1.429e-10	397-405	PR00421	THIOREDOXIN FAMILY SIGNATURE
1287	PR00421A	10.15	3.160e-09	48-56	PR00421	THIOREDOXIN FAMILY SIGNATURE
1287	PR00421B	11.40	1.000e-13	56-65	PR00421	THIOREDOXIN FAMILY SIGNATURE
1287	PR00421B	11.40	3.348e-12	405-414	PR00421	THIOREDOXIN FAMILY SIGNATURE
1287	PR00421C	13.60	5.286e-10	446-457	PR00421	THIOREDOXIN FAMILY SIGNATURE
1287	PR00421C	13.60	5.500e-09	96-107	PR00421	THIOREDOXIN FAMILY SIGNATURE
1288	BL00251A	14.27	1.383e-10	121-138	BL00251	TNF family proteins.
1288	BL00251B	11.40	5.200e-17	171-190	BL00251	TNF family proteins.
1288	BL00251C	13.97	5.250e-14	238-256	BL00251	TNF family proteins.
1288	BL00251D	12.03	1.529e-09	269-280	BL00251	TNF family proteins.
1289	BL00387A	14.69	3.423e-14	44-58	BL00387	Inorganic pyrophosphatase proteins.
1289	BL00387B	27.02	4.103e-31	72-109	BL00387	Inorganic pyrophosphatase proteins.
1289	BL00387C	20.60	1.310e-24	133-163	BL00387	Inorganic pyrophosphatase proteins.
1289	BL00387D	21.31	6.786e-23	167-199	BL00387	Inorganic pyrophosphatase proteins.
1290	BL00115Z	3.12	7.022e-09	255-303	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1290	BL00478B	14.79	3.500e-12	405-419	BL00478	LIM domain proteins.
1290	BL00478B	14.79	3.739e-14	463-477	BL00478	LIM domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1290	BL00478B	14.79	6.000e-12	530-544	BL00478	LIM domain proteins.
1290	DM00984B	15.18	4.822e-25	420-474	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.
1290	DM00984C	7.66	8.036e-11	475-488	DM00984	w MYOD MYOBLAST DETERMINATION SHORT.
1292	BL00470A	16.25	6.077e-11	57-77	BL00470	Isocitrate and isopropylmalate dehydrogenases proteins.
1292	BL00470C	15.43	4.375e-11	162-176	BL00470	Isocitrate and isopropylmalate dehydrogenases proteins.
1292	BL00470D	21.75	8.500e-13	269-299	BL00470	Isocitrate and isopropylmalate dehydrogenases proteins.
1293	BL00325A	24.83	2.125e-26	61-92	BL00325	Actin-depolymerizing proteins.
1293	BL00325B	21.66	1.000e-40	93-138	BL00325	Actin-depolymerizing proteins.
1293	PR00006A	13.46	2.000e-31	17-41	PR00006	COFILIN/DESTRIN FAMILY SIGNATURE
1293	PR00006B	4.38	1.391e-27	79-99	PR00006	COFILIN/DESTRIN FAMILY SIGNATURE
1293	PR00006C	9.30	1.500e-28	100-121	PR00006	COFILIN/DESTRIN FAMILY SIGNATURE
1293	PR00006D	14.99	9.750e-21	122-138	PR00006	COFILIN/DESTRIN FAMILY SIGNATURE
1293	PR00006E	9.61	1.462e-14	153-165	PR00006	COFILIN/DESTRIN FAMILY SIGNATURE
1294	BL00183	28.97	6.586e-33	50-97	BL00183	Ubiquitin-conjugating enzymes proteins.
1295	BL00113A	12.74	7.508e-09	8-24	BL00113	Adenylate kinase proteins.
1295	BL00211A	12.23	1.000e-09	9-20	BL00211	ABC transporters family proteins.
1295	BL00567A	10.66	8.714e-09	6-24	BL00567	Phosphoribulokinase proteins.
1295	BL00674B	4.46	9.392e-09	4-25	BL00674	AAA-protein family proteins.
1295	BL00856A	17.25	4.176e-11	8-20	BL00856	Guanylate kinase proteins.
1295	BL00856B	9.61	2.565e-22	36-56	BL00856	Guanylate kinase proteins.
1295	BL00856C	29.21	1.409e-38	64-111	BL00856	Guanylate kinase proteins.
1295	PR00449A	13.20	3.596e-10	5-26	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1297	BL00291A	4.49	3.586e-09	55-89	BL00291	Prion protein.
1297	BL00309A	19.16	5.065e-16	125-149	BL00309	Vertebrate galactoside-binding lectin proteins.
1297	BL00309B	12.11	4.500e-16	150-164	BL00309	Vertebrate galactoside-binding lectin proteins.
1297	BL00309C	18.65	1.000e-22	171-195	BL00309	Vertebrate galactoside-binding lectin proteins.
1297	BL00604F	5.96	4.709e-09	23-67	BL00604	Synaptophysin / synaptoporin proteins.
1297	DM00250B	13.84	3.593e-12	40-63	DM00250	kw ANNEXIN ANTIGEN PROLINE TUMOR.
1300	BL01113A	17.99	5.091e-11	94-120	BL01113	Clq domain proteins.
1303	BL00019A	12.56	3.475e-13	45-55	BL00019	Actinin-type actin-binding domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1303	BL00019B	13.34	8.096e-10	70-92	BL00019	Actinin-type actin-binding domain proteins.
1303	BL00019B	13.34	8.548e-16	1992-2014	BL00019	Actinin-type actin-binding domain proteins.
1303	BL00019C	14.66	5.171e-32	118-153	BL00019	Actinin-type actin-binding domain proteins.
1303	BL00019D	15.33	2.703e-23	2455-2484	BL00019	Actinin-type actin-binding domain proteins.
1303	BL00019F	19.68	3.195e-15	154-175	BL00019	Actinin-type actin-binding domain proteins.
1303	PR00401C	13.16	1.750e-09	1717-1728	PR00401	SH2 DOMAIN SIGNATURE
1306	BL01239	16.10	1.000e-40	17-70	BL01239	Dynein light chain type 1 proteins.
1307	BL00463	8.22	5.071e-09	125-136	BL00463	Fungal Zn(2)-Cys(6) binuclear cluster domain proteins.
1309	BL01207A	12.21	9.069e-18	66-81	BL01207	Glypicans proteins.
1309	BL01207B	23.69	3.423e-37	193-238	BL01207	Glypicans proteins.
1309	BL01207C	19.08	9.308e-39	252-287	BL01207	Glypicans proteins.
1309	BL01207D	23.23	5.655e-29	423-457	BL01207	Glypicans proteins.
1309	BL01207E	13.70	7.375e-16	496-512	BL01207	Glypicans proteins.
1310	BL00142	8.38	1.857e-09	210-220	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
1310	BL01177C	17.39	5.333e-11	712-730	BL01177	Anaphylatoxin domain proteins.
1310	BL01180A	15.41	4.130e-11	220-231	BL01180	CUB domain proteins profile.
1310	BL01180B	11.58	3.647e-11	488-498	BL01180	CUB domain proteins profile.
1310	BL01180B	11.58	4.000e-09	644-654	BL01180	CUB domain proteins profile.
1310	BL01180B	11.58	4.750e-09	800-810	BL01180	CUB domain proteins profile.
1310	BL01180B	11.58	6.625e-09	917-927	BL01180	CUB domain proteins profile.
1310	BL01180B	11.58	8.364e-13	375-385	BL01180	CUB domain proteins profile.
1310	BL01180C	17.69	1.000e-10	394-407	BL01180	CUB domain proteins profile.
1310	BL01180C	17.69	4.500e-09	936-949	BL01180	CUB domain proteins profile.
1310	BL01180C	17.69	8.000e-09	663-676	BL01180	CUB domain proteins profile.
1310	BL01187B	12.04	2.174e-13	718-733	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1310	BL01187B	12.04	6.250e-17	563-578	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1310	PR00010C	11.16	4.273e-10	723-733	PR00010	TYPE II EGF-LIKE SIGNATURE
1310	PR00480A	19.40	3.250e-17	151-169	PR00480	ASTACIN FAMILY SIGNATURE
1310	PR00480B	15.41	9.143e-21	205-223	PR00480	ASTACIN FAMILY SIGNATURE
1310	PR00480C	12.53	1.300e-17	224-241	PR00480	ASTACIN FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1310	PR00480D	14.26	7.545e-17	263-278	PR00480	ASTACIN FAMILY SIGNATURE
1310	PR00480E	14.96	6.727e-12	305-318	PR00480	ASTACIN FAMILY SIGNATURE
1311	BL00892A	18.17	8.412e-30	27-57	BL00892	HIT family proteins.
1311	BL00892B	16.86	1.964e-22	93-116	BL00892	HIT family proteins.
1311	PR00332A	10.15	9.625e-18	18-34	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE
1311	PR00332B	13.62	1.000e-23	39-57	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE
1311	PR00332C	7.37	2.200e-13	106-116	PR00332	HISTIDINE TRIAD FAMILY SIGNATURE
1312	BL00854A	33.93	9.036e-29	64-109	BL00854	Proteasome B-type subunits proteins.
1312	BL00854C	29.92	1.794e-14	171-199	BL00854	Proteasome B-type subunits proteins.
1312	BL00854D	13.76	2.800e-09	222-231	BL00854	Proteasome B-type subunits proteins.
1312	PR00141A	11.36	3.613e-17	67-82	PR00141	PROTEASOME COMPONENT SIGNATURE
1312	PR00141B	11.15	5.304e-14	188-199	PR00141	PROTEASOME COMPONENT SIGNATURE
1312	PR00141C	11.15	3.368e-10	199-210	PR00141	PROTEASOME COMPONENT SIGNATURE
1312	PR00141D	12.45	1.923e-12	224-235	PR00141	PROTEASOME COMPONENT SIGNATURE
1313	BL00226A	12.77	1.360e-14	71-85	BL00226	Intermediate filaments proteins.
1313	BL00226B	23.86	7.545e-17	171-218	BL00226	Intermediate filaments proteins.
1313	BL00226C	13.23	5.800e-13	236-266	BL00226	Intermediate filaments proteins.
1313	BL00226D	19.10	1.500e-30	336-382	BL00226	Intermediate filaments proteins.
1314	DM01753B	6.47	1.247e-09	276-285	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.
1314	DM01753B	6.47	1.750e-13	538-547	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.
1314	DM01753B	6.47	8.767e-09	139-148	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.
1314	DM01753C	17.64	1.735e-09	199-237	DM01753	6 kw OSTEOLAST MAJOR IMMUNOGENIC MPB70.
1315	BL00046	12.95	1.000e-40	36-90	BL00046	Histone H2A proteins.
1315	PD01672F	8.62	7.029e-09	35-68	PD01672	+ TRANSPORT EXCHANGER NA H TRANS.
1315	PR00620A	11.03	1.429e-24	16-38	PR00620	HISTONE H2A SIGNATURE
1315	PR00620B	8.47	8.909e-17	46-61	PR00620	HISTONE H2A SIGNATURE
1315	PR00620C	10.19	2.862e-15	61-74	PR00620	HISTONE H2A SIGNATURE
1315	PR00620D	11.39	3.172e-15	75-89	PR00620	HISTONE H2A SIGNATURE
1315	PR00620E	8.91	3.025e-12	89-101	PR00620	HISTONE H2A SIGNATURE
1315	PR00620F	7.29	6.226e-16	102-120	PR00620	HISTONE H2A SIGNATURE
1317	BL00188	30.29	9.036e-32	640-685	BL00188	Biotin-requiring enzymes attachment site proteins.
1317	BL00189A	19.58	5.279e-12	651-685	BL00189	2-oxo acid dehydrogenases acyltransferase component lipoyl bi.
1317	BL00866B	36.29	2.286e-31	234-279	BL00866	Carbamoyl-phosphate synthase subdomain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1317	BL00866C	23.26	1.621e-18	320-354	BL00866	Carbamoyl-phosphate synthase subdomain proteins.
1317	BL00866C	23.26	5.034e-18	9-43	BL00866	Carbamoyl-phosphate synthase subdomain proteins.
1317	PD00187	10.12	3.118e-15	188-203	PD00187	LIGASE BIOSYNTHESIS SYNTHETASE.
1318	BL00226B	23.86	6.128e-09	77-124	BL00226	Intermediate filaments proteins.
1318	BL00326D	8.76	1.000e-40	62-102	BL00326	Tropomyosins proteins.
1318	BL00326D	8.76	7.729e-09	6-46	BL00326	Tropomyosins proteins.
1318	PR00194D	9.57	1.300e-23	17-40	PR00194	TROPOMYOSIN SIGNATURE
1318	PR00194E	8.74	3.250e-30	73-98	PR00194	TROPOMYOSIN SIGNATURE
1323	PD01485A	12.50	7.250e-10	129-141	PD01485	INITIATION FACTOR PROTEIN TRANSLATION BIO.
1323	PD01485B	23.41	1.333e-37	211-251	PD01485	INITIATION FACTOR PROTEIN TRANSLATION BIO.
1323	PD01485C	20.40	4.600e-36	257-291	PD01485	INITIATION FACTOR PROTEIN TRANSLATION BIO.
1325	PR00308A	5.90	6.918e-11	45-59	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
1325	PR00308C	3.83	7.312e-09	48-57	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE
1325	PR00456E	3.06	9.316e-09	41-55	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE
1326	BL00464A	29.41	9.700e-23	17-53	BL00464	Ribosomal protein L22 proteins.
1326	BL00464B	28.48	4.960e-35	106-150	BL00464	Ribosomal protein L22 proteins.
1328	BL00854A	33.93	4.405e-24	48-93	BL00854	Proteasome B-type subunits proteins.
1328	BL00854C	29.92	5.615e-12	154-182	BL00854	Proteasome B-type subunits proteins.
1328	PR00141A	11.36	8.800e-11	51-66	PR00141	PROTEASOME COMPONENT SIGNATURE
1329	BL00509A	14.33	3.400e-12	520-530	BL00509	Ras GTPase-activating proteins.
1329	BL00509B	10.28	4.960e-11	771-781	BL00509	Ras GTPase-activating proteins.
1329	PF00168C	27.49	7.375e-09	653-678	PF00168	C2 domain proteins.
1329	PR00401A	14.00	7.075e-09	20-34	PR00401	SH2 DOMAIN SIGNATURE
1329	PR00401E	14.10	5.235e-09	84-98	PR00401	SH2 DOMAIN SIGNATURE
1330	BL00113A	12.74	8.338e-09	223-239	BL00113	Adenylate kinase proteins.
1330	BL00674A	16.91	2.636e-17	184-204	BL00674	AAA-protein family proteins.
1330	BL00674B	4.46	6.294e-25	219-240	BL00674	AAA-protein family proteins.
1330	BL00674C	22.60	3.077e-35	252-294	BL00674	AAA-protein family proteins.
1330	BL00674D	23.41	1.000e-40	311-357	BL00674	AAA-protein family proteins.
1330	BL00674E	15.24	9.143e-17	389-408	BL00674	AAA-protein family proteins.
1330	BL00675A	24.86	4.488e-09	222-265	BL00675	Sigma-54 interaction domain proteins ATP-binding region A proteins.
1330	PR00300A	9.56	3.318e-	222-240	PR00300	ATP-DEPENDENT CLP

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			PROTEASE ATP-BINDING SUBUNIT SIGNATURE
1330	PR00819B	10.83	9.100e-10	221-236	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE
1330	PR00830A	8.41	9.018e-13	226-245	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE
1330	PR00918A	13.76	7.181e-10	216-236	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE
1331	BL00284A	15.64	8.714e-16	77-100	BL00284	Serpins proteins.
1331	BL00284B	17.99	8.091e-12	176-196	BL00284	Serpins proteins.
1331	BL00284C	28.56	3.700e-26	203-244	BL00284	Serpins proteins.
1331	BL00284D	16.34	7.279e-12	312-338	BL00284	Serpins proteins.
1331	BL00284E	19.15	1.333e-17	391-415	BL00284	Serpins proteins.
1332	BL00250A	21.24	6.000e-15	211-246	BL00250	TGF-beta family proteins.
1332	BL00250B	27.37	1.305e-09	272-307	BL00250	TGF-beta family proteins.
1339	BL00831A	16.12	5.598e-09	32-60	BL00831	Ribosomal protein L27 proteins.
1339	BL00831B	21.15	6.348e-19	61-100	BL00831	Ribosomal protein L27 proteins.
1339	PR00063A	11.71	1.614e-09	34-58	PR00063	RIBOSOMAL PROTEIN L27 SIGNATURE
1339	PR00063B	15.24	9.700e-11	59-83	PR00063	RIBOSOMAL PROTEIN L27 SIGNATURE
1342	BL00652A	3.16	4.000e-09	22-28	BL00652	TNFR/NGFR family cysteine-rich region proteins.
1342	PF00084B	9.45	4.375e-10	122-133	PF00084	Sushi domain proteins (SCR repeat proteins.
1342	PF00084C	11.25	3.571e-10	274-283	PF00084	Sushi domain proteins (SCR repeat proteins.
1349	BL00113A	12.74	9.031e-09	187-203	BL00113	Adenylate kinase proteins.
1349	BL00516B	29.10	1.000e-08	314-356	BL00516	Alkylbase DNA glycosidases alka family proteins.
1349	BL00674A	16.91	7.000e-15	148-168	BL00674	AAA-protein family proteins.
1349	BL00674B	4.46	4.000e-27	183-204	BL00674	AAA-protein family proteins.
1349	BL00674C	22.60	4.273e-38	216-258	BL00674	AAA-protein family proteins.
1349	BL00674D	23.41	6.500e-39	275-321	BL00674	AAA-protein family proteins.
1349	BL00674E	15.24	6.478e-16	353-372	BL00674	AAA-protein family proteins.
1349	BL00675A	24.86	8.538e-09	186-229	BL00675	Sigma-54 interaction domain proteins ATP-binding region A proteins.
1349	PR00300A	9.56	4.409e-11	186-204	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE
1349	PR00819B	10.83	1.318e-09	185-200	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE
1349	PR00830A	8.41	5.810e-12	190-209	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE
1349	PR00918A	13.76	5.988e-10	180-200	PR00918	CALICIVIRUS NON-STRUCTURAL POLYPROTEIN FAMILY SIGNATURE
1352	BL00904A	8.30	9.936e-	320-369	BL00904	Protein

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			prenyltransferases alpha subunit repeat proteins proteins.
1352	DM00215	19.43	6.464e-10	304-336	DM00215	PROLINE-RICH PROTEIN.3.
1353	BL00674A	16.91	5.500e-13	174-194	BL00674	AAA-protein family proteins.
1353	BL00674A	16.91	5.696e-09	1-21	BL00674	AAA-protein family proteins.
1353	BL00674B	4.46	6.500e-24	209-230	BL00674	AAA-protein family proteins.
1353	BL00674C	22.60	5.846e-35	242-284	BL00674	AAA-protein family proteins.
1353	BL00674D	23.41	1.000e-40	301-347	BL00674	AAA-protein family proteins.
1353	BL00674E	15.24	8.826e-16	379-398	BL00674	AAA-protein family proteins.
1353	BL00675A	24.86	5.613e-09	212-255	BL00675	Sigma-54 interaction domain proteins ATP-binding region A proteins.
1353	PR00300A	9.56	1.887e-10	212-230	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE
1353	PR00819B	10.83	1.529e-09	211-226	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE
1353	PR00830A	8.41	2.714e-11	216-235	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE
1353	PR00887F	12.74	7.889e-09	267-284	PR00887	STRUCTURE-SPECIFIC RECOGNITION PROTEIN SIGNATURE
1354	BL00678	9.67	1.000e-08	233-243	BL00678	Trp-Asp (WD) repeat proteins proteins.
1354	BL00678	9.67	7.158e-09	184-194	BL00678	Trp-Asp (WD) repeat proteins proteins.
1354	PR00320A	16.74	2.853e-10	74-88	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320A	16.74	4.706e-10	28-42	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320A	16.74	6.049e-09	231-245	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320B	12.19	8.875e-09	182-196	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320C	13.01	5.320e-10	74-88	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320C	13.01	5.680e-10	28-42	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1354	PR00320C	13.01	9.500e-12	182-196	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1357	BL00115Z	3.12	8.412e-09	172-220	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1357	BL00412C	10.28	6.932e-09	183-216	BL00412	Neuromodulin (GAP-43) proteins.
1362	BL01145A	13.73	1.000e-40	3-44	BL01145	Ribosomal protein L34e proteins.
1362	BL01145B	14.65	2.636e-20	88-110	BL01145	Ribosomal protein L34e proteins.
1363	PR00058A	16.66	1.375e-26	20-39	PR00058	RIBOSOMAL PROTEIN L5 SIGNATURE
1363	PR00058B	8.75	1.529e-27	43-62	PR00058	RIBOSOMAL PROTEIN L5 SIGNATURE
1365	BL00112A	22.23	1.000e-40	94-135	BL00112	ATP:guanido phosphotransferases proteins.
1365	BL00112B	15.87	9.217e-31	155-186	BL00112	ATP:guanido phosphotransferases proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1365	BL00112C	21.77	1.000e-40	187-240	BL00112	ATP:guanido phosphotransferases proteins.
1365	BL00112D	12.22	1.000e-40	242-286	BL00112	ATP:guanido phosphotransferases proteins.
1365	BL00112E	17.75	3.455e-37	304-333	BL00112	ATP:guanido phosphotransferases proteins.
1365	BL00112F	21.37	1.000e-40	350-400	BL00112	ATP:guanido phosphotransferases proteins.
1366	PR00800A	15.23	9.565e-09	99-118	PR00800	AROMATIC-L-AMINO-ACID DECARBOXYLASE SIGNATURE
1367	BL00213A	12.95	9.526e-10	37-50	BL00213	Lipocalin proteins.
1367	BL00213B	8.78	8.000e-10	120-130	BL00213	Lipocalin proteins.
1367	PR00179A	13.78	5.680e-10	37-49	PR00179	LIPOCALIN SIGNATURE
1367	PR00179B	9.56	1.000e-12	120-132	PR00179	LIPOCALIN SIGNATURE
1367	PR00179C	19.02	1.000e-10	148-163	PR00179	LIPOCALIN SIGNATURE
1369	PR00050A	11.28	5.865e-09	65-80	PR00050	COLD SHOCK PROTEIN SIGNATURE
1370	PR00456F	5.86	6.400e-12	101-112	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE
1371	BL00194	12.16	9.438e-15	24-36	BL00194	Thioredoxin family proteins.
1371	PR00421A	10.15	2.286e-10	23-31	PR00421	THIOREDOXIN FAMILY SIGNATURE
1371	PR00421B	11.40	6.625e-13	31-40	PR00421	THIOREDOXIN FAMILY SIGNATURE
1371	PR00421C	13.60	8.615e-12	70-81	PR00421	THIOREDOXIN FAMILY SIGNATURE
1372	BL00478B	14.79	3.348e-14	157-171	BL00478	LIM domain proteins.
1372	BL00478B	14.79	4.913e-14	48-62	BL00478	LIM domain proteins.
1374	BL00030B	7.03	8.105e-09	50-59	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1377	BL00154A	11.86	5.500e-16	188-205	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154B	15.44	2.800e-31	332-368	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154C	12.38	6.000e-23	370-388	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154D	12.57	3.769e-13	508-518	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154E	20.37	8.615e-38	593-633	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154F	8.23	3.813e-27	712-735	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL00154G	21.18	9.526e-30	738-771	BL00154	E1-E2 ATPases phosphorylation site proteins.
1377	BL01047B	19.73	8.000e-09	721-741	BL01047	Heavy-metal-associated domain proteins.
1377	BL01228D	17.44	3.684e-12	713-737	BL01228	Hypothetical cof family proteins.
1377	PR00119A	17.34	3.000e-15	214-228	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1377	PR00119B	13.94	2.800e-20	374-388	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
1377	PR00119C	11.01	4.500e-12	587-598	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
1377	PR00119D	9.56	3.571e-13	609-619	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
1377	PR00119E	8.48	5.200e-24	715-734	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
1377	PR00119F	11.81	7.750e-13	739-751	PR00119	P-TYPE CATION-TRANSPORTING ATPASE SUPERFAMILY SIGNATURE
1377	PR00120C	9.90	5.800e-19	715-731	PR00120	H+-TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE
1377	PR00121A	6.71	9.053e-18	103-117	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121B	7.83	4.214e-26	130-150	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121C	9.40	1.000e-24	294-316	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121D	16.72	1.209e-28	367-388	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121E	13.97	4.667e-23	505-523	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121F	6.70	7.750e-27	787-808	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121G	6.89	8.875e-26	854-874	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121H	12.14	5.950e-26	916-936	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1377	PR00121I	15.47	8.500e-28	950-974	PR00121	SODIUM/POTASSIUM-TRANSPORTING ATPASE SIGNATURE
1379	PR00833H	2.30	6.423e-09	329-343	PR00833	POLLEN ALLERGEN POA PI SIGNATURE
1381	BL00478B	14.79	2.800e-11	279-293	BL00478	LIM domain proteins.
1382	BL01294A	5.15	1.571e-09	23-34	BL01294	Uncharacterized protein family UPF0038 proteins.
1382	PR00988A	6.39	8.500e-17	20-37	PR00988	URIDINE KINASE SIGNATURE
1382	PR00988B	11.60	2.915e-09	57-68	PR00988	URIDINE KINASE SIGNATURE
1382	PR00988C	13.64	6.108e-14	104-119	PR00988	URIDINE KINASE SIGNATURE
1382	PR00988D	5.95	6.878e-10	160-170	PR00988	URIDINE KINASE SIGNATURE
1382	PR00988E	8.27	3.872e-11	174-185	PR00988	URIDINE KINASE SIGNATURE
1382	PR00988F	12.23	7.828e-15	196-209	PR00988	URIDINE KINASE SIGNATURE
1383	BL01115A	10.22	2.768e-10	60-103	BL01115	GTP-binding nuclear protein ran proteins.
1383	BL01215A	9.75	3.968e-09	57-83	BL01215	Mrp family proteins.
1383	PR00449A	13.20	4.706e-19	60-81	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1383	PR00449B	14.34	7.000e-	83-99	PR00449	TRANSFORMING PROTEIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			15			P21 RAS SIGNATURE
1383	PR00449C	17.27	8.579e-18	100-122	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1383	PR00449D	10.79	3.769e-16	163-176	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1383	PR00449E	13.50	1.450e-16	199-221	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1384	PR00495A	9.18	3.700e-25	27-45	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495B	10.99	1.099e-24	47-65	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495C	10.22	7.492e-26	74-94	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495D	11.96	3.571e-24	97-115	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495E	13.09	5.114e-26	118-138	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495F	7.55	3.492e-24	147-167	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1384	PR00495G	6.74	1.529e-21	168-183	PR00495	OBESITY FACTOR (LEPTIN) SIGNATURE
1386	BL00039A	18.44	4.600e-30	57-95	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1386	BL00039B	19.19	2.200e-20	97-122	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1386	BL00039C	15.63	2.500e-21	181-204	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1386	BL00039D	21.67	1.000e-40	330-375	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1386	DM01537B	21.63	1.786e-11	304-350	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.
1386	PF00271	7.99	1.000e-08	361-368	PF00271	Helicases conserved C-terminal domain proteins.
1388	PD00078B	13.14	7.600e-12	141-153	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.
1388	PF00023A	16.03	1.750e-10	187-202	PF00023	Ank repeat proteins.
1388	PF00023A	16.03	3.250e-09	148-163	PF00023	Ank repeat proteins.
1388	PF00023B	14.20	9.100e-12	144-153	PF00023	Ank repeat proteins.
1390	BL00492D	13.23	5.865e-09	315-351	BL00492	Clusterin proteins.
1390	PR00497A	6.92	5.553e-10	554-571	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE
1391	BL01118A	12.46	4.000e-13	36-50	BL01118	Translation initiation factor SUI1 proteins.
1391	BL01118B	26.75	9.308e-33	53-90	BL01118	Translation initiation factor SUI1 proteins.
1395	PF00429	31.08	7.300e-15	383-432	PF00429	ENV polyprotein (coat polyprotein).
1395	PR00415D	12.72	8.403e-09	328-343	PR00415	ACONITASE FAMILY SIGNATURE
1395	PR00783F	12.33	3.700e-09	446-466	PR00783	MAJOR INTRINSIC PROTEIN FAMILY SIGNATURE
1396	DM01022C	19.84	3.571e-09	103-122	DM01022	LRR REPEAT.
1396	PR00019A	11.19	2.565e-10	131-144	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1396	PR00019B	11.36	4.000e-11	268-281	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1396	PR00019B	11.36	4.600e-10	220-233	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1396	PR00019B	11.36	7.840e-09	128-141	PR00019	LEUCINE-RICH REPEAT SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1397	BL00299	28.84	1.000e-40	16-67	BL00299	Ubiquitin domain proteins.
1397	PD01457A	16.51	1.000e-40	77-121	PD01457	RIBOSOMAL PROTEIN 40S ZINC-FINGER METAL.
1397	PD01457B	13.00	1.000e-31	124-148	PD01457	RIBOSOMAL PROTEIN 40S ZINC-FINGER METAL.
1397	PR00348A	7.86	2.000e-26	11-31	PR00348	UBIQUITIN SIGNATURE
1397	PR00348B	5.78	2.800e-27	32-52	PR00348	UBIQUITIN SIGNATURE
1397	PR00348C	20.03	1.643e-27	53-74	PR00348	UBIQUITIN SIGNATURE
1398	BL00280	24.61	3.000e-29	165-208	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1398	BL00280	24.61	4.857e-34	43-86	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1398	BL00280	24.61	5.215e-10	104-147	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1398	PR00759A	14.51	3.045e-11	33-47	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1398	PR00759A	14.51	7.900e-09	155-169	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1398	PR00759B	11.26	1.231e-09	183-193	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1398	PR00759B	11.26	1.290e-10	61-71	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1398	PR00759C	14.15	3.483e-13	193-208	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1398	PR00759C	14.15	5.636e-12	71-86	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1399	BL00388A	23.14	5.875e-40	5-50	BL00388	Proteasome A-type subunits proteins.
1399	BL00388B	31.38	6.538e-29	64-105	BL00388	Proteasome A-type subunits proteins.
1399	BL00388C	18.79	2.000e-22	119-140	BL00388	Proteasome A-type subunits proteins.
1399	BL00388D	20.71	1.391e-26	147-177	BL00388	Proteasome A-type subunits proteins.
1399	BL00854A	33.93	9.000e-11	36-81	BL00854	Proteasome B-type subunits proteins.
1399	PF00227	14.68	5.950e-09	12-23	PF00227	Proteasome A-type and B-type.
1401	BL00113A	12.74	9.031e-09	171-187	BL00113	Adenylate kinase proteins.
1401	BL00674A	16.91	4.857e-14	132-152	BL00674	AAA-protein family proteins.
1401	BL00674B	4.46	5.235e-25	167-188	BL00674	AAA-protein family proteins.
1401	BL00674C	22.60	9.308e-35	200-242	BL00674	AAA-protein family proteins.
1401	BL00674D	23.41	4.176e-40	259-305	BL00674	AAA-protein family proteins.
1401	BL00674E	15.24	8.200e-20	337-356	BL00674	AAA-protein family proteins.
1401	PR00051A	10.68	8.382e-09	167-187	PR00051	BACTERIAL CHROMOSOMAL REPLICATION INITIATOR (DNAA) SIGNATURE
1401	PR00300A	9.56	4.682e-11	170-188	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE
1401	PR00819B	10.83	2.482e-	169-184	PR00819	CBXX/CFQX SUPERFAMILY

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			SIGNATURE
1401	PR00830A	8.41	9.673e-13	174-193	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16) SIGNATURE
1403	BL00282	16.88	5.800e-09	127-149	BL00282	Kazal serine protease inhibitors family proteins.
1403	BL00612B	11.35	4.600e-09	169-201	BL00612	Osteonectin domain proteins.
1404	BL00229A	23.57	3.591e-09	60-98	BL00229	Tau and MAP proteins tubulin-binding domain proteins.
1404	PR00456F	5.86	6.400e-12	102-113	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE
1408	BL00989A	11.66	4.000e-12	5-18	BL00989	Clathrin adaptor complexes small chain proteins.
1408	BL00989B	26.51	1.000e-40	66-116	BL00989	Clathrin adaptor complexes small chain proteins.
1408	PR00317F	10.90	5.935e-09	103-117	PR00317	EPENDYMIN SIGNATURE
1409	BL00194	12.16	3.813e-15	547-559	BL00194	Thioredoxin family proteins.
1409	BL00194	12.16	6.727e-17	198-210	BL00194	Thioredoxin family proteins.
1409	BL00194	12.16	8.071e-16	83-95	BL00194	Thioredoxin family proteins.
1409	PR00421A	10.15	1.429e-10	546-554	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421A	10.15	3.143e-10	82-90	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421A	10.15	6.571e-10	197-205	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421B	11.40	1.783e-12	205-214	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421B	11.40	7.000e-14	90-99	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421B	11.40	7.750e-13	554-563	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421C	13.60	1.346e-09	596-607	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421C	13.60	7.231e-09	248-259	PR00421	THIOREDOXIN FAMILY SIGNATURE
1409	PR00421C	13.60	9.308e-09	133-144	PR00421	THIOREDOXIN FAMILY SIGNATURE
1410	BL00567A	10.66	6.459e-11	21-39	BL00567	Phosphoribulokinase proteins.
1410	BL01294A	5.15	3.872e-12	22-33	BL01294	Uncharacterized protein family UPF0038 proteins.
1410	BL01294B	7.90	5.065e-12	46-60	BL01294	Uncharacterized protein family UPF0038 proteins.
1410	BL01294C	22.06	5.219e-26	71-108	BL01294	Uncharacterized protein family UPF0038 proteins.
1410	BL01294E	20.47	3.800e-23	157-197	BL01294	Uncharacterized protein family UPF0038 proteins.
1410	PR00988A	6.39	6.276e-12	19-36	PR00988	URIDINE KINASE SIGNATURE
1411	BL00132A	26.07	3.329e-09	50-90	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.
1411	PR00765A	12.09	2.500e-09	76-88	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE
1411	PR00765B	15.57	2.800e-12	102-116	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14)

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						FAMILY SIGNATURE
1411	PR00765C	12.55	3.659e-09	181-189	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE
1411	PR00765D	14.16	9.053e-11	240-253	PR00765	CARBOXYPEPTIDASE A METALLOPROTEASE (M14) FAMILY SIGNATURE
1412	BL00203	13.94	5.979e-10	91-136	BL00203	Vertebrate metallothioneins proteins.
1412	BL00243I	31.77	2.521e-09	503-545	BL00243	Integrins beta chain cysteine-rich domain proteins.
1412	BL01177B	13.61	6.400e-16	200-215	BL01177	Anaphylatoxin domain proteins.
1412	BL01177C	17.39	2.875e-20	448-466	BL01177	Anaphylatoxin domain proteins.
1412	BL01177C	17.39	5.286e-09	492-510	BL01177	Anaphylatoxin domain proteins.
1412	BL01177D	17.50	3.739e-17	474-491	BL01177	Anaphylatoxin domain proteins.
1412	BL01177E	20.64	1.375e-26	496-522	BL01177	Anaphylatoxin domain proteins.
1412	BL01187A	9.98	1.000e-12	439-450	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187A	9.98	4.789e-11	260-271	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187A	9.98	4.857e-10	479-490	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187A	9.98	6.625e-09	397-408	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187A	9.98	9.571e-10	523-534	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187A	9.98	9.625e-09	214-225	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187B	12.04	3.250e-14	415-430	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187B	12.04	4.600e-10	190-205	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187B	12.04	5.333e-12	373-388	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187B	12.04	5.500e-09	498-513	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	BL01187B	12.04	6.478e-13	454-469	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1412	PR00010A	11.79	9.308e-09	441-452	PR00010	TYPE II EGF-LIKE SIGNATURE
1412	PR00010C	11.16	5.714e-09	420-430	PR00010	TYPE II EGF-LIKE SIGNATURE
1412	PR00538B	10.45	8.688e-09	108-127	PR00538	MUSCARINIC M1 RECEPTOR SIGNATURE
1412	PR00907B	11.29	9.766e-10	494-510	PR00907	THROMBOMODULIN SIGNATURE
1413	BL00030A	14.39	6.143e-13	346-364	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1413	BL00030A	14.39	9.000e-10	260-278	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1413	BL00030B	7.03	6.211e-09	295-304	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1413	BL00030B	7.03	8.800e-10	382-391	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1413	BL00291A	4.49	7.506e-10	418-452	BL00291	Prion protein.
1413	BL00412D	16.54	7.245e-09	130-180	BL00412	Neuromodulin (GAP-43) proteins.
1414	BL00054A	25.71	9.591e-34	29-69	BL00054	Ribosomal protein S11 proteins.
1414	BL00054B	16.72	1.000e-36	106-147	BL00054	Ribosomal protein S11 proteins.
1416	BL01199	8.49	7.923e-12	124-137	BL01199	Ribosomal protein L1 proteins.
1418	PR00019A	11.19	7.261e-10	256-269	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1418	PR00019A	11.19	7.600e-12	186-199	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1418	PR00019B	11.36	3.880e-09	253-266	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1418	PR00019B	11.36	5.000e-11	183-196	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1419	PD00210	15.25	3.400e-15	112-127	PD00210	PROTEIN ANTIOXIDANT PEROXIDASE RED.
1421	BL00213A	12.95	4.316e-10	40-53	BL00213	Lipocalin proteins.
1421	PR00179A	13.78	2.080e-10	40-52	PR00179	LIPOCALIN SIGNATURE
1421	PR00179B	9.56	7.375e-12	120-132	PR00179	LIPOCALIN SIGNATURE
1422	BL01171	19.94	1.000e-40	30-67	BL01171	Ribosomal protein L21e proteins.
1423	BL00361A	11.94	9.206e-13	52-67	BL00361	Ribosomal protein S10 proteins.
1423	BL00361B	18.34	5.750e-22	69-91	BL00361	Ribosomal protein S10 proteins.
1423	PR00971A	13.33	2.432e-09	19-32	PR00971	RIBOSOMAL PROTEIN S10 FAMILY SIGNATURE
1423	PR00971B	11.31	2.742e-13	54-69	PR00971	RIBOSOMAL PROTEIN S10 FAMILY SIGNATURE
1423	PR00971C	11.85	6.906e-16	76-90	PR00971	RIBOSOMAL PROTEIN S10 FAMILY SIGNATURE
1424	BL00050A	23.71	9.250e-27	94-126	BL00050	Ribosomal protein L23 proteins.
1424	BL00050B	14.81	8.125e-12	133-146	BL00050	Ribosomal protein L23 proteins.
1424	PR00925B	3.73	3.089e-10	12-24	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE
1427	PR00326A	8.75	5.979e-14	245-265	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE
1427	PR00449A	13.20	9.813e-11	243-264	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1429	PR00776A	10.77	1.844e-29	30-54	PR00776	HEMOGLOBINASE (C13) CYSTEINE PROTEASE SIGNATURE
1429	PR00776B	15.39	5.154e-30	55-84	PR00776	HEMOGLOBINASE (C13) CYSTEINE PROTEASE SIGNATURE
1429	PR00776C	11.51	9.357e-18	102-117	PR00776	HEMOGLOBINASE (C13) CYSTEINE PROTEASE SIGNATURE
1429	PR00776D	11.56	7.231e-22	131-150	PR00776	HEMOGLOBINASE (C13) CYSTEINE PROTEASE SIGNATURE
1429	PR00776E	12.29	1.375e-19	179-195	PR00776	HEMOGLOBINASE (C13) CYSTEINE PROTEASE SIGNATURE
1430	BL00951A	15.10	7.750e-39	2-37	BL00951	ER lumen protein retaining receptor proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1430	BL00951B	14.23	3.100e-31	38-68	BL00951	ER lumen protein retaining receptor proteins.
1430	BL00951C	19.35	1.000e-40	93-141	BL00951	ER lumen protein retaining receptor proteins.
1430	BL00951D	13.94	6.000e-38	142-176	BL00951	ER lumen protein retaining receptor proteins.
1430	PR00660A	13.28	9.591e-21	4-23	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660B	13.72	4.000e-24	31-51	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660C	11.32	6.211e-17	52-68	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660D	12.01	7.750e-26	120-140	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660E	11.35	3.625e-16	142-156	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660F	12.40	7.818e-22	156-174	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1430	PR00660G	11.77	8.500e-20	184-199	PR00660	ER LUMEN PROTEIN RETAINING RECEPTOR SIGNATURE
1431	BL00291A	4.49	7.103e-09	42-76	BL00291	Prion protein.
1431	BL00420A	20.42	1.000e-08	1000-1028	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.000e-09	241-269	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.000e-09	538-566	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.138e-09	667-695	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.138e-09	934-962	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.415e-09	166-194	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.590e-10	514-542	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.655e-11	685-713	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.692e-09	349-377	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.692e-09	616-644	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.692e-09	631-659	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.831e-09	688-716	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	1.885e-10	562-590	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1431	BL00420A	20.42	1.969e-09	682-710	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.108e-09	817-845	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.246e-09	451-479	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.662e-09	334-362	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.800e-09	424-452	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.964e-11	400-428	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	2.964e-11	919-947	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.077e-09	895-923	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.077e-09	94-122	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.215e-09	478-506	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.361e-10	163-191	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.361e-10	781-809	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.423e-12	328-356	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.508e-10	853-881	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.631e-09	304-332	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.769e-09	712-740	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	3.908e-09	487-515	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	4.323e-09	751-779	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	4.462e-09	640-668	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	4.541e-10	115-143	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	4.738e-09	415-443	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	4.877e-09	190-218	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	5.015e-09	319-347	BL00420	Speract receptor repeat proteins domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1431	BL00420A	20.42	5.091e-11	787-815	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	5.569e-09	322-350	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	5.582e-11	550-578	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	5.846e-09	244-272	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.016e-10	172-200	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.073e-11	208-236	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.400e-09	226-254	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.538e-09	448-476	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.607e-10	193-221	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.607e-10	628-656	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.677e-09	136-164	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.727e-11	256-284	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.754e-10	778-806	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	6.902e-10	901-929	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.369e-09	301-329	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.369e-09	493-521	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.508e-09	154-182	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.646e-09	439-467	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.646e-09	952-980	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.750e-12	460-488	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.873e-11	583-611	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.923e-09	48-76	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.923e-09	865-893	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	7.923e-	922-950	BL00420	Speract receptor repeat

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			proteins domain proteins.
1431	BL00420A	20.42	8.062e-09	283-311	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.062e-09	637-665	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.062e-09	838-866	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.200e-11	595-623	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.377e-10	313-341	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.377e-10	397-425	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.377e-10	721-749	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.525e-10	517-545	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.615e-09	352-380	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.615e-09	406-434	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.691e-11	127-155	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.754e-09	373-401	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.754e-09	457-485	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.754e-09	475-503	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.820e-10	331-359	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.855e-11	913-941	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	8.892e-09	292-320	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.031e-09	427-455	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.031e-09	565-593	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.031e-09	910-938	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.262e-10	253-281	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.446e-09	856-884	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.509e-11	100-128	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1431	BL00420A	20.42	9.509e-11	874-902	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.585e-09	799-827	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.723e-09	376-404	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.723e-09	481-509	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.852e-10	106-134	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.852e-10	238-266	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL00420A	20.42	9.852e-10	91-119	BL00420	Speract receptor repeat proteins domain proteins.
1431	BL01113A	17.99	1.000e-08	397-423	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.000e-09	898-924	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.173e-09	145-171	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.243e-13	313-339	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.519e-09	418-444	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.692e-09	136-162	BL01113	Clq domain proteins.
1431	BL01113A	17.99	1.923e-12	493-519	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.227e-11	391-417	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.340e-10	39-65	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.385e-09	1009-1035	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.385e-09	910-936	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.532e-10	304-330	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.558e-09	289-315	BL01113	Clq domain proteins.
1431	BL01113A	17.99	2.846e-12	45-71	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.077e-12	190-216	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.250e-09	382-408	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.250e-09	478-504	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.423e-09	51-77	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.423e-09	799-825	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.769e-09	808-834	BL01113	Clq domain proteins.
1431	BL01113A	17.99	3.769e-09	94-120	BL01113	Clq domain proteins.
1431	BL01113A	17.99	4.064e-10	127-153	BL01113	Clq domain proteins.
1431	BL01113A	17.99	4.068e-11	48-74	BL01113	Clq domain proteins.
1431	BL01113A	17.99	4.115e-09	634-660	BL01113	Clq domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1431	BL01113A	17.99	4.255e-10	460-486	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.273e-11	208-234	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.288e-09	172-198	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.447e-10	295-321	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.447e-10	781-807	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.447e-10	922-948	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.462e-09	433-459	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.462e-09	805-831	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.635e-09	121-147	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.682e-11	286-312	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.808e-09	250-276	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.808e-09	445-471	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.981e-09	163-189	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.981e-09	166-192	BL01113	C1q domain proteins.
1431	BL01113A	17.99	4.981e-09	667-693	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.021e-10	1000-1026	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.021e-10	520-546	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.091e-11	97-123	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.327e-09	151-177	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.327e-09	352-378	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.404e-10	184-210	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.596e-10	1081-1107	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.596e-10	469-495	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.596e-10	856-882	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.615e-12	640-666	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.673e-09	148-174	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.673e-09	865-891	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.705e-11	106-132	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.865e-13	193-219	BL01113	C1q domain proteins.
1431	BL01113A	17.99	5.979e-10	1054-1080	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.019e-09	847-873	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.192e-09	142-168	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.192e-09	310-336	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.365e-09	583-609	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.365e-09	850-876	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1431	BL01113A	17.99	6.538e-09	541-567	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.538e-09	57-83	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.538e-12	547-573	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.538e-12	796-822	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.712e-09	370-396	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.712e-09	853-879	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.745e-10	631-657	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.885e-09	256-282	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.936e-10	199-225	BL01113	C1q domain proteins.
1431	BL01113A	17.99	6.936e-10	337-363	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.000e-12	1090-1116	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.058e-09	322-348	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.128e-10	139-165	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.319e-10	328-354	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.319e-10	874-900	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.511e-10	658-684	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.750e-09	100-126	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.750e-09	472-498	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.750e-11	451-477	BL01113	C1q domain proteins.
1431	BL01113A	17.99	7.923e-12	892-918	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.054e-13	649-675	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.096e-09	793-819	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.269e-09	532-558	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.468e-10	130-156	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.773e-11	904-930	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.788e-09	394-420	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.851e-10	925-951	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.962e-09	118-144	BL01113	C1q domain proteins.
1431	BL01113A	17.99	8.977e-11	613-639	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.043e-10	556-582	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.077e-12	919-945	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.135e-09	1087-1113	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.135e-09	175-201	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.135e-09	901-927	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.182e-11	868-894	BL01113	C1q domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1431	BL01113A	17.99	9.234e-10	787-813	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.308e-09	346-372	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.308e-09	928-954	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.308e-12	883-909	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.426e-10	319-345	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.591e-11	859-885	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.795e-11	484-510	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.809e-10	406-432	BL01113	C1q domain proteins.
1431	BL01113A	17.99	9.827e-09	241-267	BL01113	C1q domain proteins.
1431	DM01418A	20.83	1.000e-40	1156-1203	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1431	DM01418B	22.51	1.000e-40	1253-1294	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1431	DM01418C	20.48	6.276e-39	1324-1365	DM01418	352 FIBRILLAR COLLAGEN CARBOXYL-TERMINAL.
1431	PR00049D	0.00	1.571e-10	1086-1100	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1431	PR00049D	0.00	9.571e-10	56-70	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1433	BL00259	9.80	9.400e-14	93-103	BL00259	Gastrin / cholecystokinin family proteins.
1433	PD01115A	12.27	9.750e-12	1-23	PD01115	PRECURSOR AMPHIBIAN SKIN SIGNAL.
1435	PR00019B	11.36	5.950e-10	179-192	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1437	BL00141A	12.10	2.636e-19	110-125	BL00141	Eukaryotic and viral aspartyl proteases proteins.
1437	BL00141B	12.14	7.231e-11	214-225	BL00141	Eukaryotic and viral aspartyl proteases proteins.
1437	BL00141C	9.74	9.471e-09	266-275	BL00141	Eukaryotic and viral aspartyl proteases proteins.
1437	BL00141D	6.28	5.154e-10	310-319	BL00141	Eukaryotic and viral aspartyl proteases proteins.
1437	BL00141E	14.32	1.900e-23	402-425	BL00141	Eukaryotic and viral aspartyl proteases proteins.
1437	PR00792A	11.54	4.273e-24	103-123	PR00792	PEPSIN (A1) ASPARTIC PROTEASE FAMILY SIGNATURE
1437	PR00792B	12.78	4.682e-11	261-274	PR00792	PEPSIN (A1) ASPARTIC PROTEASE FAMILY SIGNATURE
1437	PR00792C	9.10	1.000e-11	310-321	PR00792	PEPSIN (A1) ASPARTIC PROTEASE FAMILY SIGNATURE
1437	PR00792D	12.74	5.000e-17	401-416	PR00792	PEPSIN (A1) ASPARTIC PROTEASE FAMILY SIGNATURE
1438	BL00420A	20.42	1.000e-08	48-76	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	1.415e-09	72-100	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	1.590e-10	75-103	BL00420	Speract receptor repeat proteins domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1438	BL00420A	20.42	2.180e-10	45-73	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	4.109e-11	33-61	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	7.055e-11	84-112	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	8.082e-10	36-64	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL00420A	20.42	9.410e-10	87-115	BL00420	Speract receptor repeat proteins domain proteins.
1438	BL01113A	17.99	1.000e-13	45-71	BL01113	C1q domain proteins.
1438	BL01113A	17.99	1.519e-09	78-104	BL01113	C1q domain proteins.
1438	BL01113A	17.99	4.405e-13	54-80	BL01113	C1q domain proteins.
1438	BL01113A	17.99	5.050e-21	36-62	BL01113	C1q domain proteins.
1438	BL01113A	17.99	5.154e-12	81-107	BL01113	C1q domain proteins.
1438	BL01113A	17.99	5.655e-16	33-59	BL01113	C1q domain proteins.
1438	BL01113A	17.99	6.538e-09	30-56	BL01113	C1q domain proteins.
1438	BL01113A	17.99	7.818e-14	39-65	BL01113	C1q domain proteins.
1438	BL01113A	17.99	8.085e-10	75-101	BL01113	C1q domain proteins.
1438	BL01113A	17.99	8.154e-12	42-68	BL01113	C1q domain proteins.
1438	BL01113A	17.99	8.851e-10	84-110	BL01113	C1q domain proteins.
1438	BL01113A	17.99	9.481e-09	90-116	BL01113	C1q domain proteins.
1438	BL01113B	18.26	6.400e-33	139-174	BL01113	C1q domain proteins.
1438	BL01113C	13.18	1.462e-15	206-225	BL01113	C1q domain proteins.
1438	BL01113D	7.47	1.000e-11	240-249	BL01113	C1q domain proteins.
1438	PR00007A	19.33	4.938e-19	133-159	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE
1438	PR00007B	14.16	7.429e-20	160-179	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE
1438	PR00007C	15.60	1.225e-15	206-227	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE
1438	PR00007D	9.64	6.885e-11	238-248	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE
1439	BL01115A	10.22	6.786e-10	6-49	BL01115	GTP-binding nuclear protein ran proteins.
1439	PR00449A	13.20	3.045e-17	6-27	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1439	PR00449B	14.34	1.000e-10	29-45	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1439	PR00449C	17.27	2.895e-18	46-68	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1439	PR00449D	10.79	2.800e-15	108-121	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1439	PR00449E	13.50	4.240e-14	156-178	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1440	PR00492A	11.92	5.714e-18	57-72	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE
1440	PR00492B	9.77	6.684e-	73-91	PR00492	RHO PROTEIN GDP

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			23			DISSOCIATION INHIBITOR SIGNATURE
1440	PR00492C	9.68	7.107e-21	119-135	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE
1440	PR00492D	14.82	2.350e-19	136-151	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE
1440	PR00492E	13.98	1.000e-16	152-164	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE
1440	PR00492F	13.70	7.943e-24	178-195	PR00492	RHO PROTEIN GDP DISSOCIATION INHIBITOR SIGNATURE
1441	BL00224A	7.42	4.600e-25	26-47	BL00224	Clathrin light chain proteins.
1441	BL00224B	16.94	1.000e-40	106-158	BL00224	Clathrin light chain proteins.
1441	BL00224C	16.60	1.000e-40	163-216	BL00224	Clathrin light chain proteins.
1442	PR00759B	11.26	8.385e-09	74-84	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1443	BL00353A	9.60	1.000e-40	2-50	BL00353	HMG1/2 proteins.
1443	BL00353A	9.60	5.661e-11	3-51	BL00353	HMG1/2 proteins.
1443	BL00353B	11.47	1.000e-40	78-127	BL00353	HMG1/2 proteins.
1443	BL00353C	14.83	1.000e-40	128-174	BL00353	HMG1/2 proteins.
1443	BL00412D	16.54	3.939e-09	165-215	BL00412	Neuromodulin (GAP-43) proteins.
1443	BL00412D	16.54	4.620e-10	160-210	BL00412	Neuromodulin (GAP-43) proteins.
1443	BL00412D	16.54	5.776e-09	162-212	BL00412	Neuromodulin (GAP-43) proteins.
1443	BL00412D	16.54	6.283e-10	161-211	BL00412	Neuromodulin (GAP-43) proteins.
1443	BL00412D	16.54	7.061e-09	159-209	BL00412	Neuromodulin (GAP-43) proteins.
1443	BL00412D	16.54	7.648e-11	164-214	BL00412	Neuromodulin (GAP-43) proteins.
1443	PR00886A	10.08	1.643e-30	40-62	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1443	PR00886B	9.88	3.250e-26	63-83	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1443	PR00886C	11.84	3.250e-23	110-128	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1443	PR00886D	15.72	6.786e-24	128-147	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1443	PR00886E	8.85	5.101e-09	63-83	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1443	PR00886E	8.85	9.182e-26	147-167	PR00886	HIGH MOBILITY GROUP (HMG1/HMG2) PROTEIN SIGNATURE
1444	PR00690A	10.86	9.866e-09	782-800	PR00690	ADHESIN FAMILY SIGNATURE
1446	BL00048	6.39	6.625e-09	11-37	BL00048	Protamine P1 proteins.
1449	DM00179	13.97	7.158e-10	107-116	DM00179	w KINASE ALPHA ADHESION T-CELL.
1453	BL00056A	28.90	3.769e-32	75-114	BL00056	Ribosomal protein S17 proteins.
1453	BL00056B	20.86	6.727e-	123-146	BL00056	Ribosomal protein S17

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			23			proteins.
1453	PR00973A	20.76	2.565e-20	89-112	PR00973	RIBOSOMAL PROTEIN S17 FAMILY SIGNATURE
1453	PR00973B	13.27	6.625e-12	123-133	PR00973	RIBOSOMAL PROTEIN S17 FAMILY SIGNATURE
1453	PR00973C	10.86	1.300e-09	133-140	PR00973	RIBOSOMAL PROTEIN S17 FAMILY SIGNATURE
1454	BL01019A	13.20	9.520e-13	46-85	BL01019	ADP-ribosylation factors family proteins.
1454	BL01115A	10.22	5.075e-11	12-55	BL01115	GTP-binding nuclear protein ran proteins.
1454	PR00449A	13.20	5.846e-21	12-33	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1454	PR00449B	14.34	5.500e-13	35-51	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1454	PR00449C	17.27	3.700e-24	53-75	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1454	PR00449D	10.79	3.368e-13	115-128	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1454	PR00449E	13.50	6.684e-17	150-172	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1458	BL00284A	15.64	2.742e-15	166-189	BL00284	Serpins proteins.
1458	BL00284B	17.99	6.182e-12	258-278	BL00284	Serpins proteins.
1458	BL00284C	28.56	6.400e-25	285-326	BL00284	Serpins proteins.
1458	BL00284D	16.34	7.070e-12	396-422	BL00284	Serpins proteins.
1458	BL00284E	19.15	7.968e-16	474-498	BL00284	Serpins proteins.
1458	PD02080A	10.03	9.750e-10	1-16	PD02080	T-CELL GLYCOPROTEIN CD8 CHAIN SURFACE ALPHA PRE.
1458	PR00743B	14.95	8.831e-09	206-226	PR00743	GLYCOSYL HYDROLASE FAMILY 36 SIGNATURE
1459	BL00192A	11.90	4.857e-30	5-44	BL00192	Cytochrome b/b6 heme-ligand proteins.
1459	BL00192B	9.13	1.000e-40	62-107	BL00192	Cytochrome b/b6 heme-ligand proteins.
1459	BL00192C	7.84	9.325e-40	124-171	BL00192	Cytochrome b/b6 heme-ligand proteins.
1459	BL00192D	10.29	4.176e-36	196-231	BL00192	Cytochrome b/b6 heme-ligand proteins.
1459	BL00192E	13.29	1.000e-40	247-294	BL00192	Cytochrome b/b6 heme-ligand proteins.
1459	BL00192F	14.83	1.900e-32	318-367	BL00192	Cytochrome b/b6 heme-ligand proteins.
1460	BL00580A	17.63	7.652e-37	14-49	BL00580	Ribosomal protein L32e proteins.
1460	BL00580B	19.83	6.850e-40	50-86	BL00580	Ribosomal protein L32e proteins.
1462	BL00166A	14.82	7.429e-10	66-77	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1462	BL00166B	16.92	3.348e-17	104-125	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1462	BL00166C	18.93	9.129e-23	161-187	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1462	BL00166D	22.87	4.375e-22	213-248	BL00166	Enoyl-CoA hydratase/isomerase proteins.
1463	BL00226A	12.77	2.080e-14	83-97	BL00226	Intermediate filaments proteins.
1463	BL00226B	23.86	5.050e-38	183-230	BL00226	Intermediate filaments proteins.
1463	BL00226C	13.23	6.850e-	248-278	BL00226	Intermediate filaments

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			25			proteins.
1463	BL00226D	19.10	1.000e-40	349-395	BL00226	Intermediate filaments proteins.
1463	BL00226D	19.10	9.100e-09	296-342	BL00226	Intermediate filaments proteins.
1464	BL00039A	18.44	1.871e-23	21-59	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1464	BL00039B	19.19	4.064e-11	277-302	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1464	BL00039C	15.63	1.720e-11	364-387	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1464	BL00039D	21.67	1.900e-29	568-613	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.
1465	BL00222B	11.09	4.420e-10	60-75	BL00222	Insulin-like growth factor binding proteins.
1465	BL00273	12.24	8.286e-09	64-76	BL00273	Heat-stable enterotoxins proteins.
1465	BL00282	16.88	4.234e-12	111-133	BL00282	Kazal serine protease inhibitors family proteins.
1465	PR00290B	9.78	4.326e-09	122-133	PR00290	KAZAL-TYPE SERINE PROTEASE INHIBITOR SIGNATURE
1465	PR00834A	9.80	3.659e-11	213-225	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1465	PR00834B	10.09	5.500e-14	234-254	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1465	PR00834C	15.43	3.613e-20	275-299	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1465	PR00834D	12.14	6.455e-18	313-330	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1465	PR00834E	13.63	5.355e-13	335-352	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1465	PR00834F	10.91	9.526e-12	427-439	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE
1466	PR00939A	8.95	2.636e-09	135-144	PR00939	C2HC-TYPE ZINC-FINGER SIGNATURE
1466	PR00939A	8.95	8.714e-11	96-105	PR00939	C2HC-TYPE ZINC-FINGER SIGNATURE
1466	PR00939B	13.27	2.588e-09	81-89	PR00939	C2HC-TYPE ZINC-FINGER SIGNATURE
1467	BL00288A	17.47	3.333e-34	17-46	BL00288	Tissue inhibitors of metalloproteinases proteins.
1467	BL00288B	9.44	5.500e-14	62-72	BL00288	Tissue inhibitors of metalloproteinases proteins.
1467	BL00288C	14.62	3.829e-16	78-92	BL00288	Tissue inhibitors of metalloproteinases proteins.
1467	BL00288D	25.76	1.000e-40	100-144	BL00288	Tissue inhibitors of metalloproteinases proteins.
1467	BL00288E	17.24	4.333e-26	145-167	BL00288	Tissue inhibitors of metalloproteinases proteins.
1468	PR00450C	12.22	4.214e-11	98-119	PR00450	RECOVERIN FAMILY SIGNATURE
1469	DM01282A	17.37	7.179e-10	62-83	DM01282	w INTEGRASE CP4-57 SYT P4.
1470	BL00359A	20.66	4.000e-21	106-141	BL00359	Ribosomal protein L11 proteins.
1470	BL00359B	23.07	4.231e-24	142-182	BL00359	Ribosomal protein L11 proteins.
1470	BL00359C	22.18	6.586e-	197-230	BL00359	Ribosomal protein L11

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			22			proteins.
1470	BL01108A	20.33	1.000e-08	126-158	BL01108	Ribosomal protein L24 proteins.
1472	BL00390	27.44	1.000e-40	16-70	BL00390	Sodium and potassium ATPases beta subunits proteins.
1473	BL00536A	14.17	1.000e-40	449-490	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536A	14.17	9.647e-11	53-94	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536B	18.17	1.000e-40	498-541	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536B	18.17	3.947e-09	97-140	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536C	15.91	1.000e-40	559-597	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536D	22.91	1.000e-40	621-664	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536E	16.94	3.753e-09	744-774	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536E	16.94	8.435e-34	841-871	BL00536	Ubiquitin-activating enzyme proteins.
1473	BL00536F	13.65	1.000e-40	872-910	BL00536	Ubiquitin-activating enzyme proteins.
1476	BL00227A	24.55	3.250e-39	1-34	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1476	BL00227B	19.29	1.000e-40	50-104	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1476	BL00227C	25.48	1.000e-40	111-162	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1476	BL00227D	18.46	1.000e-40	220-273	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1476	BL00227E	24.15	8.500e-34	324-358	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1476	BL00227F	21.16	1.000e-40	372-425	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1477	PD01443B	15.02	1.000e-40	20-70	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443C	9.45	3.455e-40	78-112	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443D	8.36	8.031e-26	113-134	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443E	9.22	1.273e-34	136-162	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443F	13.86	1.000e-40	163-213	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443G	11.15	1.000e-40	228-272	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443H	11.91	3.032e-31	273-298	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443H	11.91	6.032e-11	552-577	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443H	11.91	8.835e-13	415-440	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443I	10.25	1.000e-	299-335	PD01443	INHIBITOR CALPAIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			CALPASTATIN REPEAT THIOL PROT.
1477	PD01443J	4.11	1.545e-15	523-556	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443J	4.11	2.756e-40	386-419	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443J	4.11	5.425e-10	243-276	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443K	9.19	1.000e-40	420-458	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443K	9.19	3.571e-23	278-316	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443K	9.19	9.914e-15	557-595	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443L	14.60	1.000e-40	459-501	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443M	11.28	1.000e-40	521-554	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443M	11.28	7.387e-09	241-274	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443M	11.28	7.861e-14	384-417	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443N	11.76	1.000e-40	555-592	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443N	11.76	4.744e-09	142-179	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443N	11.76	7.341e-19	418-455	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443N	11.76	9.563e-14	276-313	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1477	PD01443O	6.25	4.600e-33	640-667	PD01443	INHIBITOR CALPAIN CALPASTATIN REPEAT THIOL PROT.
1479	PR00318C	12.09	8.254e-09	268-285	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1479	PR00440C	9.54	7.000e-09	268-285	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1480	BL00719A	16.66	6.885e-12	32-45	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719B	17.24	5.333e-22	207-231	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719C	30.44	3.000e-37	324-368	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719D	22.90	4.103e-37	369-406	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719E	16.22	2.909e-18	436-451	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719F	17.71	5.765e-14	533-548	BL00719	Glycosyl hydrolases family 2 proteins.
1480	BL00719G	25.30	4.000e-23	588-617	BL00719	Glycosyl hydrolases family 2 proteins.
1480	PR00132A	13.45	8.541e-13	126-141	PR00132	GLYCOSYL HYDROLASE FAMILY 2 SIGNATURE
1480	PR00132B	10.72	2.688e-18	338-352	PR00132	GLYCOSYL HYDROLASE FAMILY 2 SIGNATURE
1480	PR00132C	18.68	5.500e-	369-387	PR00132	GLYCOSYL HYDROLASE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			20			FAMILY 2 SIGNATURE
1480	PR00132D	16.76	9.036e-19	437-452	PR00132	GLYCOSYL HYDROLASE FAMILY 2 SIGNATURE
1480	PR00132E	20.16	8.054e-14	534-549	PR00132	GLYCOSYL HYDROLASE FAMILY 2 SIGNATURE
1481	BL00678	9.67	1.947e-09	423-433	BL00678	Trp-Asp (WD) repeat proteins proteins.
1481	PF00646A	14.37	8.594e-09	237-250	PF00646	F-box domain proteins.
1481	PR00320A	16.74	2.059e-10	421-435	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1481	PR00320A	16.74	3.382e-10	513-527	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1481	PR00320B	12.19	4.857e-10	421-435	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1481	PR00320C	13.01	7.480e-10	421-435	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1481	PR00320C	13.01	7.900e-09	513-527	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1483	BL01115A	10.22	1.000e-40	11-54	BL01115	GTP-binding nuclear protein ran proteins.
1483	BL01115B	10.81	1.000e-40	91-134	BL01115	GTP-binding nuclear protein ran proteins.
1483	BL01115C	10.52	2.200e-39	140-170	BL01115	GTP-binding nuclear protein ran proteins.
1483	BL01115D	14.49	1.360e-28	184-215	BL01115	GTP-binding nuclear protein ran proteins.
1483	PR00442A	6.46	8.013e-09	12-27	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1483	PR00449A	13.20	1.000e-16	11-32	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1483	PR00449B	14.34	5.320e-10	34-50	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1483	PR00449C	17.27	4.750e-16	52-74	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1483	PR00449D	10.79	9.053e-13	113-126	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1483	PR00449E	13.50	1.391e-15	146-168	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1483	PR00627A	10.81	1.265e-19	24-38	PR00627	GTP-BINDING NUCLEAR PROTEIN RAN/TC4 FAMILY SIGNATURE
1483	PR00627B	11.05	6.538e-25	71-89	PR00627	GTP-BINDING NUCLEAR PROTEIN RAN/TC4 FAMILY SIGNATURE
1483	PR00627C	11.68	9.400e-29	91-112	PR00627	GTP-BINDING NUCLEAR PROTEIN RAN/TC4 FAMILY SIGNATURE
1483	PR00627D	12.54	1.000e-21	127-145	PR00627	GTP-BINDING NUCLEAR PROTEIN RAN/TC4 FAMILY SIGNATURE
1483	PR00627E	14.59	1.529e-24	165-187	PR00627	GTP-BINDING NUCLEAR PROTEIN RAN/TC4 FAMILY SIGNATURE
1484	BL00290A	20.89	6.143e-17	140-162	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1484	BL00290B	13.17	4.750e-16	197-214	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1484	PF00969A	22.07	9.719e-33	11-53	PF00969	Class II histocompatibility antigen, beta domain proteins.
1484	PF00969B	9.97	1.000e-40	55-90	PF00969	Class II histocompatibility antigen, beta domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1484	PF00969C	27.72	1.000e-40	94-143	PF00969	Class II histocompatibility antigen, beta domain proteins.
1484	PF00969D	14.02	7.375e-35	151-180	PF00969	Class II histocompatibility antigen, beta domain proteins.
1484	PF00969E	11.49	7.686e-35	209-243	PF00969	Class II histocompatibility antigen, beta domain proteins.
1486	BL00309C	18.65	2.241e-09	62-86	BL00309	Vertebrate galactoside-binding lectin proteins.
1487	BL00824B	9.21	3.676e-09	349-368	BL00824	Elongation factor 1 beta/beta'/delta chain proteins.
1487	PF00956A	11.88	1.000e-13	121-131	PF00956	Nucleosome assembly protein (NAP).
1487	PF00956B	23.14	1.000e-40	162-202	PF00956	Nucleosome assembly protein (NAP).
1487	PF00956C	7.72	6.850e-22	216-233	PF00956	Nucleosome assembly protein (NAP).
1487	PF00956D	7.51	3.700e-12	295-305	PF00956	Nucleosome assembly protein (NAP).
1488	BL00284A	15.64	1.000e-18	50-73	BL00284	Serpins proteins.
1488	BL00284B	17.99	1.273e-12	149-169	BL00284	Serpins proteins.
1488	BL00284C	28.56	5.821e-27	179-220	BL00284	Serpins proteins.
1488	BL00284D	16.34	1.500e-14	291-317	BL00284	Serpins proteins.
1488	BL00284E	19.15	3.842e-21	374-398	BL00284	Serpins proteins.
1489	BL00420B	22.67	3.951e-34	28-82	BL00420	Speract receptor repeat proteins domain proteins.
1489	BL00420C	11.90	3.864e-10	113-123	BL00420	Speract receptor repeat proteins domain proteins.
1489	PR00258A	11.46	8.054e-16	24-40	PR00258	SPERACT RECEPTOR SIGNATURE
1489	PR00258B	9.63	3.531e-15	43-54	PR00258	SPERACT RECEPTOR SIGNATURE
1489	PR00258C	9.05	4.643e-11	58-68	PR00258	SPERACT RECEPTOR SIGNATURE
1489	PR00258D	14.41	7.968e-15	89-103	PR00258	SPERACT RECEPTOR SIGNATURE
1489	PR00258E	13.33	1.486e-13	112-124	PR00258	SPERACT RECEPTOR SIGNATURE
1490	BL00474A	9.96	2.800e-15	46-56	BL00474	Ribosomal protein L3 proteins.
1490	BL00474B	21.72	7.500e-24	80-109	BL00474	Ribosomal protein L3 proteins.
1490	BL00474C	21.74	6.571e-34	211-245	BL00474	Ribosomal protein L3 proteins.
1490	BL00474D	29.47	8.650e-36	252-288	BL00474	Ribosomal protein L3 proteins.
1491	BL00227A	24.55	8.200e-36	1-34	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1491	BL00227B	19.29	1.000e-40	52-106	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1491	BL00227C	25.48	1.000e-40	113-164	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1491	BL00227D	18.46	1.000e-	222-275	BL00227	Tubulin subunits alpha,

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			beta, and gamma proteins.
1491	BL00227E	24.15	5.000e-37	326-360	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1491	BL00227F	21.16	1.000e-40	382-435	BL00227	Tubulin subunits alpha, beta, and gamma proteins.
1493	BL00018	7.41	6.870e-09	172-184	BL00018	EF-hand calcium-binding domain proteins.
1493	PR00049D	0.00	9.214e-10	63-77	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1494	DM01111A	10.80	5.500e-34	7-35	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111B	9.44	1.000e-40	36-72	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111C	9.35	9.100e-35	93-121	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111D	16.76	1.000e-40	152-197	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111E	17.28	1.000e-40	238-286	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111E	17.28	7.632e-10	398-446	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111F	18.22	6.684e-40	305-340	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111G	10.39	1.000e-40	341-381	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111G	10.39	5.376e-11	181-221	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111G	10.39	9.622e-09	259-299	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111H	12.57	1.000e-40	382-423	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111I	15.32	5.846e-36	424-453	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111J	19.19	8.941e-40	454-487	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111K	19.10	4.000e-38	494-523	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111L	11.93	3.500e-33	524-551	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1494	DM01111M	10.67	8.500e-30	560-583	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.
1495	BL01310	14.74	2.432e-29	133-168	BL01310	ATP1G1 / PLM / MAT8 family proteins.
1496	BL01221A	17.26	1.000e-22	1-28	BL01221	PMP-22 / EMP / MP20 family proteins.
1496	BL01221B	13.29	4.818e-12	34-47	BL01221	PMP-22 / EMP / MP20 family proteins.
1496	BL01221C	26.20	2.303e-12	56-100	BL01221	PMP-22 / EMP / MP20 family proteins.
1496	BL01221C	26.20	5.500e-33	59-103	BL01221	PMP-22 / EMP / MP20 family proteins.
1496	BL01221D	13.99	6.276e-27	139-165	BL01221	PMP-22 / EMP / MP20 family proteins.
1497	BL00094A	13.03	6.192e-16	1139-1159	BL00094	C-5 cytosine-specific DNA methylases proteins.
1497	BL00094B	16.39	1.000e-14	1218-1233	BL00094	C-5 cytosine-specific DNA methylases proteins.
1497	BL00094C	9.14	2.800e-11	1260-1271	BL00094	C-5 cytosine-specific DNA methylases proteins.
1497	BL00094D	14.24	8.636e-14	1298-1317	BL00094	C-5 cytosine-specific DNA methylases proteins.
1497	BL00094E	14.45	8.920e-15	1546-1561	BL00094	C-5 cytosine-specific DNA methylases

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1497	BL00094F	13.12	9.280e-10	1573-1582	BL00094	C-5 cytosine-specific DNA methylases proteins.
1497	PF01140D	15.54	3.407e-09	212-246	PF01140	Matrix protein (MA), p15.
1497	PR00105A	10.36	4.900e-13	1140-1156	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE
1497	PR00105B	12.32	2.800e-12	1259-1273	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE
1497	PR00105C	10.86	1.000e-10	1305-1318	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE
1498	PR00801A	10.74	4.913e-25	2-22	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801B	11.34	1.094e-22	30-46	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801C	10.94	8.258e-22	49-67	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801D	13.48	8.463e-22	83-100	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801E	9.31	5.829e-26	103-122	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801F	17.66	3.596e-25	122-141	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801G	10.72	1.000e-21	141-157	PR00801	ADRENOMEDULLIN SIGNATURE
1498	PR00801H	10.32	3.512e-19	161-178	PR00801	ADRENOMEDULLIN SIGNATURE
1499	BL00303A	21.77	5.000e-26	4-40	BL00303	S-100/ICaBP type calcium binding protein.
1499	BL00303B	26.15	1.900e-29	48-84	BL00303	S-100/ICaBP type calcium binding protein.
1503	BL00027	26.43	4.000e-11	27-69	BL00027	'Homeobox' domain proteins.
1504	BL00913B	10.94	7.706e-11	86-101	BL00913	Iron-containing alcohol dehydrogenases proteins.
1504	BL00913C	7.62	4.375e-11	136-145	BL00913	Iron-containing alcohol dehydrogenases proteins.
1504	BL00913D	24.20	8.981e-17	170-203	BL00913	Iron-containing alcohol dehydrogenases proteins.
1504	BL00913E	21.38	9.203e-09	269-302	BL00913	Iron-containing alcohol dehydrogenases proteins.
1506	BL00298A	10.97	1.000e-40	13-57	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298B	15.64	1.000e-40	73-119	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298C	16.40	1.000e-40	120-163	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298D	17.97	1.000e-40	176-215	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298E	27.30	1.000e-40	267-321	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298F	11.21	1.000e-40	353-407	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298G	24.57	1.000e-	410-464	BL00298	Heat shock hsp90

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			proteins family proteins.
1506	BL00298H	20.50	1.000e-40	498-551	BL00298	Heat shock hsp90 proteins family proteins.
1506	BL00298I	30.07	1.000e-40	602-655	BL00298	Heat shock hsp90 proteins family proteins.
1506	PR00775A	9.90	1.692e-24	13-33	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775B	3.52	2.286e-29	34-56	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775C	10.68	1.474e-19	83-100	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775D	8.91	1.000e-22	101-118	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775E	8.06	1.000e-27	126-148	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775F	12.76	7.188e-21	177-194	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1506	PR00775G	10.64	5.800e-22	195-213	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1507	BL00223A	15.59	7.158e-12	270-303	BL00223	Annexins repeat proteins domain proteins.
1507	BL00223A	15.59	8.113e-16	38-71	BL00223	Annexins repeat proteins domain proteins.
1507	BL00223A	15.59	9.625e-32	110-143	BL00223	Annexins repeat proteins domain proteins.
1507	BL00223B	28.47	1.000e-40	180-229	BL00223	Annexins repeat proteins domain proteins.
1507	BL00223C	24.79	1.000e-40	257-311	BL00223	Annexins repeat proteins domain proteins.
1507	BL00223C	24.79	6.760e-18	97-151	BL00223	Annexins repeat proteins domain proteins.
1507	PR00196A	11.16	3.423e-15	119-141	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196A	11.16	7.136e-23	47-69	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196B	10.68	7.300e-17	87-103	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196C	10.36	6.870e-23	114-135	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196C	10.36	7.750e-12	274-295	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196D	21.86	4.103e-25	198-224	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196E	9.19	1.333e-23	278-298	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196E	9.19	7.353e-12	118-138	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196F	13.89	2.714e-15	306-321	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196G	11.72	4.353e-09	162-175	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00196G	11.72	6.000e-16	322-335	PR00196	ANNEXIN FAMILY SIGNATURE
1507	PR00197B	7.56	7.652e-17	47-69	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197C	7.50	2.394e-10	87-103	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197D	7.50	2.500e-09	274-295	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197D	7.50	6.906e-18	114-135	PR00197	ANNEXIN TYPE I SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1507	PR00197E	11.89	9.077e-15	198-224	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197F	9.03	2.561e-09	118-138	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197F	9.03	9.690e-21	278-298	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00197H	11.98	1.988e-09	322-335	PR00197	ANNEXIN TYPE I SIGNATURE
1507	PR00198A	10.33	1.818e-17	3-15	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198B	8.71	3.842e-29	47-69	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198C	14.32	9.679e-20	87-103	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198D	7.65	2.206e-10	274-295	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198D	7.65	4.000e-28	114-135	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198E	14.67	8.364e-35	198-224	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198F	7.98	1.082e-10	254-261	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198G	8.09	6.250e-27	278-298	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198G	8.09	8.319e-10	118-138	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00198H	12.05	1.429e-18	322-335	PR00198	ANNEXIN TYPE II SIGNATURE
1507	PR00199B	6.86	1.971e-11	119-141	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199B	6.86	5.605e-15	47-69	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199B	6.86	8.634e-09	204-226	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199C	13.84	9.786e-09	87-103	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199D	5.65	1.281e-17	114-135	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199D	5.65	4.931e-10	274-295	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199F	16.19	5.862e-09	113-139	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199F	16.19	7.750e-12	198-224	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199G	9.09	5.860e-10	119-144	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199G	9.09	9.645e-17	279-304	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00199H	12.62	4.044e-09	322-335	PR00199	ANNEXIN TYPE III SIGNATURE
1507	PR00200B	7.39	5.099e-11	47-69	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200B	7.39	9.465e-11	119-141	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200D	10.01	7.554e-11	87-103	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200E	10.00	2.111e-14	114-135	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200E	10.00	5.825e-10	274-295	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200F	13.72	9.100e-10	198-224	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200G	9.43	4.038e-20	278-304	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200G	9.43	6.143e-12	118-144	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200H	13.68	2.753e-11	322-335	PR00200	ANNEXIN TYPE IV SIGNATURE
1507	PR00200H	13.68	3.118e-09	162-175	PR00200	ANNEXIN TYPE IV SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1507	PR00201A	6.05	3.069e-12	119-141	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201A	6.05	6.838e-16	47-69	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201D	10.49	1.495e-12	114-135	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201D	10.49	6.940e-10	274-295	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201E	12.37	8.129e-11	198-224	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201G	11.02	1.231e-19	278-304	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201G	11.02	7.888e-12	118-144	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00201H	12.04	7.413e-13	322-335	PR00201	ANNEXIN TYPE V SIGNATURE
1507	PR00202B	11.44	1.287e-12	118-141	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202B	11.44	7.680e-11	46-69	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202D	5.58	7.028e-09	274-295	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202D	5.58	9.242e-12	114-135	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202E	13.00	9.400e-10	198-224	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202G	8.01	5.417e-11	118-144	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202G	8.01	8.606e-25	278-304	PR00202	ANNEXIN TYPE VI SIGNATURE
1507	PR00202H	9.20	5.050e-10	322-335	PR00202	ANNEXIN TYPE VI SIGNATURE
1508	BL01144	25.07	1.000e-40	22-73	BL01144	Ribosomal protein L31e proteins.
1509	PR00738A	16.27	2.500e-20	158-178	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738B	11.01	2.241e-18	194-211	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738C	11.37	7.500e-26	223-244	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738D	14.00	4.000e-21	277-294	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738E	14.48	8.364e-16	322-340	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738F	11.93	6.500e-15	344-357	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738G	15.05	1.000e-19	481-497	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1509	PR00738H	11.43	5.846e-18	498-515	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1510	BL00854A	33.93	1.818e-26	58-103	BL00854	Proteasome B-type subunits proteins.
1510	BL00854C	29.92	8.435e-19	168-196	BL00854	Proteasome B-type subunits proteins.
1511	BL00487A	8.84	2.125e-12	30-39	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487B	16.59	1.000e-40	61-98	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487C	10.90	8.043e-13	153-165	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487D	26.53	1.000e-40	242-294	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487E	16.12	1.000e-40	299-343	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487F	18.79	1.000e-40	380-420	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487G	26.82	9.500e-38	439-480	BL00487	IMP dehydrogenase / GMP reductase proteins.
1511	BL00487H	15.21	3.368e-17	490-506	BL00487	IMP dehydrogenase / GMP reductase proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1511	BL00557D	17.76	1.297e-12	361-402	BL00557	FMN-dependent alpha-hydroxy acid dehydrogenases proteins.
1511	BL00911G	19.64	3.654e-09	359-389	BL00911	Dihydroorotate dehydrogenase proteins.
1513	PR00019A	11.19	4.000e-09	207-220	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1513	PR00019B	11.36	1.720e-09	230-243	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1513	PR00019B	11.36	9.640e-09	204-217	PR00019	LEUCINE-RICH REPEAT SIGNATURE
1514	BL00019D	15.33	3.520e-17	818-847	BL00019	Actinin-type actin-binding domain proteins.
1514	PD01351B	13.72	4.981e-11	233-258	PD01351	PROTEIN REPEAT NEUROFILAMENT TRIPL.
1514	PF00992A	16.67	2.895e-09	607-641	PF00992	Troponin.
1516	BL00417A	7.74	6.704e-13	5-32	BL00417	Synaptobrevin proteins.
1516	BL00417B	18.48	2.414e-19	33-86	BL00417	Synaptobrevin proteins.
1516	PR00219A	8.98	9.156e-13	10-29	PR00219	SYNAPTOSOMAL SIGNATURE
1518	BL00191J	11.37	6.447e-17	128-149	BL00191	Cytochrome b5 family, heme-binding domain proteins.
1518	BL00191K	17.38	4.951e-27	184-227	BL00191	Cytochrome b5 family, heme-binding domain proteins.
1518	BL00559I	13.63	7.366e-21	58-86	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.
1518	BL00559J	19.63	9.348e-16	128-179	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.
1518	BL00559K	13.17	7.563e-17	201-227	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.
1518	BL00559L	13.60	1.514e-14	270-287	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.
1518	PR00371D	14.55	2.313e-13	180-199	PR00371	FLAVOPROTEIN PYRIDINE NUCLEOTIDE CYTOCHROME REDUCTASE SIGNATURE
1518	PR00406A	11.92	4.375e-13	75-86	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE
1518	PR00406C	13.10	7.750e-12	141-155	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE
1518	PR00406D	10.02	7.387e-19	180-199	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE
1518	PR00406E	8.37	9.400e-09	218-229	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE
1518	PR00406F	3.97	4.240e-10	274-282	PR00406	CYTOCHROME B5 REDUCTASE SIGNATURE
1518	PR00409F	12.70	6.612e-10	180-199	PR00409	PHthalate DIOXYGENASE REDUCTASE FAMILY SIGNATURE
1518	PR00410D	12.97	4.676e-09	180-199	PR00410	PHENOL HYDROXYLASE REDUCTASE FAMILY SIGNATURE
1519	BL00297A	17.58	1.000e-40	7-43	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297B	22.91	1.000e-	46-94	BL00297	Heat shock hsp70

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			proteins family proteins.
1519	BL00297C	9.51	1.000e-40	134-185	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297D	11.95	1.000e-40	195-234	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297E	18.56	8.800e-40	292-335	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297F	11.84	6.400e-29	356-383	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297G	21.87	1.000e-40	390-444	BL00297	Heat shock hsp70 proteins family proteins.
1519	BL00297H	15.46	1.000e-40	453-506	BL00297	Heat shock hsp70 proteins family proteins.
1519	PR00301A	14.84	3.368e-16	5-18	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301B	15.36	1.692e-17	33-45	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301C	8.62	9.609e-10	55-63	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301D	15.51	5.500e-27	142-162	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301E	8.11	2.286e-14	203-213	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301F	13.98	1.429e-19	331-347	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301G	13.78	6.143e-25	363-383	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301H	8.81	2.421e-21	390-409	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1519	PR00301I	12.76	2.125e-22	471-487	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE
1520	BL00960B	24.47	9.471e-09	195-239	BL00960	BTG1 family proteins.
1520	PR00738A	16.27	6.538e-17	125-145	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738B	11.01	1.000e-18	161-178	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738C	11.37	3.483e-23	190-211	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738D	14.00	4.194e-19	245-262	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738E	14.48	5.500e-16	290-308	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738F	11.93	3.455e-14	312-325	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738G	15.05	1.000e-20	452-468	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1520	PR00738H	11.43	9.308e-18	469-486	PR00738	GLYCOSYL HYDROLASE FAMILY 20 SIGNATURE
1521	BL00030B	7.03	2.200e-10	103-112	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1522	BL00540A	15.06	8.636e-40	5-45	BL00540	Ferritin iron-binding regions proteins.
1522	BL00540B	18.82	1.000e-40	96-150	BL00540	Ferritin iron-binding regions proteins.
1522	BL00540C	13.00	4.649e-12	161-172	BL00540	Ferritin iron-binding regions proteins.
1524	BL00362	24.67	3.348e-35	88-130	BL00362	Ribosomal protein S15 proteins.
1525	BL00406A	9.95	1.000e-40	9-43	BL00406	Actins proteins.
1525	BL00406B	5.47	1.000e-40	85-139	BL00406	Actins proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1525	BL00406C	6.75	1.000e-40	144-198	BL00406	Actins proteins.
1525	BL00406D	12.58	1.000e-40	271-325	BL00406	Actins proteins.
1525	BL00406E	8.44	1.000e-40	328-377	BL00406	Actins proteins.
1525	PR00190A	7.24	1.375e-13	28-37	PR00190	ACTIN SIGNATURE
1525	PR00190B	9.98	1.000e-15	51-62	PR00190	ACTIN SIGNATURE
1525	PR00190C	11.49	4.789e-30	63-85	PR00190	ACTIN SIGNATURE
1525	PR00190D	19.23	3.520e-24	86-104	PR00190	ACTIN SIGNATURE
1525	PR00190E	7.16	1.450e-19	117-130	PR00190	ACTIN SIGNATURE
1525	PR00190F	7.80	1.321e-24	142-161	PR00190	ACTIN SIGNATURE
1525	PR00190G	12.62	1.600e-21	238-254	PR00190	ACTIN SIGNATURE
1526	BL00798A	14.97	5.200e-17	7-21	BL00798	Aldo/keto reductase family proteins.
1526	BL00798B	16.01	5.500e-28	35-59	BL00798	Aldo/keto reductase family proteins.
1526	BL00798C	11.15	7.480e-15	68-80	BL00798	Aldo/keto reductase family proteins.
1526	BL00798D	7.65	5.235e-17	92-108	BL00798	Aldo/keto reductase family proteins.
1526	BL00798E	20.32	1.000e-40	177-214	BL00798	Aldo/keto reductase family proteins.
1526	BL00798F	23.30	1.000e-40	238-286	BL00798	Aldo/keto reductase family proteins.
1526	PR00069A	16.01	8.364e-29	35-59	PR00069	ALDO-KETO REDUCTASE SIGNATURE
1526	PR00069B	11.33	1.000e-21	95-113	PR00069	ALDO-KETO REDUCTASE SIGNATURE
1526	PR00069C	16.03	4.000e-19	145-162	PR00069	ALDO-KETO REDUCTASE SIGNATURE
1526	PR00069D	19.36	1.529e-32	181-210	PR00069	ALDO-KETO REDUCTASE SIGNATURE
1526	PR00069E	18.14	6.870e-25	228-252	PR00069	ALDO-KETO REDUCTASE SIGNATURE
1527	BL00086	20.87	2.421e-21	427-458	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.
1527	PR00385A	14.97	8.448e-11	306-323	PR00385	P450 SUPERFAMILY SIGNATURE
1527	PR00385B	10.22	4.300e-09	324-337	PR00385	P450 SUPERFAMILY SIGNATURE
1527	PR00385D	13.11	4.000e-09	428-437	PR00385	P450 SUPERFAMILY SIGNATURE
1527	PR00385E	12.66	6.571e-09	437-448	PR00385	P450 SUPERFAMILY SIGNATURE
1527	PR00463E	17.37	9.542e-11	315-341	PR00463	E-CLASS P450 GROUP I SIGNATURE
1527	PR00464E	18.28	4.696e-09	352-372	PR00464	E-CLASS P450 GROUP II SIGNATURE
1527	PR00464I	14.64	9.654e-09	437-460	PR00464	E-CLASS P450 GROUP II SIGNATURE
1528	PR00049D	0.00	9.929e-10	180-194	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE
1529	BL00678	9.67	1.692e-11	80-90	BL00678	Trp-Asp (WD) repeat proteins proteins.
1529	BL00678	9.67	1.947e-09	167-177	BL00678	Trp-Asp (WD) repeat proteins proteins.
1529	BL00678	9.67	8.615e-11	122-132	BL00678	Trp-Asp (WD) repeat proteins proteins.
1529	PR00320A	16.74	1.439e-09	207-221	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320A	16.74	3.143e-	78-92	PR00320	G-PROTEIN BETA WD-40

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			13			REPEAT SIGNATURE
1529	PR00320A	16.74	3.382e-10	31-45	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320A	16.74	7.207e-11	165-179	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320A	16.74	8.560e-12	120-134	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320B	12.19	1.257e-10	31-45	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320B	12.19	2.174e-13	120-134	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320B	12.19	4.484e-11	165-179	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320B	12.19	4.825e-09	207-221	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320B	12.19	7.231e-12	78-92	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320C	13.01	1.000e-10	78-92	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320C	13.01	2.800e-10	120-134	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320C	13.01	7.000e-12	207-221	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320C	13.01	8.043e-11	165-179	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1529	PR00320C	13.01	9.700e-09	31-45	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE
1530	BL01082	20.37	5.000e-34	51-90	BL01082	Ribosomal protein L7Ae proteins.
1530	PR00881A	9.94	3.455e-12	35-49	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1530	PR00881B	9.01	4.484e-12	54-67	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1530	PR00881C	12.76	9.526e-13	70-80	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1530	PR00881D	11.60	2.440e-14	80-94	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1530	PR00883A	6.49	5.500e-18	8-21	PR00883	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN SIGNATURE
1530	PR00883B	8.76	8.364e-19	21-36	PR00883	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN SIGNATURE
1530	PR00883C	8.52	2.000e-14	38-48	PR00883	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN SIGNATURE
1530	PR00883D	13.33	2.200e-16	82-94	PR00883	HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN SIGNATURE
1530	PR00884D	11.07	9.217e-10	80-90	PR00884	RIBOSOMAL PROTEIN HS6 SIGNATURE
1531	BL00296A	17.20	5.648e-10	12-65	BL00296	Chaperonins cpn60 proteins.
1531	BL00296B	15.98	4.115e-13	76-129	BL00296	Chaperonins cpn60 proteins.
1531	BL00296F	19.66	3.826e-09	476-513	BL00296	Chaperonins cpn60 proteins.
1531	BL00750A	20.07	8.286e-36	25-67	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750B	16.17	2.000e-39	69-118	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750C	25.65	8.579e-23	152-183	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750D	16.16	5.875e-13	199-217	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750E	24.59	8.313e-	294-330	BL00750	Chaperonins TCP-1

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			21			proteins.
1531	BL00750F	18.40	3.880e-29	368-408	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750G	20.12	4.300e-31	429-468	BL00750	Chaperonins TCP-1 proteins.
1531	BL00750H	21.44	2.731e-23	486-520	BL00750	Chaperonins TCP-1 proteins.
1531	PR00298B	13.59	7.353e-11	88-115	PR00298	60 KD CHAPERONIN SIGNATURE
1531	PR00304A	9.20	3.605e-15	34-50	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1531	PR00304B	11.60	2.059e-17	56-74	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1531	PR00304C	8.69	1.250e-18	86-105	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1531	PR00304D	11.04	9.757e-17	371-393	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1531	PR00304E	7.79	8.043e-13	405-417	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE
1532	BL00021B	13.33	2.435e-10	487-504	BL00021	Kringle domain proteins.
1532	BL00021D	24.56	1.105e-09	656-697	BL00021	Kringle domain proteins.
1532	BL00022B	7.54	9.100e-09	174-180	BL00022	EGF-like domain proteins.
1532	BL00134A	11.96	5.114e-14	487-503	BL00134	Serine proteases, trypsin family, histidine proteins.
1532	BL00134B	15.99	3.382e-13	648-671	BL00134	Serine proteases, trypsin family, histidine proteins.
1532	BL00134C	13.45	5.500e-12	684-697	BL00134	Serine proteases, trypsin family, histidine proteins.
1532	BL004950	13.75	6.040e-09	675-703	BL00495	Apple domain proteins.
1532	BL01187B	12.04	6.538e-16	165-180	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1532	BL01253G	11.34	5.382e-11	647-660	BL01253	Type I fibronectin domain proteins.
1532	BL01253H	13.15	9.587e-09	666-700	BL01253	Type I fibronectin domain proteins.
1532	PR00010C	11.16	3.571e-09	170-180	PR00010	TYPE II EGF-LIKE SIGNATURE
1532	PR00722A	12.27	8.258e-13	488-503	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1532	PR00722B	12.51	3.625e-09	553-567	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1532	PR00722C	10.87	8.105e-12	647-659	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1533	BL00021B	13.33	5.431e-11	460-477	BL00021	Kringle domain proteins.
1533	BL00134A	11.96	4.094e-15	460-476	BL00134	Serine proteases, trypsin family, histidine proteins.
1533	BL00134B	15.99	5.378e-12	626-649	BL00134	Serine proteases, trypsin family, histidine proteins.
1533	BL00134C	13.45	5.125e-12	662-675	BL00134	Serine proteases, trypsin family, histidine proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1533	BL00495K	12.58	4.845e-09	462-494	BL00495	Apple domain proteins.
1533	BL01180B	11.58	2.875e-09	65-75	BL01180	CUB domain proteins profile.
1533	BL01187B	12.04	9.550e-14	147-162	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.
1533	BL01253D	4.84	7.960e-09	460-473	BL01253	Type I fibronectin domain proteins.
1533	PF00084B	9.45	8.875e-10	379-390	PF00084	Sushi domain proteins (SCR repeat proteins.
1533	PR00722A	12.27	7.120e-15	461-476	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1533	PR00722B	12.51	6.625e-12	525-539	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1533	PR00722C	10.87	3.864e-11	625-637	PR00722	CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1) SIGNATURE
1533	PR00907B	11.29	8.364e-10	143-159	PR00907	THROMBOMODULIN SIGNATURE
1535	BL00018	7.41	1.000e-09	57-69	BL00018	EF-hand calcium-binding domain proteins.
1535	BL00018	7.41	3.400e-12	130-142	BL00018	EF-hand calcium-binding domain proteins.
1535	BL00303B	26.15	6.344e-10	45-81	BL00303	S-100/ICaBP type calcium binding protein.
1535	PR00450C	12.22	4.480e-10	89-110	PR00450	RECOVERIN FAMILY SIGNATURE
1535	PR00450C	12.22	5.320e-10	16-37	PR00450	RECOVERIN FAMILY SIGNATURE
1535	PR00450C	12.22	6.520e-10	52-73	PR00450	RECOVERIN FAMILY SIGNATURE
1536	BL00319C	17.12	9.289e-09	383-416	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1536	BL00412D	16.54	2.565e-10	364-414	BL00412	Neuromodulin (GAP-43) proteins.
1536	BL00412D	16.54	2.929e-09	350-400	BL00412	Neuromodulin (GAP-43) proteins.
1536	BL00412D	16.54	4.398e-09	348-398	BL00412	Neuromodulin (GAP-43) proteins.
1536	BL00412D	16.54	8.714e-09	354-404	BL00412	Neuromodulin (GAP-43) proteins.
1536	BL00412D	16.54	9.265e-09	339-389	BL00412	Neuromodulin (GAP-43) proteins.
1536	BL00422C	16.18	1.176e-09	384-411	BL00422	Granins proteins.
1536	BL00422C	16.18	8.059e-09	376-403	BL00422	Granins proteins.
1536	BL00803A	14.83	2.688e-14	35-48	BL00803	Calreticulin family proteins.
1536	BL00803B	17.08	8.714e-18	63-81	BL00803	Calreticulin family proteins.
1536	BL00803C	11.13	6.063e-26	91-113	BL00803	Calreticulin family proteins.
1536	BL00803D	16.08	1.000e-15	128-138	BL00803	Calreticulin family proteins.
1536	BL00803E	16.55	2.588e-31	166-196	BL00803	Calreticulin family proteins.
1536	BL00803F	10.95	2.000e-37	225-255	BL00803	Calreticulin family proteins.
1536	BL00803F	10.95	2.179e-11	191-221	BL00803	Calreticulin family proteins.
1536	BL00803F	10.95	7.268e-22	208-238	BL00803	Calreticulin family proteins.
1536	BL00803F	10.95	9.516e-	242-272	BL00803	Calreticulin family

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			09			proteins.
1536	BL00803G	14.33	1.000e-40	258-302	BL00803	Calreticulin family proteins.
1536	BL00803G	14.33	1.127e-19	244-288	BL00803	Calreticulin family proteins.
1536	BL00803G	14.33	7.429e-16	272-316	BL00803	Calreticulin family proteins.
1536	BL00803H	16.02	4.000e-10	309-325	BL00803	Calreticulin family proteins.
1536	BL00803H	16.02	7.375e-14	337-353	BL00803	Calreticulin family proteins.
1536	PD00301B	5.49	6.538e-09	371-381	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.
1536	PF00992A	16.67	8.986e-10	363-397	PF00992	Troponin.
1536	PR00626A	14.35	1.500e-18	100-118	PR00626	CALRETICULIN SIGNATURE
1536	PR00626B	14.12	2.200e-20	126-142	PR00626	CALRETICULIN SIGNATURE
1536	PR00626C	9.70	7.882e-14	232-245	PR00626	CALRETICULIN SIGNATURE
1536	PR00626C	9.70	9.100e-18	215-228	PR00626	CALRETICULIN SIGNATURE
1536	PR00626D	8.30	6.520e-09	208-230	PR00626	CALRETICULIN SIGNATURE
1536	PR00626D	8.30	8.017e-13	256-278	PR00626	CALRETICULIN SIGNATURE
1536	PR00626D	8.30	8.071e-30	242-264	PR00626	CALRETICULIN SIGNATURE
1536	PR00626E	11.30	3.676e-19	266-285	PR00626	CALRETICULIN SIGNATURE
1536	PR00626E	11.30	7.632e-24	280-299	PR00626	CALRETICULIN SIGNATURE
1536	PR00626F	15.79	5.500e-21	313-333	PR00626	CALRETICULIN SIGNATURE
1537	BL00303A	21.77	5.286e-30	4-40	BL00303	S-100/ICaBP type calcium binding protein.
1537	BL00303B	26.15	1.000e-29	51-87	BL00303	S-100/ICaBP type calcium binding protein.
1538	BL00983A	5.84	7.261e-10	12-20	BL00983	Ly-6 / u-PAR domain proteins.
1538	BL00983B	8.19	1.643e-12	22-31	BL00983	Ly-6 / u-PAR domain proteins.
1538	BL00983C	12.69	3.500e-15	80-95	BL00983	Ly-6 / u-PAR domain proteins.
1539	BL00261A	23.97	5.500e-34	29-62	BL00261	Glycoprotein hormones beta chain proteins.
1539	BL00261B	25.64	6.885e-37	77-120	BL00261	Glycoprotein hormones beta chain proteins.
1539	PR00438A	13.54	1.000e-09	50-59	PR00438	GROWTH FACTOR CYSTINE KNOT SUPERFAMILY SIGNATURE
1540	BL00280	24.61	1.391e-37	132-175	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1540	BL00280	24.61	2.241e-33	61-104	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1540	BL00280	24.61	3.500e-29	224-267	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1540	PR00759A	14.51	5.500e-11	122-136	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759A	14.51	8.579e-12	51-65	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759B	11.26	1.692e-	79-89	PR00759	BASIC PROTEASE (KUNITZ-

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			11			TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759B	11.26	2.385e-11	150-160	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759B	11.26	8.269e-11	242-252	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759C	14.15	1.000e-13	89-104	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759C	14.15	1.818e-15	160-175	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1540	PR00759C	14.15	3.727e-12	252-267	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1541	BL01104A	14.65	1.000e-40	13-51	BL01104	Ribosomal protein L13e proteins.
1541	BL01104B	15.12	1.000e-40	83-129	BL01104	Ribosomal protein L13e proteins.
1541	BL01104C	15.14	9.550e-28	174-201	BL01104	Ribosomal protein L13e proteins.
1543	BL01031A	10.55	4.429e-09	19-28	BL01031	Heat shock hsp20 proteins family profile.
1543	BL01031B	15.78	5.200e-19	73-93	BL01031	Heat shock hsp20 proteins family profile.
1543	BL01031C	17.68	8.412e-21	101-125	BL01031	Heat shock hsp20 proteins family profile.
1543	PR00299A	13.53	8.448e-16	2-14	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299B	17.53	1.000e-16	19-31	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299C	8.47	2.317e-20	69-89	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299D	8.56	5.974e-16	91-104	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299E	12.26	6.455e-25	106-125	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299F	13.20	9.289e-21	128-149	PR00299	ALPHA CRYSTALLIN SIGNATURE
1543	PR00299G	5.58	4.825e-16	156-171	PR00299	ALPHA CRYSTALLIN SIGNATURE
1544	BL01101A	16.07	1.000e-40	9-53	BL01101	Casein kinase II regulatory subunit proteins.
1544	BL01101B	10.94	9.000e-31	72-96	BL01101	Casein kinase II regulatory subunit proteins.
1544	BL01101C	15.36	8.714e-37	97-126	BL01101	Casein kinase II regulatory subunit proteins.
1544	BL01101D	16.87	1.000e-40	127-168	BL01101	Casein kinase II regulatory subunit proteins.
1544	PR00472A	8.03	7.600e-23	8-24	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE
1544	PR00472B	14.84	1.000e-19	25-39	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE
1544	PR00472C	12.38	5.154e-28	80-101	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE
1544	PR00472D	10.36	4.857e-28	105-126	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1544	PR00472E	13.85	3.769e-27	127-148	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE
1544	PR00472F	9.76	3.368e-23	155-172	PR00472	CASEIN KINASE II REGULATORY SUBUNIT FAMILY SIGNATURE
1545	BL00023	24.31	4.545e-27	382-418	BL00023	Type II fibronectin collagen-binding domain proteins.
1545	BL00023	24.31	8.920e-33	442-478	BL00023	Type II fibronectin collagen-binding domain proteins.
1545	BL01253A	20.33	4.720e-09	589-617	BL01253	Type I fibronectin domain proteins.
1545	PR00012A	9.68	1.450e-14	221-232	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012A	9.68	3.250e-14	2297-2308	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012A	9.68	4.250e-13	596-607	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012A	9.68	4.789e-09	85-96	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012A	9.68	7.316e-09	174-185	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012A	9.68	8.269e-10	266-277	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	1.957e-10	572-580	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	4.273e-12	2317-2325	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	5.021e-10	105-113	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	5.909e-12	525-533	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	6.339e-09	196-204	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	6.707e-11	2274-2282	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	8.475e-09	287-295	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	8.902e-11	616-624	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00012B	8.28	9.043e-10	152-160	PR00012	FIBRONECTIN TYPE I REPEAT SIGNATURE
1545	PR00013A	12.26	1.500e-09	386-395	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
1545	PR00013A	12.26	5.875e-12	446-455	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
1545	PR00013B	14.75	2.385e-13	457-469	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
1545	PR00013C	12.29	2.607e-18	474-489	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
1545	PR00013C	12.29	4.400e-14	414-429	PR00013	FIBRONECTIN TYPE II REPEAT SIGNATURE
1545	PR00014A	8.22	4.750e-11	1946-1955	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014A	8.22	9.591e-09	1040-1049	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014B	14.77	1.000e-08	1956-1966	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014B	14.77	8.500e-09	864-874	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	1.391e-09	797-815	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	1.500e-11	2148-2166	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	1.783e-09	1254-1272	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	2.800e-10	688-706	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1545	PR00014C	15.44	2.800e-12	1890-1908	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	4.857e-13	1980-1998	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	6.400e-10	1525-1543	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	6.400e-10	1709-1727	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	6.400e-10	887-905	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	6.478e-09	1619-1637	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	7.000e-11	1435-1453	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1545	PR00014C	15.44	8.650e-10	1345-1363	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1546	BL00086	20.87	1.429e-20	452-483	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.
1546	PR00359I	11.13	5.378e-09	462-473	PR00359	B-CLASS P450 SIGNATURE
1546	PR00385A	14.97	7.882e-16	326-343	PR00385	P450 SUPERFAMILY SIGNATURE
1546	PR00385C	16.94	2.421e-10	379-390	PR00385	P450 SUPERFAMILY SIGNATURE
1546	PR00385D	13.11	5.000e-09	453-462	PR00385	P450 SUPERFAMILY SIGNATURE
1546	PR00385E	12.66	5.714e-09	462-473	PR00385	P450 SUPERFAMILY SIGNATURE
1546	PR00408A	14.69	5.680e-15	126-141	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408B	13.00	4.194e-09	142-152	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408C	13.23	5.655e-18	203-221	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408D	15.44	5.500e-21	326-343	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408E	9.47	4.545e-13	344-357	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408F	11.33	1.486e-18	372-390	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408G	13.17	9.667e-10	435-443	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408H	12.37	1.000e-12	453-462	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00408I	8.49	2.125e-14	462-473	PR00408	MITOCHONDRIAL P450 SIGNATURE
1546	PR00463G	18.24	9.833e-10	418-442	PR00463	E-CLASS P450 GROUP I SIGNATURE
1546	PR00463I	15.02	8.525e-09	462-485	PR00463	E-CLASS P450 GROUP I SIGNATURE
1546	PR00464C	18.84	9.000e-11	315-343	PR00464	E-CLASS P450 GROUP II SIGNATURE
1546	PR00464E	18.28	7.511e-11	373-393	PR00464	E-CLASS P450 GROUP II SIGNATURE
1546	PR00464I	14.64	6.651e-11	462-485	PR00464	E-CLASS P450 GROUP II SIGNATURE
1546	PR00465D	14.64	6.824e-12	374-390	PR00465	E-CLASS P450 GROUP IV SIGNATURE
1546	PR00465F	13.37	6.940e-11	423-441	PR00465	E-CLASS P450 GROUP IV SIGNATURE
1548	BL00301A	12.41	3.842e-13	9-20	BL00301	GTP-binding elongation factors proteins.
1548	BL00301B	20.09	5.500e-31	90-121	BL00301	GTP-binding elongation factors proteins.
1548	BL00301C	11.73	8.200e-15	423-436	BL00301	GTP-binding elongation factors proteins.
1548	BL00880	17.52	9.214e-09	99-148	BL00880	Acyl-CoA-binding protein.
1548	BL01176B	8.74	5.547e-	87-124	BL01176	Initiation factor 2

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			12			proteins.
1548	PR00315A	11.81	1.818e-15	9-22	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE
1548	PR00315B	11.66	5.800e-10	68-76	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE
1548	PR00315C	13.85	7.750e-13	88-98	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE
1548	PR00315D	10.84	2.895e-11	104-115	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE
1548	PR00315E	12.29	3.864e-09	148-157	PR00315	GTP-BINDING ELONGATION FACTOR SIGNATURE
1549	BL00514A	11.68	6.885e-12	40-49	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514B	16.42	4.000e-15	150-165	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514C	17.41	1.000e-40	206-242	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514D	15.35	7.000e-16	251-263	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514E	14.28	4.000e-19	272-288	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514F	11.65	5.091e-15	304-318	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514G	15.98	1.947e-37	351-380	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	BL00514H	14.95	3.368e-28	390-414	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.
1549	PR00171A	10.00	8.875e-09	384-394	PR00171	SUGAR TRANSPORTER SIGNATURE
1551	BL00615B	12.25	3.423e-09	207-220	BL00615	C-type lectin domain proteins.
1551	PR00770A	13.71	1.231e-24	2-25	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770B	11.43	9.325e-17	88-103	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770C	12.19	5.886e-17	109-125	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770D	13.82	8.364e-21	126-142	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770E	8.53	1.000e-22	153-171	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770F	13.79	1.250e-26	172-191	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1551	PR00770G	7.65	3.512e-23	195-212	PR00770	EOSINOPHIL MAJOR BASIC PROTEIN SIGNATURE
1552	BL00213A	12.95	8.105e-10	31-44	BL00213	Lipocalin proteins.
1552	PR00179A	13.78	5.050e-11	31-43	PR00179	LIPOCALIN SIGNATURE
1552	PR00179B	9.56	5.034e-11	112-124	PR00179	LIPOCALIN SIGNATURE
1552	PR00179C	19.02	8.909e-09	139-154	PR00179	LIPOCALIN SIGNATURE
1553	BL00164A	11.58	1.529e-27	32-54	BL00164	Enolase proteins.
1553	BL00164B	16.22	1.000e-40	98-140	BL00164	Enolase proteins.
1553	BL00164C	15.66	1.000e-40	144-193	BL00164	Enolase proteins.
1553	BL00164D	21.97	2.588e-38	220-262	BL00164	Enolase proteins.
1553	BL00164E	8.80	9.100e-	287-301	BL00164	Enolase proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			20			
1553	BL00164F	10.48	3.813e-39	313-348	BL00164	Enolase proteins.
1553	BL00164G	12.13	1.000e-40	380-418	BL00164	Enolase proteins.
1553	PR00148A	10.11	1.783e-18	35-49	PR00148	ENOLASE SIGNATURE
1553	PR00148B	8.60	7.000e-21	107-123	PR00148	ENOLASE SIGNATURE
1553	PR00148C	15.33	2.800e-16	164-177	PR00148	ENOLASE SIGNATURE
1553	PR00148D	14.46	1.360e-15	317-328	PR00148	ENOLASE SIGNATURE
1553	PR00148E	13.62	4.500e-17	340-354	PR00148	ENOLASE SIGNATURE
1553	PR00148F	10.19	1.643e-23	369-386	PR00148	ENOLASE SIGNATURE
1554	BL00086	20.87	4.938e-24	438-469	BL00086	Cytochrome P450 cysteine heme-iron ligand proteins.
1554	PR00359F	24.20	1.738e-09	382-409	PR00359	B-CLASS P450 SIGNATURE
1554	PR00359I	11.13	3.189e-09	448-459	PR00359	B-CLASS P450 SIGNATURE
1554	PR00385A	14.97	7.750e-18	311-328	PR00385	P450 SUPERFAMILY SIGNATURE
1554	PR00385B	10.22	8.650e-12	329-342	PR00385	P450 SUPERFAMILY SIGNATURE
1554	PR00385C	16.94	6.684e-10	364-375	PR00385	P450 SUPERFAMILY SIGNATURE
1554	PR00385D	13.11	1.857e-10	439-448	PR00385	P450 SUPERFAMILY SIGNATURE
1554	PR00385E	12.66	2.800e-11	448-459	PR00385	P450 SUPERFAMILY SIGNATURE
1554	PR00408D	15.44	9.211e-12	311-328	PR00408	MITOCHONDRIAL P450 SIGNATURE
1554	PR00463A	11.40	3.659e-10	72-91	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463B	17.50	9.077e-12	96-117	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463C	12.85	6.684e-18	187-205	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463D	14.02	8.875e-18	300-317	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463E	17.37	4.150e-25	320-346	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463F	17.63	1.818e-16	363-381	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463G	18.24	5.680e-19	404-428	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463H	12.41	5.154e-13	438-448	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00463I	15.02	5.500e-20	448-471	PR00463	E-CLASS P450 GROUP I SIGNATURE
1554	PR00464C	18.84	4.000e-11	300-328	PR00464	E-CLASS P450 GROUP II SIGNATURE
1554	PR00464D	17.40	4.545e-12	329-346	PR00464	E-CLASS P450 GROUP II SIGNATURE
1554	PR00464H	13.32	3.423e-09	435-448	PR00464	E-CLASS P450 GROUP II SIGNATURE
1554	PR00464I	14.64	2.532e-10	448-471	PR00464	E-CLASS P450 GROUP II SIGNATURE
1554	PR00465F	13.37	3.400e-09	409-427	PR00465	E-CLASS P450 GROUP IV SIGNATURE
1555	BL01191A	15.57	1.000e-40	13-63	BL01191	Ribosomal protein S3Ae proteins.
1555	BL01191B	13.33	1.000e-40	89-139	BL01191	Ribosomal protein S3Ae proteins.
1555	BL01191C	16.50	1.000e-40	180-231	BL01191	Ribosomal protein S3Ae proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1556	BL01209	9.31	2.500e-14	124-136	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1556	BL01209	9.31	8.342e-12	44-56	BL01209	LDL-receptor class A (LDLRA) domain proteins.
1556	PR00261A	11.02	6.053e-17	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261A	11.02	7.338e-12	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261B	14.12	2.385e-15	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261B	14.12	9.630e-12	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261C	11.37	5.607e-09	78-99	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261C	11.37	8.174e-13	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261C	11.37	8.603e-17	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261D	12.47	1.915e-16	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261D	12.47	5.257e-11	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261E	11.08	3.813e-13	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261E	11.08	8.714e-11	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261F	11.57	6.824e-12	115-136	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1556	PR00261F	11.57	7.750e-12	35-56	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE
1557	BL00025	17.17	2.853e-17	89-109	BL00025	P-type 'Trefoil' domain proteins.
1557	BL00129A	26.21	1.000e-40	359-404	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL00129B	19.19	3.667e-25	473-499	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL00129C	15.12	6.211e-32	594-621	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL00129D	16.76	1.000e-40	632-675	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL00129E	22.60	1.692e-32	696-731	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL00129F	26.19	1.000e-29	827-864	BL00129	Glycosyl hydrolases family 31 proteins.
1557	BL01103H	11.98	7.840e-09	738-749	BL01103	Aspartate-semialdehyde dehydrogenase proteins.
1557	PR00680B	10.34	5.359e-10	99-111	PR00680	P-TYPE TREFOIL DOMAIN SIGNATURE
1558	BL01033A	16.94	2.929e-17	25-46	BL01033	Globins profile.
1558	BL01033B	13.81	1.000e-15	93-104	BL01033	Globins profile.
1558	PR00612D	9.76	2.976e-10	80-93	PR00612	ALPHA HAEMOGLOBIN SIGNATURE
1558	PR00613B	9.02	9.270e-	25-48	PR00613	MYOGLOBIN SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			10			
1558	PR00613C	10.22	9.630e-09	58-78	PR00613	MYOGLOBIN SIGNATURE
1558	PR00814A	12.94	1.000e-22	30-46	PR00814	BETA HAEMOGLOBIN SIGNATURE
1558	PR00814B	9.18	3.571e-20	48-63	PR00814	BETA HAEMOGLOBIN SIGNATURE
1558	PR00814C	9.20	8.615e-19	72-89	PR00814	BETA HAEMOGLOBIN SIGNATURE
1558	PR00814D	15.25	2.286e-09	94-99	PR00814	BETA HAEMOGLOBIN SIGNATURE
1558	PR00814E	10.17	4.414e-14	128-144	PR00814	BETA HAEMOGLOBIN SIGNATURE
1559	PR00014A	8.22	7.955e-09	443-452	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1559	PR00014C	15.44	8.826e-09	578-596	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1560	BL00222A	11.34	9.438e-11	45-55	BL00222	Insulin-like growth factor binding proteins.
1560	BL00222B	11.09	7.300e-17	65-80	BL00222	Insulin-like growth factor binding proteins.
1560	BL00222C	22.97	1.409e-29	237-264	BL00222	Insulin-like growth factor binding proteins.
1560	BL00484B	9.04	1.000e-17	238-251	BL00484	Thyroglobulin type-1 repeat proteins
1560	BL00484C	17.01	5.737e-15	262-276	BL00484	Thyroglobulin type-1 repeat proteins
1561	BL00222B	11.09	7.333e-15	55-70	BL00222	Insulin-like growth factor binding proteins.
1561	BL00222C	22.97	2.161e-24	203-230	BL00222	Insulin-like growth factor binding proteins.
1561	BL00484B	9.04	6.143e-16	204-217	BL00484	Thyroglobulin type-1 repeat proteins
1561	BL00484C	17.01	1.375e-14	228-242	BL00484	Thyroglobulin type-1 repeat proteins
1562	BL00322A	9.23	1.000e-40	30-81	BL00322	Histone H3 proteins.
1562	BL00322B	13.68	1.000e-40	83-135	BL00322	Histone H3 proteins.
1562	PR00622A	6.52	1.391e-19	3-17	PR00622	HISTONE H3 SIGNATURE
1562	PR00622B	6.92	1.409e-19	17-31	PR00622	HISTONE H3 SIGNATURE
1562	PR00622C	8.83	1.391e-28	34-55	PR00622	HISTONE H3 SIGNATURE
1562	PR00622D	12.71	1.273e-22	58-75	PR00622	HISTONE H3 SIGNATURE
1562	PR00622E	15.81	1.281e-21	80-98	PR00622	HISTONE H3 SIGNATURE
1562	PR00622F	19.51	1.265e-22	98-114	PR00622	HISTONE H3 SIGNATURE
1562	PR00622G	13.24	1.300e-28	114-135	PR00622	HISTONE H3 SIGNATURE
1563	BL00290A	20.89	1.000e-14	221-243	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1563	BL00290A	20.89	2.800e-16	31-53	BL00290	Immunoglobulins and major histocompatibility complex proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1563	BL00290B	13.17	4.000e-21	278-295	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1564	BL00345B	21.28	9.118e-30	304-354	BL00345	Ets-domain proteins.
1564	BL00354A	3.83	8.875e-10	244-253	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (A+T-hook).
1564	BL00354B	3.16	6.468e-09	241-253	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (A+T-hook).
1564	PR00454B	20.78	8.380e-12	299-317	PR00454	ETS DOMAIN SIGNATURE
1564	PR00454C	11.24	5.119e-14	318-336	PR00454	ETS DOMAIN SIGNATURE
1564	PR00454D	10.89	5.860e-11	337-355	PR00454	ETS DOMAIN SIGNATURE
1564	PR00929A	3.25	6.571e-09	244-254	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE
1564	PR00929B	4.38	5.018e-09	242-253	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE
1564	PR00929C	5.26	4.736e-10	242-252	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE
1564	PR00930D	5.16	9.407e-09	233-252	PR00930	HIGH MOBILITY GROUP PROTEIN (HMGY) SIGNATURE
1565	BL00290A	20.89	7.882e-14	224-246	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1565	BL00290A	20.89	9.526e-13	34-56	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1565	BL00290B	13.17	6.625e-19	281-298	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1565	PR00818B	6.95	1.614e-09	164-180	PR00818	ISLET AMYLOID PROTEIN (AMYLIN) SIGNATURE
1566	BL00299	28.84	7.943e-26	97-148	BL00299	Ubiquitin domain proteins.
1568	PF01105B	25.12	2.016e-20	154-205	PF01105	emp24/gp25L/p24 family.
1569	BL00380F	9.76	9.705e-09	38-48	BL00380	Rhodanese proteins.
1569	BL00383E	10.35	1.692e-10	256-266	BL00383	Tyrosine specific protein phosphatases proteins.
1569	BL00415R	7.93	7.655e-11	302-341	BL00415	Synapsins proteins.
1569	PR00700D	12.47	4.462e-11	253-271	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1569	PR00716C	17.65	7.750e-09	26-46	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE
1570	BL00712A	6.23	6.000e-25	2-21	BL00712	Ribosomal protein S17e proteins.
1570	BL00712B	12.56	1.000e-40	28-65	BL00712	Ribosomal protein S17e proteins.
1570	BL00712C	9.67	1.900e-13	98-107	BL00712	Ribosomal protein S17e proteins.
1571	BL00388A	23.14	3.483e-37	6-51	BL00388	Proteasome A-type subunits proteins.
1571	BL00388B	31.38	2.731e-29	62-103	BL00388	Proteasome A-type subunits proteins.
1571	BL00388C	18.79	2.385e-19	117-138	BL00388	Proteasome A-type subunits proteins.
1571	BL00388D	20.71	4.462e-24	144-174	BL00388	Proteasome A-type subunits proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1572	BL01002B	7.39	3.118e-14	14-27	BL01002	Translationally controlled tumor protein.
1572	BL01002C	21.97	6.143e-26	45-75	BL01002	Translationally controlled tumor protein.
1572	BL01002D	18.24	4.706e-26	109-136	BL01002	Translationally controlled tumor protein.
1573	BL00298C	16.40	1.000e-40	28-71	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298D	17.97	1.000e-40	84-123	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298E	27.30	1.000e-40	178-232	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298F	11.21	1.000e-40	264-318	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298G	24.57	1.000e-40	321-375	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298H	20.50	1.000e-40	409-462	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00298I	30.07	1.000e-40	513-566	BL00298	Heat shock hsp90 proteins family proteins.
1573	BL00412D	16.54	5.989e-10	121-171	BL00412	Neuromodulin (GAP-43) proteins.
1573	PR00775D	8.91	1.000e-22	9-26	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1573	PR00775E	8.06	5.500e-28	34-56	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1573	PR00775F	12.76	7.188e-21	85-102	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1573	PR00775G	10.64	1.750e-23	103-121	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1574	BL00076A	18.83	9.163e-13	14-43	BL00076	Pyridine nucleotide-disulphide oxidoreductases class-I.
1574	BL00504A	10.76	3.712e-10	15-36	BL00504	Fumarate reductase / succinate dehydrogenase FAD-binding site proteins.
1574	BL00623A	12.60	5.500e-10	15-33	BL00623	GMC oxidoreductases proteins.
1574	BL00836D	22.30	1.574e-10	15-51	BL00836	Alanine dehydrogenase & pyridine nucleotide transhydrogenase.
1574	BL00977A	20.76	4.051e-09	15-66	BL00977	FAD-dependent glycerol-3-phosphate dehydrogenase proteins.
1574	BL00982A	18.41	1.000e-13	17-48	BL00982	Bacterial-type phytoene dehydrogenase proteins.
1574	BL01280A	15.97	8.740e-09	15-55	BL01280	Glucose inhibited division protein A family proteins.
1574	PR00368A	17.76	1.865e-10	15-37	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE
1574	PR00368C	15.74	3.656e-09	15-40	PR00368	FAD-DEPENDENT PYRIDINE NUCLEOTIDE REDUCTASE SIGNATURE
1574	PR00370A	3.35	7.932e-10	15-30	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1574	PR00411A	15.95	6.365e-10	15-37	PR00411	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-I SIGNATURE
1574	PR00419A	14.89	4.214e-09	15-37	PR00419	ADRENODOXIN REDUCTASE FAMILY SIGNATURE
1574	PR00420A	14.78	6.750e-16	15-37	PR00420	AROMATIC-RING HYDROXYLASE (FLAVOPROTEIN MONOOXYGENASE) SIGNATURE
1574	PR00469F	16.51	6.241e-09	11-35	PR00469	PYRIDINE NUCLEOTIDE DISULPHIDE REDUCTASE CLASS-II SIGNATURE
1574	PR00757A	6.64	2.324e-22	15-34	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757B	12.54	2.286e-30	101-123	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757C	13.48	1.600e-30	183-204	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757D	6.41	3.571e-29	206-228	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757E	11.48	1.000e-27	303-322	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757F	15.60	1.129e-28	389-408	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757G	4.34	5.345e-30	410-432	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757H	9.22	1.096e-23	441-458	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1574	PR00757I	12.66	3.368e-29	471-493	PR00757	FLAVIN-CONTAINING AMINE OXIDASE SIGNATURE
1575	BL00290A	20.89	2.421e-13	224-246	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1575	BL00290A	20.89	4.600e-16	34-56	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1575	BL00290B	13.17	4.000e-21	281-298	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1576	BL00290A	20.89	6.684e-13	129-151	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1576	BL00290B	13.17	9.308e-15	186-203	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1577	BL00469	22.22	1.000e-40	78-132	BL00469	Nucleoside diphosphate kinases proteins.
1578	BL00113A	12.74	4.600e-09	142-158	BL00113	Adenylate kinase proteins.
1578	BL00291A	4.49	8.448e-09	47-81	BL00291	Prion protein.
1578	BL00674B	4.46	8.909e-11	138-159	BL00674	AAA-protein family proteins.
1578	PR00300A	9.56	5.442e-09	141-159	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE
1578	PR00449A	13.20	1.692e-10	139-160	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1578	PR00449D	10.79	6.400e-15	241-254	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1578	PR00449E	13.50	1.529e-11	276-298	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1578	PR00830A	8.41	8.644e-09	145-164	PR00830	ENDOPEPTIDASE LA (LON) SERINE PROTEASE (S16)

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SIGNATURE
1579	BL01257A	11.15	1.000e-40	2-44	BL01257	Ribosomal protein L10e proteins.
1579	BL01257B	12.56	1.000e-40	62-101	BL01257	Ribosomal protein L10e proteins.
1579	BL01257C	11.43	1.000e-40	102-136	BL01257	Ribosomal protein L10e proteins.
1579	BL01257D	18.80	1.000e-40	137-176	BL01257	Ribosomal protein L10e proteins.
1579	PF00774D	10.59	9.250e-10	189-214	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.
1580	BL01204A	17.74	1.000e-40	19-66	BL01204	NF-kappa-B/Rel/dorsal domain proteins.
1580	BL01204B	15.41	4.000e-16	113-126	BL01204	NF-kappa-B/Rel/dorsal domain proteins.
1580	BL01204C	13.93	9.727e-18	150-168	BL01204	NF-kappa-B/Rel/dorsal domain proteins.
1580	BL01204D	16.42	1.000e-40	185-228	BL01204	NF-kappa-B/Rel/dorsal domain proteins.
1580	BL01204E	13.83	8.875e-31	233-257	BL01204	NF-kappa-B/Rel/dorsal domain proteins.
1580	PR00057A	10.14	1.450e-24	25-42	PR00057	TRANSCRIPTION FACTOR NF-KB SIGNATURE
1580	PR00057B	11.81	5.629e-15	175-189	PR00057	TRANSCRIPTION FACTOR NF-KB SIGNATURE
1580	PR00057C	7.43	4.462e-25	208-228	PR00057	TRANSCRIPTION FACTOR NF-KB SIGNATURE
1580	PR00057D	11.94	1.563e-24	239-257	PR00057	TRANSCRIPTION FACTOR NF-KB SIGNATURE
1580	PR00057E	15.74	4.000e-14	280-294	PR00057	TRANSCRIPTION FACTOR NF-KB SIGNATURE
1581	BL00284A	15.64	7.231e-17	54-77	BL00284	Serpins proteins.
1581	BL00284B	17.99	1.783e-15	155-175	BL00284	Serpins proteins.
1581	BL00284C	28.56	4.913e-31	184-225	BL00284	Serpins proteins.
1581	BL00284D	16.34	6.538e-18	296-322	BL00284	Serpins proteins.
1581	BL00284E	19.15	8.875e-23	378-402	BL00284	Serpins proteins.
1582	BL01251A	17.37	4.240e-31	1-36	BL01251	Proliferating cell nuclear antigen proteins.
1582	BL01251B	17.25	1.000e-40	37-82	BL01251	Proliferating cell nuclear antigen proteins.
1582	BL01251C	19.35	1.000e-40	108-157	BL01251	Proliferating cell nuclear antigen proteins.
1582	BL01251D	23.72	1.000e-40	197-250	BL01251	Proliferating cell nuclear antigen proteins.
1582	PR00339A	5.83	6.400e-21	10-29	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE
1582	PR00339B	9.94	3.250e-20	34-52	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE
1582	PR00339C	13.91	7.158e-29	56-80	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE
1582	PR00339D	12.90	8.650e-26	110-132	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE
1582	PR00339E	14.05	2.000e-18	203-217	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1582	PR00339F	10.56	1.000e-22	241-258	PR00339	PROLIFERATING CELL NUCLEAR ANTIGEN (CYCLIN) SIGNATURE
1583	BL00507A	8.79	4.643e-09	309-329	BL00507	Nickel-dependent hydrogenases large subunit proteins.
1583	PD02870A	14.10	1.563e-17	39-55	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1583	PD02870B	18.83	7.968e-34	93-125	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1583	PD02870C	24.41	9.419e-31	136-170	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1583	PD02870D	15.74	4.000e-33	192-226	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1583	PD02870E	12.75	1.545e-16	244-260	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1583	PD02870F	22.82	4.536e-22	301-325	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1584	BL01024A	10.26	1.000e-40	26-72	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024B	8.91	1.000e-40	90-130	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024C	7.80	1.000e-40	150-188	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024D	13.22	1.000e-40	189-225	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024E	11.96	1.000e-40	226-269	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024F	9.42	1.000e-40	270-320	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024G	11.09	1.000e-40	321-352	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	BL01024H	13.88	1.000e-40	393-445	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.
1584	PR00600A	11.61	6.000e-26	35-55	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600B	11.27	1.500e-37	70-98	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600C	10.70	3.842e-35	99-127	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600D	10.70	4.667e-36	176-203	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600E	12.87	1.000e-34	204-231	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600F	18.73	9.625e-36	232-260	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600G	8.77	6.143e-35	261-288	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600H	8.99	5.500e-36	289-316	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600I	10.13	6.625e-34	317-342	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600J	12.56	7.000e-	343-369	PR00600	PROTEIN PHOSPHATASE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			37			PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1584	PR00600K	11.12	3.647e-37	413-442	PR00600	PROTEIN PHOSPHATASE PP2A 55KD REGULATORY SUBUNIT SIGNATURE
1585	DM00372A	19.18	1.000e-40	19-63	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1585	DM00372B	20.31	9.763e-35	82-126	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1585	DM00372C	23.69	6.921e-23	321-356	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1586	BL00214A	21.17	1.257e-18	5-30	BL00214	Cytosolic fatty-acid binding proteins.
1586	BL00214B	26.51	6.516e-26	46-90	BL00214	Cytosolic fatty-acid binding proteins.
1586	PR00178A	15.07	5.846e-17	6-26	PR00178	FATTY ACID-BINDING PROTEIN SIGNATURE
1586	PR00178B	10.52	5.800e-10	40-51	PR00178	FATTY ACID-BINDING PROTEIN SIGNATURE
1586	PR00178C	20.54	3.919e-19	66-93	PR00178	FATTY ACID-BINDING PROTEIN SIGNATURE
1586	PR00178D	13.52	3.132e-14	112-130	PR00178	FATTY ACID-BINDING PROTEIN SIGNATURE
1587	BL00107A	18.39	3.842e-18	768-798	BL00107	Protein kinases ATP-binding region proteins.
1587	BL00107B	13.31	9.100e-14	835-850	BL00107	Protein kinases ATP-binding region proteins.
1587	BL00239B	25.15	2.849e-14	634-681	BL00239	Receptor tyrosine kinase class II proteins.
1587	BL00239C	18.75	3.684e-13	755-777	BL00239	Receptor tyrosine kinase class II proteins.
1587	BL00239D	16.81	4.356e-11	780-805	BL00239	Receptor tyrosine kinase class II proteins.
1587	BL00239E	17.14	6.891e-32	807-856	BL00239	Receptor tyrosine kinase class II proteins.
1587	BL00239F	28.15	1.632e-19	862-906	BL00239	Receptor tyrosine kinase class II proteins.
1587	BL00240A	22.72	6.516e-20	21-49	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240B	24.70	9.500e-20	417-440	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240C	22.58	1.000e-40	574-622	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240D	23.07	1.000e-40	623-677	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240E	11.56	1.000e-40	754-791	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240F	17.74	1.000e-40	806-853	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00240G	28.45	1.000e-40	854-906	BL00240	Receptor tyrosine kinase class III proteins.
1587	BL00790M	8.74	5.747e-09	759-780	BL00790	Receptor tyrosine kinase class V

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1587	BL00790N	13.25	1.098e-11	781-807	BL00790	Receptor tyrosine kinase class V proteins.
1587	BL00790O	7.68	3.302e-15	814-846	BL00790	Receptor tyrosine kinase class V proteins.
1587	BL00790Q	15.61	3.536e-10	873-921	BL00790	Receptor tyrosine kinase class V proteins.
1587	BL50001B	17.40	4.130e-10	765-785	BL50001	Src homology 2 (SH2) domain proteins profile.
1587	BL50001D	11.00	4.750e-09	835-845	BL50001	Src homology 2 (SH2) domain proteins profile.
1587	PR00109A	15.00	8.615e-15	663-676	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1587	PR00109B	12.27	5.500e-18	768-786	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1587	PR00109C	12.85	2.500e-14	817-827	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1587	PR00109D	17.04	7.158e-23	836-858	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1587	PR00109E	14.41	1.321e-16	881-903	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1590	BL00442B	14.98	5.765e-09	237-248	BL00442	Glutamine amidotransferases class-I proteins.
1591	BL00962A	11.87	1.600e-10	13-25	BL00962	Ribosomal protein S2 proteins.
1591	BL00962B	36.15	4.600e-36	28-81	BL00962	Ribosomal protein S2 proteins.
1591	BL00962C	15.90	9.591e-17	94-111	BL00962	Ribosomal protein S2 proteins.
1591	BL00962D	22.51	5.500e-35	119-162	BL00962	Ribosomal protein S2 proteins.
1591	PR00395A	16.93	6.464e-15	15-33	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1591	PR00395B	10.55	1.771e-10	45-54	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1591	PR00395C	16.17	1.000e-17	94-111	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1591	PR00395D	13.04	7.000e-17	119-136	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1591	PR00395E	14.46	4.103e-11	136-147	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1591	PR00395F	10.56	6.400e-16	157-171	PR00395	RIBOSOMAL PROTEIN S2 SIGNATURE
1592	BL00740B	19.76	3.813e-09	690-710	BL00740	MAM domain proteins.
1592	PR00597A	12.96	1.000e-25	375-396	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597A	12.96	4.575e-09	742-763	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597B	9.78	5.629e-09	85-101	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597B	9.78	7.000e-20	464-480	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597C	14.19	9.000e-23	489-507	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597D	12.77	4.522e-24	522-542	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597D	12.77	7.723e-09	144-164	PR00597	GELSOLIN FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1592	PR00597E	13.46	4.130e-21	576-596	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597F	16.29	4.522e-21	634-653	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597G	8.55	1.429e-28	690-712	PR00597	GELSOLIN FAMILY SIGNATURE
1592	PR00597H	15.32	5.500e-22	719-738	PR00597	GELSOLIN FAMILY SIGNATURE
1595	BL01019A	13.20	3.629e-09	46-85	BL01019	ADP-ribosylation factors family proteins.
1595	BL01115A	10.22	2.688e-14	12-55	BL01115	GTP-binding nuclear protein ran proteins.
1595	PR00449A	13.20	7.000e-20	12-33	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1595	PR00449B	14.34	7.500e-12	35-51	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1595	PR00449C	17.27	5.500e-24	53-75	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1595	PR00449D	10.79	5.500e-14	115-128	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1595	PR00449E	13.50	5.263e-17	150-172	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1596	BL00578A	14.24	2.800e-37	1-31	BL00578	Ribosomal protein S6e proteins.
1596	BL00578B	15.15	1.000e-40	39-89	BL00578	Ribosomal protein S6e proteins.
1596	BL00578C	9.53	1.000e-40	120-157	BL00578	Ribosomal protein S6e proteins.
1596	BL00578D	16.68	1.000e-40	164-213	BL00578	Ribosomal protein S6e proteins.
1597	BL00472B	14.67	8.448e-12	31-48	BL00472	Small cytokines (intercrine/chemokine) C-C subfamily signatur.
1597	PR00436D	12.23	1.106e-10	72-95	PR00436	INTERLEUKIN-8 SIGNATURE
1598	DM00895E	15.72	3.333e-11	527-551	DM00895	7 kw REVERSE TRANSCRIPTASE RNA POLYMERASE.
1598	DM01354A	11.77	4.462e-29	13-40	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354B	14.71	9.280e-33	41-68	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354C	8.79	5.680e-21	69-86	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354D	10.59	4.960e-32	87-114	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354E	18.69	3.025e-28	115-144	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354F	14.56	7.943e-37	145-180	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354G	11.57	9.500e-37	181-211	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354H	18.00	8.071e-30	212-251	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354I	15.55	2.800e-39	252-292	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354J	15.12	8.541e-31	293-324	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354K	9.35	1.200e-30	325-356	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354L	11.73	4.000e-30	357-383	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354M	12.50	4.960e-33	384-413	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354N	13.17	1.000e-40	414-458	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354O	8.73	1.000e-40	465-510	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354P	9.18	3.308e-	511-544	DM01354	kw TRANSCRIPTASE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			REVERSE II ORF2.
1598	DM01354Q	9.23	1.000e-40	545-599	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354R	8.50	5.714e-31	600-629	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354S	11.61	7.300e-26	630-650	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354T	9.48	1.000e-40	651-693	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354U	12.24	7.171e-21	740-759	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354V	12.97	1.000e-40	760-806	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354W	12.64	6.760e-23	807-826	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354X	13.86	1.000e-40	827-865	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354Y	10.69	1.000e-40	876-915	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1598	DM01354Z	9.06	1.000e-40	1190-1238	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1600	BL00322A	9.23	1.000e-40	32-83	BL00322	Histone H3 proteins.
1600	BL00322B	13.68	1.000e-40	85-137	BL00322	Histone H3 proteins.
1600	PR00622A	6.52	1.391e-19	5-19	PR00622	HISTONE H3 SIGNATURE
1600	PR00622B	6.92	1.409e-19	19-33	PR00622	HISTONE H3 SIGNATURE
1600	PR00622C	8.83	1.391e-28	36-57	PR00622	HISTONE H3 SIGNATURE
1600	PR00622D	12.71	1.273e-22	60-77	PR00622	HISTONE H3 SIGNATURE
1600	PR00622E	15.81	1.281e-21	82-100	PR00622	HISTONE H3 SIGNATURE
1600	PR00622F	19.51	1.265e-22	100-116	PR00622	HISTONE H3 SIGNATURE
1600	PR00622G	13.24	1.300e-28	116-137	PR00622	HISTONE H3 SIGNATURE
1601	BL00065A	31.92	4.682e-27	115-156	BL00065	D-isomer specific 2-hydroxyacid dehydrogenases NAD-binding si.
1601	BL00065B	16.97	7.652e-19	179-203	BL00065	D-isomer specific 2-hydroxyacid dehydrogenases NAD-binding si.
1601	BL00065C	27.25	6.000e-37	253-303	BL00065	D-isomer specific 2-hydroxyacid dehydrogenases NAD-binding si.
1601	BL00071A	5.81	8.258e-09	184-195	BL00071	Glyceraldehyde 3-phosphate dehydrogenase proteins.
1603	BL00388A	23.14	5.500e-39	8-53	BL00388	Proteasome A-type subunits proteins.
1603	BL00388B	31.38	7.207e-27	66-107	BL00388	Proteasome A-type subunits proteins.
1603	BL00388C	18.79	4.706e-16	121-142	BL00388	Proteasome A-type subunits proteins.
1603	BL00388D	20.71	6.897e-23	149-179	BL00388	Proteasome A-type subunits proteins.
1603	PF00227	14.68	6.294e-10	15-26	PF00227	Proteasome A-type and B-type.
1604	BL00053A	8.83	5.320e-12	5-17	BL00053	Ribosomal protein S8 proteins.
1604	BL00053B	14.56	4.789e-14	58-75	BL00053	Ribosomal protein S8 proteins.
1604	BL00053C	16.71	5.500e-26	98-130	BL00053	Ribosomal protein S8 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1607	BL01170A	12.34	9.143e-40	139-174	BL01170	Ribosomal protein L6e proteins.
1607	BL01170B	19.54	5.821e-37	251-288	BL01170	Ribosomal protein L6e proteins.
1607	PD01457A	16.51	9.845e-09	67-111	PD01457	RIBOSOMAL PROTEIN 40S ZINC-FINGER METAL.
1608	BL50040A	12.98	1.450e-14	4-15	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040B	13.65	7.000e-30	53-78	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040C	22.62	3.739e-38	135-177	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040D	17.41	1.000e-40	273-322	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040E	18.79	1.000e-40	327-381	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040F	18.99	5.320e-40	384-421	BL50040	Elongation factor 1 gamma chain profile.
1608	BL50040G	8.15	1.900e-13	427-437	BL50040	Elongation factor 1 gamma chain profile.
1608	DM01181C	17.27	6.055e-12	125-162	DM01181	7 kw 103-1A LACTOYLGLUTATHIONE GLUTATHIONE LYASE.
1608	PF00043	21.83	9.735e-11	57-86	PF00043	Glutathione S-transferases.
1609	BL01052A	16.12	2.875e-35	3-34	BL01052	Calponin family repeat proteins.
1609	BL01052B	15.31	5.219e-26	52-77	BL01052	Calponin family repeat proteins.
1609	BL01052C	18.51	1.000e-40	88-127	BL01052	Calponin family repeat proteins.
1609	BL01052D	10.26	4.462e-24	175-194	BL01052	Calponin family repeat proteins.
1609	PR00888A	11.87	7.750e-18	3-17	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888B	13.72	1.321e-14	22-35	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888C	12.27	2.286e-17	52-67	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888D	16.09	9.550e-19	89-105	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888E	11.81	2.800e-18	105-120	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888F	7.44	4.600e-18	126-140	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888G	12.73	9.438e-15	163-176	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00888H	9.97	8.269e-20	176-191	PR00888	SMOOTH MUSCLE PROTEIN/CALPONIN FAMILY SIGNATURE
1609	PR00889E	12.18	7.300e-11	172-187	PR00889	CALPONIN SIGNATURE
1609	PR00890A	8.61	1.000e-26	34-53	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
1609	PR00890B	8.75	6.318e-19	62-77	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
1609	PR00890C	8.22	1.600e-19	85-98	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
1609	PR00890D	16.17	1.130e-13	119-128	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN)

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						SIGNATURE
1609	PR00890E	14.34	1.429e-27	136-155	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
1609	PR00890F	12.92	1.643e-17	162-174	PR00890	SMOOTH MUSCLE PROTEIN 22-ALPHA (TRANSGELIN) SIGNATURE
1612	PR00194A	7.86	7.652e-09	180-197	PR00194	TROPOMYOSIN SIGNATURE
1614	DM00934A	20.07	8.663e-11	7-54	DM00934	kw DIHYDROFLAVONOL YOL151W YDR541C YGL157W.
1616	BL00605	27.67	1.000e-40	74-127	BL00605	ATP synthase c subunit proteins.
1616	PR00124A	8.81	2.125e-17	70-89	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE
1616	PR00124A	8.81	8.603e-09	72-91	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE
1616	PR00124B	14.66	1.000e-15	91-106	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE
1616	PR00124C	12.42	3.250e-27	108-133	PR00124	ATP SYNTHASE C SUBUNIT SIGNATURE
1618	BL00310E	19.92	8.875e-12	257-281	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1618	BL00310F	23.26	3.377e-10	291-345	BL00310	Lysosome-associated membrane glycoproteins duplicated domain proteins.
1618	PR00336A	12.86	6.455e-24	158-182	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1618	PR00336B	15.42	9.027e-13	269-283	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1618	PR00336C	14.47	9.438e-11	306-318	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1618	PR00336D	9.96	5.705e-19	319-341	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1618	PR00336E	11.59	1.711e-12	341-353	PR00336	LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN SIGNATURE
1619	BL00280	24.61	5.091e-38	317-360	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.
1619	BL00319A	17.62	1.000e-40	77-125	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	BL00319B	17.02	2.440e-29	173-198	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	BL00319C	17.12	6.143e-30	265-298	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	BL00319D	21.29	1.000e-40	365-414	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	BL00319E	12.66	1.000e-40	438-479	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	BL00319F	13.95	1.000e-40	480-522	BL00319	Amyloidogenic glycoprotein

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						extracellular domain proteins.
1619	BL00319G	16.93	1.000e-40	717-762	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.
1619	PR00203A	13.98	3.829e-21	193-211	PR00203	AMYLOID A4 PROTEIN PRECURSOR SIGNATURE
1619	PR00203B	11.38	8.500e-28	381-404	PR00203	AMYLOID A4 PROTEIN PRECURSOR SIGNATURE
1619	PR00203C	6.37	4.667e-27	692-717	PR00203	AMYLOID A4 PROTEIN PRECURSOR SIGNATURE
1619	PR00203D	13.57	2.895e-30	738-760	PR00203	AMYLOID A4 PROTEIN PRECURSOR SIGNATURE
1619	PR00759A	14.51	2.440e-10	307-321	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1619	PR00759B	11.26	7.000e-13	335-345	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1619	PR00759C	14.15	1.000e-14	345-360	PR00759	BASIC PROTEASE (KUNITZ-TYPE) INHIBITOR FAMILY SIGNATURE
1620	BL00634	34.38	1.333e-37	93-143	BL00634	Ribosomal protein L30 proteins.
1622	BL00107A	18.39	9.400e-22	1012-1042	BL00107	Protein kinases ATP-binding region proteins.
1622	BL00107B	13.31	7.300e-14	1079-1094	BL00107	Protein kinases ATP-binding region proteins.
1622	BL00239C	18.75	1.913e-10	999-1021	BL00239	Receptor tyrosine kinase class II proteins.
1622	BL00239D	16.81	9.043e-14	1024-1049	BL00239	Receptor tyrosine kinase class II proteins.
1622	BL00239E	17.14	4.436e-32	1051-1100	BL00239	Receptor tyrosine kinase class II proteins.
1622	BL00239F	28.15	2.770e-17	1106-1150	BL00239	Receptor tyrosine kinase class II proteins.
1622	BL00240A	22.72	7.500e-18	32-60	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240B	24.70	5.333e-15	575-598	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240B	24.70	5.404e-09	452-475	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240B	24.70	6.651e-10	680-703	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240C	22.58	1.000e-40	819-867	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240D	23.07	1.000e-40	868-922	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240E	11.56	3.182e-40	998-1035	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240F	17.74	1.000e-40	1050-1097	BL00240	Receptor tyrosine kinase class III proteins.
1622	BL00240G	28.45	1.000e-40	1098-1150	BL00240	Receptor tyrosine kinase class III proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1622	BL00790M	8.74	1.692e-09	1003-1024	BL00790	Receptor tyrosine kinase class V proteins.
1622	BL00790N	13.25	6.929e-13	1025-1051	BL00790	Receptor tyrosine kinase class V proteins.
1622	BL00790O	7.68	4.539e-14	1058-1090	BL00790	Receptor tyrosine kinase class V proteins.
1622	BL00790Q	15.61	8.533e-15	1117-1165	BL00790	Receptor tyrosine kinase class V proteins.
1622	BL50001B	17.40	1.000e-12	1009-1029	BL50001	Src homology 2 (SH2) domain proteins profile.
1622	BL50001D	11.00	9.100e-10	1079-1089	BL50001	Src homology 2 (SH2) domain proteins profile.
1622	DM00179	13.97	8.826e-09	304-313	DM00179	w KINASE ALPHA ADHESION T-CELL.
1622	PD02870B	18.83	9.521e-09	621-653	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1622	PD02870B	18.83	9.617e-09	716-748	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1622	PD02870D	15.74	1.200e-10	621-655	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1622	PD02870D	15.74	5.117e-09	390-424	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.
1622	PR00109A	15.00	4.808e-11	909-922	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1622	PR00109B	12.27	5.714e-19	1012-1030	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1622	PR00109C	12.85	3.118e-12	1061-1071	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1622	PR00109D	17.04	2.286e-25	1080-1102	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1622	PR00109E	14.41	7.857e-19	1125-1147	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE
1622	PR00573D	15.57	1.000e-09	1284-1299	PR00573	INTERLEUKIN 8B RECEPTOR SIGNATURE
1623	DM01354Z	9.06	5.747e-14	1-49	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.
1624	BL00262A	12.48	8.200e-09	523-540	BL00262	Insulin family proteins.
1624	BL01282B	30.49	5.243e-09	517-555	BL01282	BIR repeat proteins.
1625	BL00779A	14.01	4.667e-27	31-57	BL00779	Glycoprotein hormones alpha chain proteins.
1625	BL00779B	6.45	1.429e-20	58-73	BL00779	Glycoprotein hormones alpha chain proteins.
1625	BL00779C	14.39	1.333e-37	82-115	BL00779	Glycoprotein hormones alpha chain proteins.
1625	PR00274A	9.96	2.500e-15	30-44	PR00274	GLYCOPROTEIN HORMONE ALPHA CHAIN SIGNATURE
1625	PR00274B	9.15	8.091e-26	50-69	PR00274	GLYCOPROTEIN HORMONE ALPHA CHAIN SIGNATURE
1625	PR00274C	13.49	5.959e-22	70-87	PR00274	GLYCOPROTEIN HORMONE ALPHA CHAIN SIGNATURE
1625	PR00274D	9.71	1.900e-23	99-115	PR00274	GLYCOPROTEIN HORMONE ALPHA CHAIN SIGNATURE
1626	BL01019A	13.20	7.353e-10	203-242	BL01019	ADP-ribosylation factors family proteins.
1626	PR00318A	7.84	4.000e-18	42-57	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1626	PR00318B	14.79	4.429e-22	190-212	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1626	PR00318C	12.09	9.526e-22	219-236	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1626	PR00318D	16.28	3.625e-26	241-269	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1626	PR00318E	7.23	2.875e-11	287-296	PR00318	ALPHA G-PROTEIN (TRANSDUCIN) SIGNATURE
1626	PR00440A	9.18	9.416e-14	42-57	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1626	PR00440B	13.27	7.078e-13	190-212	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1626	PR00440C	9.54	7.197e-15	219-236	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1626	PR00440D	8.15	5.081e-16	241-269	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1626	PR00440E	11.16	3.160e-10	288-296	PR00440	G-PROTEIN ALPHA SUBUNIT GROUP 12 SIGNATURE
1626	PR00441A	10.69	5.725e-17	42-57	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1626	PR00441B	16.16	7.709e-18	190-212	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1626	PR00441C	14.17	5.245e-16	219-236	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1626	PR00441D	14.44	9.847e-20	241-269	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1626	PR00441E	8.35	8.377e-10	288-296	PR00441	G-PROTEIN ALPHA SUBUNIT GROUP I SIGNATURE
1626	PR00442A	6.46	6.865e-13	42-57	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1626	PR00442B	7.17	5.390e-13	190-213	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1626	PR00442C	17.61	5.985e-16	219-236	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1626	PR00442D	9.29	9.679e-13	241-269	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1626	PR00442E	7.23	1.273e-10	288-296	PR00442	G-PROTEIN ALPHA SUBUNIT GROUP Q SIGNATURE
1626	PR00443A	15.16	1.097e-19	42-57	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443B	9.25	3.000e-29	94-117	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443C	14.35	1.346e-29	190-212	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443D	13.15	1.205e-25	219-236	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443E	11.98	2.421e-36	241-269	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443F	12.68	1.092e-11	288-296	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1626	PR00443G	7.19	1.750e-29	334-356	PR00443	G-PROTEIN ALPHA SUBUNIT GROUP S SIGNATURE
1627	BL00030A	14.39	1.000e-12	16-34	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1627	BL00030A	14.39	1.500e-10	107-125	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1627	BL00030B	7.03	1.900e-11	146-155	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.
1628	BL00353C	14.83	4.814e-09	1-47	BL00353	HMG1/2 proteins.
1628	PR00901L	11.74	5.348e-09	77-90	PR00901	PHEROMONE B ALPHA-1 RECEPTOR SIGNATURE
1629	BL01082	20.37	7.750e-40	152-191	BL01082	Ribosomal protein L7Ae proteins.
1629	PR00881A	9.94	7.517e-13	136-150	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1629	PR00881B	9.01	4.000e-17	155-168	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1629	PR00881C	12.76	1.000e-13	171-181	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1629	PR00881D	11.60	8.500e-16	181-195	PR00881	RIBOSOMAL PROTEIN L7A/RS6 FAMILY SIGNATURE
1629	PR00882A	8.80	3.160e-22	36-53	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882B	9.47	1.000e-22	53-70	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882C	15.18	2.969e-23	73-92	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882D	14.85	6.500e-17	97-110	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882E	14.99	2.216e-21	132-152	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882F	13.81	4.273e-26	193-217	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00882G	10.27	8.500e-25	225-245	PR00882	RIBOSOMAL PROTEIN L7A FAMILY SIGNATURE
1629	PR00884C	7.05	7.409e-10	154-165	PR00884	RIBOSOMAL PROTEIN HS6 SIGNATURE
1630	BL00529A	22.06	1.000e-40	5-49	BL00529	Ribosomal protein S24e proteins.
1630	BL00529B	20.08	1.000e-40	55-99	BL00529	Ribosomal protein S24e proteins.
1631	BL00612A	12.09	7.171e-09	3-18	BL00612	Osteonectin domain proteins.
1631	PD01469	20.59	1.346e-29	357-388	PD01469	GLYCOPROTEIN PROTEIN PRECURSOR SA.
1631	PD01469	20.59	7.176e-19	451-482	PD01469	GLYCOPROTEIN PROTEIN PRECURSOR SA.
1632	BL00326A	14.01	6.651e-09	162-195	BL00326	Tropomyosins proteins.
1632	BL00326A	14.01	9.308e-37	1-34	BL00326	Tropomyosins proteins.
1632	BL00326B	7.68	1.000e-40	81-129	BL00326	Tropomyosins proteins.
1632	BL00326B	7.68	3.838e-10	39-87	BL00326	Tropomyosins proteins.
1632	BL00326C	9.99	1.000e-40	137-190	BL00326	Tropomyosins proteins.
1632	BL00326C	9.99	2.116e-09	95-148	BL00326	Tropomyosins proteins.
1632	BL00326C	9.99	3.306e-09	193-246	BL00326	Tropomyosins proteins.
1632	BL00326D	8.76	1.000e-40	220-260	BL00326	Tropomyosins proteins.
1632	BL00326D	8.76	7.511e-12	59-99	BL00326	Tropomyosins proteins.
1632	PR00194A	7.86	4.857e-21	84-101	PR00194	TROPOMYOSIN SIGNATURE
1632	PR00194B	10.24	6.143e-26	120-140	PR00194	TROPOMYOSIN SIGNATURE
1632	PR00194C	6.38	1.450e-32	145-173	PR00194	TROPOMYOSIN SIGNATURE
1632	PR00194D	9.57	1.788e-09	21-44	PR00194	TROPOMYOSIN SIGNATURE
1632	PR00194D	9.57	6.400e-23	175-198	PR00194	TROPOMYOSIN SIGNATURE
1632	PR00194E	8.74	1.000e-30	231-256	PR00194	TROPOMYOSIN SIGNATURE
1633	BL00266A	15.69	5.200e-26	46-72	BL00266	Somatotropin, prolactin and related hormones proteins.
1633	BL00266B	24.48	1.857e-29	86-123	BL00266	Somatotropin, prolactin and related hormones proteins.
1633	BL00266C	13.66	5.304e-12	146-162	BL00266	Somatotropin, prolactin and related hormones

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1633	BL00266D	12.72	1.818e-27	197-220	BL00266	Somatotropin, prolactin and related hormones proteins.
1633	PR00836A	14.40	9.471e-14	86-99	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1633	PR00836B	16.59	3.571e-15	108-126	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1633	PR00836C	11.95	2.500e-17	190-206	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1633	PR00836D	13.05	2.688e-17	206-220	PR00836	SOMATOTROPIN HORMONE FAMILY SIGNATURE
1635	BL00383A	13.34	6.000e-09	1657-1671	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383A	13.34	9.550e-14	1368-1382	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383B	7.61	6.143e-12	1393-1401	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383B	7.61	8.500e-09	1682-1690	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383C	10.10	1.000e-10	1712-1722	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383C	10.10	4.500e-13	1423-1433	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383D	11.92	7.500e-12	1787-1799	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383D	11.92	9.400e-13	1498-1510	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383E	10.35	1.000e-14	1536-1546	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383E	10.35	1.000e-14	1827-1837	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383F	15.51	7.120e-13	1865-1880	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00383F	15.51	8.941e-16	1574-1589	BL00383	Tyrosine specific protein phosphatases proteins.
1635	BL00621G	22.33	1.250e-10	1225-1278	BL00621	Tissue factor proteins.
1635	BL00790I	20.01	1.536e-09	663-693	BL00790	Receptor tyrosine kinase class V proteins.
1635	BL00790I	20.01	2.688e-10	776-806	BL00790	Receptor tyrosine kinase class V proteins.
1635	BL00790I	20.01	2.800e-10	467-497	BL00790	Receptor tyrosine kinase class V proteins.
1635	BL00790I	20.01	8.500e-12	561-591	BL00790	Receptor tyrosine kinase class V proteins.
1635	BL00790I	20.01	9.735e-13	967-997	BL00790	Receptor tyrosine kinase class V proteins.
1635	PR00014B	14.77	5.500e-09	431-441	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1635	PR00014C	15.44	5.500e-10	550-568	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1635	PR00014C	15.44	8.500e-	956-974	PR00014	FIBRONECTIN TYPE III

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			14			REPEAT SIGNATURE
1635	PR00014D	12.04	5.235e-10	878-892	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1635	PR00014D	12.04	7.000e-11	670-684	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1635	PR00014D	12.04	7.750e-09	974-988	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE
1635	PR00219C	9.04	4.450e-09	1251-1270	PR00219	SYNAPTOBREVIN SIGNATURE
1635	PR00346H	10.74	1.214e-09	1250-1273	PR00346	TISSUE FACTOR SIGNATURE
1635	PR00700A	6.96	8.714e-11	1394-1401	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700B	16.80	1.500e-24	1410-1430	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700B	16.80	4.240e-21	1699-1719	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700C	13.17	5.800e-18	1494-1511	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700C	13.17	7.353e-17	1783-1800	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700D	12.47	4.214e-22	1533-1551	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700D	12.47	7.158e-20	1824-1842	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700E	17.57	4.000e-14	1855-1870	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700E	17.57	5.304e-12	1564-1579	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700F	11.18	1.429e-12	1871-1881	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1635	PR00700F	11.18	7.353e-13	1580-1590	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE
1636	BL00152A	15.38	5.154e-21	134-159	BL00152	ATP synthase alpha and beta subunits proteins.
1636	BL00152B	21.40	4.000e-32	191-228	BL00152	ATP synthase alpha and beta subunits proteins.
1636	BL00152C	11.41	6.250e-12	291-302	BL00152	ATP synthase alpha and beta subunits proteins.
1636	BL00152D	29.00	1.000e-40	310-354	BL00152	ATP synthase alpha and beta subunits proteins.
1636	BL00152E	22.68	1.000e-32	362-399	BL00152	ATP synthase alpha and beta subunits proteins.
1637	BL00018	7.41	4.130e-09	67-79	BL00018	EF-hand calcium-binding domain proteins.
1637	BL00303A	21.77	6.667e-26	7-43	BL00303	S-100/ICaBP type calcium binding protein.
1637	BL00303B	26.15	1.000e-24	55-91	BL00303	S-100/ICaBP type calcium binding protein.
1637	PR00334B	8.69	8.286e-09	90-113	PR00334	HMW KININOGEN SIGNATURE
1639	BL00111A	9.65	3.000e-17	16-29	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111B	12.16	7.923e-15	58-69	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111C	15.75	6.850e-20	74-98	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111D	16.01	9.400e-16	114-128	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111E	11.18	1.750e-26	159-179	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111F	14.32	1.000e-40	186-232	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111G	26.36	3.769e-34	253-292	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111H	20.83	3.455e-31	317-352	BL00111	Phosphoglycerate kinase proteins.
1639	BL00111I	9.95	1.643e-	390-411	BL00111	Phosphoglycerate kinase

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			25			proteins.
1639	BL00461B	14.59	1.437e-09	201-240	BL00461	6-phosphogluconate dehydrogenase proteins.
1639	PR00477A	7.93	3.769e-20	13-29	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477B	14.50	4.857e-22	34-56	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477C	14.67	6.400e-17	114-129	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477D	12.94	1.900e-28	157-179	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477E	11.95	3.500e-22	186-208	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477F	7.63	8.000e-20	209-228	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477G	15.40	1.000e-24	333-358	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477H	5.93	6.000e-15	369-380	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1639	PR00477I	8.53	4.000e-20	392-409	PR00477	PHOSPHOGLYCERATE KINASE FAMILY SIGNATURE
1640	PR00360B	13.61	1.818e-09	40-53	PR00360	C2 DOMAIN SIGNATURE
1640	PR00360B	13.61	6.455e-11	1193-1206	PR00360	C2 DOMAIN SIGNATURE
1641	BL00115A	15.44	1.000e-40	50-88	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115B	15.42	2.957e-36	89-120	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115C	14.01	4.750e-24	182-203	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115D	19.94	1.000e-40	224-264	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115E	14.13	8.560e-31	297-325	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115F	10.77	7.107e-36	326-356	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115G	11.65	2.000e-34	357-384	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115H	14.34	2.286e-35	385-417	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115I	8.33	1.000e-40	443-497	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115J	16.71	9.143e-31	498-523	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115K	15.03	1.000e-40	524-565	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115L	12.25	6.464e-	566-597	BL00115	Eukaryotic RNA

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			37			polymerase II heptapeptide repeat proteins.
1641	BL00115M	19.19	1.000e-40	622-664	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115N	20.57	1.000e-40	665-713	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115O	16.76	1.000e-40	735-784	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115P	11.54	1.000e-40	785-824	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Q	18.08	2.575e-37	825-854	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115R	6.50	2.385e-32	855-881	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115S	18.24	6.333e-40	882-923	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115T	8.45	1.000e-40	1083-1116	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115U	10.34	2.688e-26	1117-1139	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115V	21.32	1.000e-40	1140-1189	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115W	21.01	1.000e-40	1208-1253	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115X	21.13	5.500e-35	1324-1359	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Y	11.86	1.000e-40	1360-1405	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-08	1568-1616	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1604-1652	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1611-1659	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1618-1666	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1641	BL00115Z	3.12	1.000e-40	1625-1673	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1632-1680	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1639-1687	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1646-1694	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1653-1701	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1660-1708	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1667-1715	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1674-1722	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1681-1729	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1688-1736	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1695-1743	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1702-1750	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1709-1757	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1716-1764	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1723-1771	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1730-1778	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1737-1785	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1744-1792	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1641	BL00115Z	3.12	1.000e-40	1751-1799	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1758-1806	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1765-1813	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1772-1820	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1779-1827	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1786-1834	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1793-1841	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1800-1848	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1814-1862	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1821-1869	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1828-1876	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1835-1883	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1842-1890	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1849-1897	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1856-1904	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1863-1911	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1870-1918	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1877-1925	BL00115	Eukaryotic RNA polymerase II

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1884-1932	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.000e-40	1891-1939	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.493e-35	1597-1645	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	1.779e-17	1922-1970	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	2.636e-12	1561-1609	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	3.326e-24	1590-1638	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	3.380e-12	1554-1602	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	3.512e-10	1576-1624	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	4.030e-18	1583-1631	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	4.646e-30	1905-1953	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	5.760e-17	1908-1956	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	6.000e-23	1912-1960	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	6.302e-10	1894-1942	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	6.591e-40	1807-1855	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	7.154e-09	1547-1595	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	8.174e-38	1898-1946	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	8.566e-14	1901-1949	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	9.644e-	1919-1967	BL00115	Eukaryotic RNA

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			18			polymerase II heptapeptide repeat proteins.
1641	BL00115Z	3.12	9.903e-22	1915-1963	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.
1643	BL00298A	10.97	1.000e-40	74-118	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298B	15.64	1.290e-39	134-180	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298C	16.40	2.286e-40	186-229	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298D	17.97	6.226e-33	242-281	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298E	27.30	1.000e-40	321-375	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298F	11.21	1.000e-40	409-463	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298G	24.57	5.345e-39	465-519	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298H	20.50	1.000e-40	553-606	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00298I	30.07	7.818e-34	661-714	BL00298	Heat shock hsp90 proteins family proteins.
1643	BL00422C	16.18	9.234e-10	295-322	BL00422	Granins proteins.
1643	PD01781B	27.55	2.800e-09	758-801	PD01781	PROTEASE IMMUNOGLOBULIN PRECURSO.
1643	PR00775A	9.90	3.250e-22	74-94	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775B	3.52	3.700e-26	95-117	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775C	10.68	3.727e-16	144-161	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775D	8.91	9.640e-18	162-179	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775E	8.06	6.571e-27	192-214	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775F	12.76	2.800e-15	243-260	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1643	PR00775G	10.64	9.625e-19	261-279	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE
1644	BL00299	28.84	1.000e-40	16-67	BL00299	Ubiquitin domain proteins.
1644	PF01020	15.00	1.000e-40	80-128	PF01020	Ribosomal L40e family.
1644	PR00348A	7.86	2.000e-26	11-31	PR00348	UBIQUITIN SIGNATURE
1644	PR00348B	5.78	2.800e-27	32-52	PR00348	UBIQUITIN SIGNATURE
1644	PR00348C	20.03	1.643e-27	53-74	PR00348	UBIQUITIN SIGNATURE
1646	BL00646A	25.82	6.192e-29	14-61	BL00646	Ribosomal protein S13 proteins.
1646	BL00646B	21.42	6.100e-30	110-142	BL00646	Ribosomal protein S13 proteins.
1647	BL00358A	13.06	9.690e-11	19-29	BL00358	Ribosomal protein L5 proteins.
1647	BL00358B	22.76	2.742e-38	40-85	BL00358	Ribosomal protein L5 proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1647	BL00358C	13.75	5.500e-15	99-112	BL00358	Ribosomal protein L5 proteins.
1647	BL00358D	14.26	5.500e-14	119-133	BL00358	Ribosomal protein L5 proteins.
1649	BL00290A	20.89	7.158e-13	42-64	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1649	BL00290B	13.17	4.500e-12	98-115	BL00290	Immunoglobulins and major histocompatibility complex proteins.
1650	BL01121A	9.11	9.100e-12	90-100	BL01121	Caspase family histidine proteins.
1650	BL01121B	29.68	1.346e-26	103-138	BL01121	Caspase family histidine proteins.
1650	BL01121C	13.17	5.065e-15	150-165	BL01121	Caspase family histidine proteins.
1650	BL01121D	12.34	4.343e-19	197-214	BL01121	Caspase family histidine proteins.
1650	BL01121E	23.71	5.179e-31	247-281	BL01121	Caspase family histidine proteins.
1650	BL01121F	15.43	1.783e-12	293-305	BL01121	Caspase family histidine proteins.
1650	PR00376A	14.23	5.886e-14	88-101	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1650	PR00376B	15.57	9.660e-11	106-124	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1650	PR00376C	16.28	5.574e-10	124-142	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1650	PR00376D	12.74	1.250e-10	157-165	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1650	PR00376E	12.26	5.941e-18	197-215	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1650	PR00376F	13.77	4.833e-11	266-277	PR00376	INTERLEUKIN-1B CONVERTING ENZYME SIGNATURE
1651	BL00525A	11.57	4.971e-11	12-30	BL00525	Ribosomal protein L6 proteins.
1651	BL00700A	19.34	9.308e-33	8-45	BL00700	Ribosomal protein L6 proteins 2.
1651	BL00700B	18.26	1.000e-40	62-100	BL00700	Ribosomal protein L6 proteins 2.
1651	BL00700C	11.76	4.000e-13	112-121	BL00700	Ribosomal protein L6 proteins 2.
1651	BL00700D	21.51	1.000e-40	141-184	BL00700	Ribosomal protein L6 proteins 2.
1652	BL00055	15.98	2.200e-24	90-125	BL00055	Ribosomal protein S12 proteins.
1653	BL00299	28.84	8.269e-33	16-67	BL00299	Ubiquitin domain proteins.
1653	PR00348B	5.78	2.000e-15	32-52	PR00348	UBIQUITIN SIGNATURE
1653	PR00348C	20.03	8.477e-14	53-74	PR00348	UBIQUITIN SIGNATURE
1654	BL00024A	11.49	5.000e-11	75-85	BL00024	Hemopexin domain proteins.
1654	BL00024B	21.53	3.432e-26	104-137	BL00024	Hemopexin domain proteins.
1654	BL00024C	22.98	1.000e-40	152-200	BL00024	Hemopexin domain proteins.
1654	BL00024D	17.28	4.375e-29	206-237	BL00024	Hemopexin domain proteins.
1654	BL00024E	7.58	2.406e-14	245-258	BL00024	Hemopexin domain proteins.

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
1654	BL00024F	11.30	6.786e-21	298-318	BL00024	Hemopexin domain proteins.
1654	BL00024G	13.31	2.333e-09	429-441	BL00024	Hemopexin domain proteins.
1654	BL00024G	13.31	9.308e-13	336-348	BL00024	Hemopexin domain proteins.
1654	BL00024H	11.35	2.174e-13	355-366	BL00024	Hemopexin domain proteins.
1654	BL00024H	11.35	3.600e-09	401-412	BL00024	Hemopexin domain proteins.
1654	BL00142	8.38	2.636e-11	212-222	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
1654	BL00546A	19.62	8.154e-21	55-84	BL00546	Matrixins cysteine switch.
1654	BL00546B	20.11	1.000e-40	153-196	BL00546	Matrixins cysteine switch.
1654	BL00546C	16.41	2.575e-29	206-237	BL00546	Matrixins cysteine switch.
1654	BL00546D	10.34	2.459e-14	245-258	BL00546	Matrixins cysteine switch.
1654	BL00546E	10.23	9.727e-21	298-318	BL00546	Matrixins cysteine switch.
1654	BL00546F	12.40	6.700e-13	336-348	BL00546	Matrixins cysteine switch.
1654	BL00546F	12.40	8.059e-10	429-441	BL00546	Matrixins cysteine switch.
1654	BL00546G	16.84	2.091e-15	356-375	BL00546	Matrixins cysteine switch.
1654	BL00546G	16.84	3.368e-09	310-329	BL00546	Matrixins cysteine switch.
1654	BL00546H	10.76	1.514e-10	448-458	BL00546	Matrixins cysteine switch.
1654	BL00546H	10.76	6.333e-11	401-411	BL00546	Matrixins cysteine switch.
1654	PR00138A	15.14	7.000e-13	75-88	PR00138	MATRIXIN SIGNATURE
1654	PR00138B	15.82	6.625e-16	130-145	PR00138	MATRIXIN SIGNATURE
1654	PR00138C	16.41	9.053e-33	153-181	PR00138	MATRIXIN SIGNATURE
1654	PR00138D	16.56	6.921e-25	212-237	PR00138	MATRIXIN SIGNATURE
1654	PR00138E	6.01	2.091e-14	245-258	PR00138	MATRIXIN SIGNATURE
1654	PR00480B	15.41	5.355e-11	207-225	PR00480	ASTACIN FAMILY SIGNATURE
1656	PR00449E	13.50	8.313e-18	68-90	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1657	BL01160B	19.54	2.068e-09	139-192	BL01160	Kinesin light chain repeat proteins.
1657	PF00850D	14.76	5.846e-16	829-852	PF00850	Histone deacetylase family.
1657	PF00850E	8.88	8.071e-23	863-888	PF00850	Histone deacetylase family.
1657	PF00850F	15.70	1.556e-10	901-933	PF00850	Histone deacetylase family.
1657	PF00850G	22.75	9.250e-11	940-981	PF00850	Histone deacetylase family.
1658	BL00720B	16.57	6.516e-17	347-370	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.
1658	PR00761E	14.32	9.500e-10	38-56	PR00761	BINDIN PRECURSOR SIGNATURE
1659	BL01267A	18.07	7.618e-28	12-40	BL01267	Uncharacterized protein family UPF0023 proteins.
1659	BL01267B	18.76	6.936e-	41-81	BL01267	Uncharacterized protein

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			31			family UPF0023 proteins.
1659	BL01267C	22.80	9.348e-23	125-178	BL01267	Uncharacterized protein family UPF0023 proteins.
1660	BL01100A	12.62	1.947e-24	12-38	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100B	12.73	1.000e-40	42-85	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100C	10.34	6.211e-24	86-107	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100D	14.77	9.357e-23	110-134	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100E	12.25	1.000e-40	156-199	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100F	14.30	6.595e-28	200-232	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1660	BL01100G	14.70	9.780e-19	238-259	BL01100	NNMT/PNMT/TEMT family of methyltransferases proteins.
1661	BL00548	20.58	7.000e-19	66-95	BL00548	Ribosomal protein S3 proteins.
1661	BL00765A	13.27	1.000e-08	158-178	BL00765	Phosphoglucose isomerase proteins.
1661	PF00013	5.78	4.706e-10	58-69	PF00013	KH domain proteins family of RNA binding proteins.
1662	PD01733B	20.44	4.375e-09	410-464	PD01733	APOLIPOPROTEIN PLASMA LIPID TRANSPORT H.
1663	BL00267	14.21	8.667e-10	81-90	BL00267	Tachykinin family proteins.
1664	DM00372A	19.18	1.000e-40	19-63	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1664	DM00372B	20.31	9.229e-38	82-126	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1664	DM00372C	23.69	2.552e-28	321-356	DM00372	CARCINOEMBRYONIC ANTIGEN PRECURSOR AMINO-TERMINAL DOMAIN.
1664	PD01270D	24.66	1.000e-09	378-413	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.
1665	DM01269A	23.35	1.600e-20	68-95	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.
1665	DM01269B	11.71	3.323e-09	138-147	DM01269	303 kw ACTIVATING RAN GTPASE ISOZYME.
1665	PF00638	11.91	4.600e-18	67-81	PF00638	RanBP1 domain proteins.
1666	BL00633B	13.82	7.097e-16	166-190	BL00633	Bromodomain proteins.
1666	PR00503B	9.96	9.571e-13	165-181	PR00503	BROMODOMAIN SIGNATURE
1666	PR00503C	19.84	7.563e-09	181-199	PR00503	BROMODOMAIN SIGNATURE
1666	PR00503D	20.81	2.313e-11	199-218	PR00503	BROMODOMAIN SIGNATURE
1670	BL00282	16.88	8.875e-12	464-486	BL00282	Kazal serine protease inhibitors family proteins.
1670	BL00612A	12.09	3.136e-11	3-18	BL00612	Osteonectin domain proteins.
1670	BL00612B	11.35	6.625e-29	431-463	BL00612	Osteonectin domain proteins.
1670	BL00612C	9.90	1.000e-	496-543	BL00612	Osteonectin domain

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			40			proteins.
1670	BL00612D	10.06	1.000e-40	563-613	BL00612	Osteonectin domain proteins.
1670	BL00612E	13.12	1.000e-40	617-661	BL00612	Osteonectin domain proteins.
1671	BL00061A	9.41	6.684e-11	83-93	BL00061	Short-chain dehydrogenases/reductases family proteins.
1671	BL00061B	25.79	7.158e-19	136-173	BL00061	Short-chain dehydrogenases/reductases family proteins.
1671	PR00080A	9.32	9.667e-11	83-94	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
1671	PR00080C	17.16	2.125e-10	156-175	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE
1671	PR00081A	10.53	7.000e-12	5-22	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1671	PR00081B	10.38	3.368e-10	83-94	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1671	PR00081C	15.13	6.586e-10	130-146	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE
1672	BL00139A	10.29	1.000e-14	132-141	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1672	BL00139B	10.19	6.571e-09	175-183	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1672	BL00139C	9.23	2.800e-10	275-284	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1672	BL00139D	9.24	1.818e-18	295-311	BL00139	Eukaryotic thiol (cysteine) proteases cysteine proteins.
1672	PD01919E	19.31	7.582e-10	73-98	PD01919	PROTEIN PROCESSING TRANSPORT CAPSID ASSEMBLY PR.
1672	PR00704C	11.88	6.162e-09	132-148	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE
1672	PR00705A	10.55	4.000e-21	132-147	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1672	PR00705B	10.22	2.385e-10	276-286	PR00705	PAPAIN CYSTEINE PROTEASE (C1) FAMILY SIGNATURE
1673	BL00610A	17.73	1.000e-40	60-109	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610B	23.65	1.000e-40	123-172	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610C	12.94	1.000e-40	233-284	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610D	20.97	1.000e-40	299-351	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610E	20.34	3.423e-39	392-434	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610F	29.02	1.000e-40	491-545	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	BL00610G	12.89	4.706e-25	551-573	BL00610	Sodium:neurotransmitter symporter family proteins.
1673	PR00176A	16.82	8.500e-	60-81	PR00176	SODIUM/NEUROTRANSMITTER

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			28			SYMPORTER SIGNATURE
1673	PR00176B	7.31	7.250e-18	89-108	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176C	10.84	8.714e-27	132-158	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176D	9.02	1.783e-19	260-277	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176E	11.41	7.000e-21	342-362	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176F	10.73	2.333e-20	396-415	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176G	12.48	7.857e-20	480-500	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1673	PR00176H	15.27	5.500e-21	520-540	PR00176	SODIUM/NEUROTRANSMITTER SYMPORTER SIGNATURE
1674	BL00309C	18.65	1.621e-09	62-86	BL00309	Vertebrate galactoside-binding lectin proteins.
1675	BL00113A	12.74	9.585e-09	157-173	BL00113	Adenylate kinase proteins.
1675	BL00690A	6.87	3.455e-12	160-169	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1675	BL00690B	13.38	4.938e-18	191-208	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1675	BL00690C	7.51	8.650e-11	257-266	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.
1675	DM00406	7.73	9.514e-10	392-404	DM00406	GLIADIN.
1676	BL01082	20.37	3.500e-09	47-86	BL01082	Ribosomal protein L7Ae proteins.
1676	BL01189A	14.27	1.000e-40	35-70	BL01189	Ribosomal protein S12e proteins.
1676	BL01189B	13.49	1.000e-40	71-124	BL01189	Ribosomal protein S12e proteins.
1676	PR00972A	8.01	6.625e-17	21-34	PR00972	RIBOSOMAL PROTEIN S12E FAMILY SIGNATURE
1676	PR00972B	8.62	9.000e-21	35-51	PR00972	RIBOSOMAL PROTEIN S12E FAMILY SIGNATURE
1676	PR00972C	10.31	1.500e-26	76-97	PR00972	RIBOSOMAL PROTEIN S12E FAMILY SIGNATURE
1676	PR00972D	10.15	1.000e-18	101-114	PR00972	RIBOSOMAL PROTEIN S12E FAMILY SIGNATURE
1677	PF00043	21.83	3.647e-22	54-83	PF00043	Glutathione S-transferases.
1677	PR00455B	17.47	5.227e-09	60-83	PR00455	TETR BACTERIAL REGULATORY PROTEIN HTH SIGNATURE
1678	BL00501A	21.02	7.333e-18	106-131	BL00501	Signal peptidases I serine proteins.
1678	BL00501B	12.58	9.735e-11	132-147	BL00501	Signal peptidases I serine proteins.
1678	BL00501C	9.61	4.000e-10	156-167	BL00501	Signal peptidases I serine proteins.
1678	BL00501D	16.69	1.000e-15	179-198	BL00501	Signal peptidases I serine proteins.
1678	PR00728A	13.14	1.750e-20	125-140	PR00728	EUKARYOTIC SIGNAL PEPTIDASE (S27) FAMILY SIGNATURE
1678	PR00728B	11.12	1.000e-15	184-195	PR00728	EUKARYOTIC SIGNAL PEPTIDASE (S27) FAMILY SIGNATURE
1683	BL01019A	13.20	3.859e-10	57-96	BL01019	ADP-ribosylation factors family proteins.
1683	BL01115A	10.22	9.735e-12	23-66	BL01115	GTP-binding nuclear protein ran proteins.
1683	PR00449A	13.20	3.400e-	23-44	PR00449	TRANSFORMING PROTEIN

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
			15			P21 RAS SIGNATURE
1683	PR00449B	14.34	2.800e-10	46-62	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1683	PR00449C	17.27	8.941e-19	64-86	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1683	PR00449D	10.79	3.864e-12	126-139	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1683	PR00449E	13.50	6.478e-15	161-183	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE
1684	BL00604A	9.13	8.842e-20	49-103	BL00604	Synaptophysin / synaptoporin proteins.
1684	BL00604B	9.95	1.329e-19	114-143	BL00604	Synaptophysin / synaptoporin proteins.
1684	BL00604C	14.66	5.639e-12	144-175	BL00604	Synaptophysin / synaptoporin proteins.
1684	BL00604D	12.28	5.410e-11	176-210	BL00604	Synaptophysin / synaptoporin proteins.
1684	BL00604E	8.32	1.444e-23	210-251	BL00604	Synaptophysin / synaptoporin proteins.
1684	PR00220A	10.93	8.244e-24	46-68	PR00220	SYNAPTOPHYSIN/SYNAPTOPO RIN FAMILY SIGNATURE
1684	PR00220B	15.48	4.462e-24	70-95	PR00220	SYNAPTOPHYSIN/SYNAPTOPO RIN FAMILY SIGNATURE
1684	PR00220C	11.05	4.477e-25	127-151	PR00220	SYNAPTOPHYSIN/SYNAPTOPO RIN FAMILY SIGNATURE
1684	PR00220D	8.32	7.585e-26	159-182	PR00220	SYNAPTOPHYSIN/SYNAPTOPO RIN FAMILY SIGNATURE
1684	PR00220E	3.46	6.932e-23	225-243	PR00220	SYNAPTOPHYSIN/SYNAPTOPO RIN FAMILY SIGNATURE
1685	BL00142	8.38	5.909e-11	352-362	BL00142	Neutral zinc metalloproteinases, zinc-binding region proteins.
1685	BL00427	13.93	6.918e-24	449-503	BL00427	Disintegrins proteins.
1685	PR00289A	13.62	5.000e-19	463-482	PR00289	DISINTEGRIN SIGNATURE
1685	PR00289B	11.79	2.500e-12	492-504	PR00289	DISINTEGRIN SIGNATURE
1685	PR00480B	15.41	8.500e-10	347-365	PR00480	ASTACIN FAMILY SIGNATURE
1686	BL00421A	11.79	4.600e-15	67-85	BL00421	Transmembrane 4 family proteins.
1686	BL00421B	17.62	9.000e-34	118-156	BL00421	Transmembrane 4 family proteins.
1686	BL00421C	12.89	2.333e-11	203-214	BL00421	Transmembrane 4 family proteins.
1686	BL00421E	20.97	4.500e-21	287-316	BL00421	Transmembrane 4 family proteins.
1686	PR00174A	8.67	8.105e-09	71-93	PR00174	LACY PROTON/SUGAR SYMPORTER SIGNATURE
1686	PR00259A	9.27	2.742e-21	71-94	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1686	PR00259B	14.81	6.727e-23	112-138	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1686	PR00259C	16.40	1.265e-22	139-167	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1686	PR00259D	13.50	6.250e-23	290-316	PR00259	TRANSMEMBRANE FOUR FAMILY SIGNATURE
1688	BL00291A	4.49	5.345e-09	138-172	BL00291	Prion protein.
1688	BL00291A	4.49	7.724e-09	132-166	BL00291	Prion protein.
1688	DM01724	8.14	4.553e-09	156-175	DM01724	kw ALLERGEN POLLEN CIM1 HOL-LI.
1689	PD01861A	14.06	4.836e-11	60-83	PD01861	PROTEIN NUCLEAR RIBONUCLEOPROTEIN SMALL MRNA RNA.
1691	BL00107A	18.39	6.760e-13	280-310	BL00107	Protein kinases ATP-binding region

SEQ ID NO:	Domain_ID	Score	p-value	Domain_position	Model_ID	Model_Description
						proteins.
1691	BL00107B	13.31	1.000e-14	344-359	BL00107	Protein kinases ATP-binding region proteins.
1691	DM00191A	8.16	4.840e-09	663-675	DM00191	w SPAC8A4.04C RESISTANCE SPAC8A4.05C DAUNORUBICIN.

EXAMPLE 6

Prediction of Signal Peptide Sequences contained in the Polypeptides of the Invention

5

The signal peptide regions for a plurality of the polypeptides of the invention were predicted using the Neural Network SignalP V1.1 program (Nielsen et al, (1997) Int. J. Neural Syst. 8, 581-599 herein incorporated by reference). One of skill in the art will recognize that the actual cleavage site may be different than that predicted by the computer program. The following table depicts the polypeptides of the invention that are predicted to have an N-terminal signal peptide, and lists the output from the SignalP program:

10

TABLE 5

SEQ ID NO:	Max_score	Mean_score	Cleavage_Position
865	0.979	0.879	34
870	0.896	0.685	23
876	0.979	0.854	33
893	0.941	0.838	15
895	0.989	0.619	44
897	0.954	0.805	25
898	0.897	0.486	21
904	0.959	0.826	28
906	0.931	0.729	30
919	0.958	0.608	39
921	0.980	0.932	26
923	0.970	0.872	22
930	0.943	0.602	23
934	0.897	0.678	23
937	0.956	0.597	43
938	0.882	0.547	25
939	0.967	0.532	16
942	0.926	0.509	36
943	0.896	0.540	25
954	0.997	0.951	36
959	0.979	0.751	39
960	0.983	0.637	36
964	0.964	0.819	26
968	0.943	0.645	38
969	0.969	0.597	30
970	0.958	0.821	30
973	0.945	0.587	37
974	0.910	0.623	25
988	0.991	0.971	27

SEQ ID NO:	Max_score	Mean_score	Cleavage_Position
994	0.914	0.628	26
999	0.970	0.659	21
1000	0.958	0.526	49
1004	0.979	0.941	19
1016	0.987	0.926	23
1025	0.894	0.561	28
1030	0.994	0.965	30
1033	0.962	0.865	26
1040	0.941	0.805	32
1041	0.981	0.795	45
1045	0.935	0.833	26
1046	0.962	0.558	46
1051	0.986	0.597	49
1058	0.975	0.901	19
1060	0.933	0.705	17
1062	0.982	0.513	49
1063	0.939	0.545	33
1066	0.945	0.754	47
1067	0.944	0.819	25
1072	0.989	0.673	44
1085	0.974	0.512	49
1087	0.958	0.770	16
1094	0.968	0.571	36
1095	0.968	0.617	42
1096	0.976	0.893	25
1102	0.961	0.933	20
1103	0.932	0.552	19
1114	0.980	0.568	47
1115	0.990	0.815	22
1119	0.985	0.935	21
1130	0.955	0.661	37
1134	0.985	0.614	21
1138	0.975	0.872	34
1140	0.965	0.749	23
1149	0.960	0.775	18
1151	0.991	0.727	34
1155	0.982	0.496	47
1156	0.944	0.794	29
1160	0.947	0.603	47
1162	0.954	0.745	31
1164	0.927	0.651	43
1194	0.948	0.680	27
1201	0.957	0.899	18
1207	0.975	0.935	18
1210	0.977	0.935	26
1211	0.985	0.822	47
1224	0.983	0.904	21
1228	0.951	0.544	47
1238	0.966	0.713	45
1255	0.939	0.495	39
1263	0.991	0.619	46
1266	0.992	0.806	39
1271	0.929	0.666	34
1279	0.966	0.857	20
1280	0.921	0.777	28

SEQ ID NO:	Max_score	Mean_score	Cleavage_Posit ion
1282	0.993	0.927	19
1283	0.995	0.867	22
1286	0.965	0.894	18
1287	0.986	0.935	24
1288	0.979	0.733	32
1291	0.987	0.785	28
1304	0.920	0.712	24
1307	0.927	0.586	45
1308	0.979	0.963	18
1309	0.963	0.840	24
1310	0.967	0.839	22
1314	0.995	0.929	23
1316	0.978	0.873	24
1331	0.975	0.888	19
1332	0.961	0.796	29
1333	0.965	0.873	27
1339	0.910	0.631	25
1342	0.973	0.884	34
1346	0.933	0.725	29
1356	0.975	0.821	34
1365	0.929	0.632	39
1367	0.962	0.919	22
1376	0.955	0.849	33
1384	0.987	0.576	39
1389	0.984	0.889	26
1390	0.980	0.559	36
1395	0.974	0.933	22
1396	0.967	0.941	16
1398	0.943	0.829	24
1402	0.969	0.721	41
1403	0.934	0.815	26
1405	0.920	0.505	22
1409	0.985	0.939	24
1412	0.963	0.878	29
1417	0.957	0.640	35
1418	0.946	0.873	18
1419	0.975	0.645	37
1420	0.976	0.867	24
1421	0.985	0.917	20
1429	0.980	0.908	17
1430	0.910	0.712	28
1431	0.984	0.939	22
1433	0.974	0.908	20
1437	0.966	0.542	38
1438	0.981	0.941	27
1445	0.959	0.771	26
1449	0.988	0.897	18
1452	0.966	0.782	31
1455	0.978	0.944	22
1456	0.950	0.919	19
1458	0.974	0.913	22
1465	0.983	0.957	22
1467	0.977	0.937	20
1471	0.906	0.601	22
1478	0.959	0.491	45

SEQ ID NO:	Max_score	Mean_score	Cleavage_Posit ion
1479	0.968	0.883	24
1480	0.976	0.916	22
1484	0.981	0.897	28
1485	0.972	0.956	17
1488	0.983	0.838	20
1489	0.965	0.869	18
1492	0.914	0.677	17
1495	0.945	0.825	21
1496	0.993	0.975	16
1498	0.957	0.891	19
1500	0.984	0.832	33
1509	0.996	0.921	42
1512	0.977	0.835	16
1515	0.986	0.945	20
1518	0.978	0.885	26
1520	0.996	0.924	22
1527	0.955	0.521	46
1528	0.991	0.502	48
1532	0.989	0.903	17
1533	0.987	0.971	15
1536	0.983	0.956	17
1538	0.978	0.915	25
1539	0.983	0.940	20
1540	0.965	0.799	28
1542	0.981	0.865	26
1545	0.939	0.502	9
1549	0.966	0.902	26
1551	0.990	0.965	16
1552	0.991	0.927	18
1554	0.979	0.895	31
1557	0.963	0.884	24
1559	0.977	0.922	24
1560	0.969	0.901	27
1561	0.980	0.946	25
1565	0.982	0.886	24
1568	0.962	0.801	27
1575	0.984	0.958	18
1576	0.938	0.818	25
1581	0.963	0.887	23
1583	0.970	0.935	13
1585	0.900	0.641	34
1587	0.968	0.902	19
1590	0.981	0.955	20
1592	0.966	0.909	27
1594	0.970	0.931	15
1597	0.977	0.905	23
1613	0.970	0.910	22
1618	0.976	0.840	21
1619	0.982	0.908	31
1622	0.978	0.879	26
1625	0.929	0.805	24
1631	0.991	0.972	16
1633	0.979	0.871	28
1635	0.959	0.816	19
1636	0.918	0.692	13

SEQ ID NO:	Max_score	Mean_score	Cleavage_Posit ion
1643	0.990	0.901	21
1649	0.962	0.921	20
1654	0.979	0.865	31
1663	0.989	0.966	16
1667	0.980	0.916	37
1669	0.953	0.496	34
1670	0.988	0.951	16
1672	0.966	0.913	17
1681	0.927	0.671	20
1685	0.967	0.593	36
1695	0.986	0.919	18
1697	0.898	0.716	24
1702	0.940	0.837	19
1703	0.994	0.620	43

EXAMPLE 7

Prediction of Transmembrane Regions of the Polypeptides of the Invention

Regions of the polypeptides of the invention that cross a cellular lipid bilayer or membrane were predicted using the TMPRED computer program (Hofmann et al. Biol. Chem. Hoppe-Seyler 374,166 hereby incorporated herein by reference). The following table describes the plurality of polypeptides of the invention that contain at least one predicted transmembrane domain:

TABLE 6

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
854	1	2088	115-138:2088
864	6	12660	56-78:2631 150-169:1686 243-258:1737 336-359:1556 379-394:2572 456-473:2478
871	1	1947	434-454:1947
873	4	8479	53-69:2714 136-152:2014 203-220:1906 509-526:1845
875	1	1722	118-138:1722
878	4	7527	68-86:1551 105-123:1875 272-290:1556 340-356:2545
879	6	11423	127-148:1678 281-300:2640 393-412:1662 427-447:1670 543-559:2249

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
			638-653:1524
886	4	8588	104-120:2019 243-267:2346 335-350:2222 401-425:2001
894	3	7997	141-156:3090 167-190:1601 207-226:3306
896	1	2642	44-66:2642
898	1	2578	87-106:2578
908	1	1569	958-974:1569
914	1	3089	502-524:3089
918	1	2577	469-485:2577
919	1	2819	233-254:2819
926	3	6476	161-177:2207 254-270:2180 449-467:2089
929	1	2228	121-136:2228
934	6	12682	172-187:2293 237-258:2056 279-299:1759 329-351:2812 371-386:2117 408-429:1645
937	1	2548	248-264:2548
939	1	2181	93-114:2181
941	2	3480	89-110:1685 135-154:1795
946	1	2450	385-401:2450
957	1	2151	97-117:2151
960	3	5457	598-614:1857 707-724:1544 748-764:2056
968	2	4661	49-71:2672 165-185:1989
969	4	7843	89-105:2039 164-183:2176 224-243:1514 282-299:2114
971	1	2123	100-118:2123
978	1	2143	135-148:2143
979	1	2131	49-66:2131
986	1	1710	128-143:1710
989	1	1979	112-130:1979
997	1	1929	288-303:1929
999	1	3084	178-199:3084
1005	1	3072	73-90:3072
1008	1	3073	641-660:3073
1012	1	2019	910-925:2019
1015	1	3454	396-416:3454
1016	1	3369	581-605:3369
1017	1	1618	644-663:1618
1027	6	13013	80-96:2887

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
			150-169:2073 227-243:2086 307-324:1960 404-419:1773 481-495:2234
1028	1	1790	92-107:1790
1030	1	1710	63-86:1710
1035	1	2506	94-111:2506
1040	1	1561	718-733:1561
1041	4	8350	71-88:1896 291-307:2812 387-406:1755 474-490:1887
1062	1	3368	258-278:3368
1065	1	2643	336-358:2643
1066	1	2406	49-70:2406
1067	1	2700	493-510:2700
1073	2	4203	135-168:2597 200-214:1606
1075	4	6874	50-66:1560 139-155:1995 190-213:1787 291-305:1532
1080	3	7420	116-132:2923 197-212:2709 223-239:1788
1085	1	2097	195-216:2097
1088	1	1996	74-89:1996
1090	7	13484	68-88:2007 105-119:1501 141-159:1687 220-238:2030 296-311:2033 395-410:1727 452-471:2499
1101	1	2000	403-423:2000
1102	1	3504	743-764:3504
1105	1	2219	351-369:2219
1106	6	12120	68-88:2342 128-145:1914 185-206:1521 312-329:2024 365-380:2531 433-448:1788
1111	1	1517	51-68:1517
1113	1	3180	356-380:3180
1116	1	2206	56-75:2206
1124	2	4091	83-111:2452 130-148:1639
1125	1	2998	160-181:2998
1129	1	3163	779-799:3163
1130	1	2744	102-126:2744
1133	1	2029	112-129:2029
1134	1	2206	736-757:2206

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
1140	1	2750	87-99:2750
1142	1	2922	105-123:2922
1148	1	3113	294-316:3113
1164	5	9520	483-502:1826 516-531:1837 584-605:2275 626-642:1515 674-690:2067
1165	6	11860	92-112:2331 121-141:1535 209-230:2031 336-353:1755 389-406:2107 457-472:2101
1166	4	7475	164-179:1986 229-248:2015 254-269:1577 286-306:1897
1168	6	12530	109-122:2345 195-212:1649 344-366:2101 424-439:2493 455-474:2000 476-496:1942
1170	1	2318	349-376:2318
1175	1	1582	90-108:1582
1176	1	1516	742-764:1516
1179	1	2508	135-154:2508
1185	1	1649	58-74:1649
1190	1	2235	296-312:2235
1194	1	2823	44-70:2823
1196	1	2041	187-202:2041
1199	1	3788	99-116:3788
1201	1	1553	551-566:1553
1207	4	8078	134-150:2201 237-258:1652 375-397:2178 484-501:2047
1210	1	2222	118-132:2222
1233	1	1704	49-67:1704
1255	1	2677	84-106:2677
1266	3	7330	59-76:2685 90-108:1580 195-221:3065
1271	2	3771	634-650:1766 691-709:2005
1273	2	4814	85-105:2193 216-241:2621
1280	3	6011	58-74:2642 171-188:1509 228-250:1860
1301	1	1651	112-131:1651
1304	1	1960	187-209:1960
1308	1	2729	212-229:2729

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
1309	1	2154	564-579:2154
1316	1	1634	90-105:1634
1320	1	1847	134-150:1847
1322	2	5403	83-98:2412 160-175:2991
1324	1	2129	128-147:2129
1327	1	1645	115-131:1645
1333	1	2378	122-138:2378
1334	1	2681	52-76:2681
1342	1	1520	365-380:1520
1343	1	2312	139-155:2312
1356	1	2292	101-129:2292
1376	1	1606	606-621:1606
1377	4	8637	100-113:2419 294-313:2702 787-808:1889 985-1001:1627
1379	2	5222	197-218:2416 277-297:2806
1380	1	2398	102-120:2398
1389	4	9882	177-192:3257 235-261:2052 276-291:1761 363-381:2812
1393	2	4456	66-82:2701 110-126:1755
1395	2	3335	263-279:1511 325-342:1824
1400	1	1793	95-113:1793
1402	2	4648	229-245:1641 313-333:3007
1417	2	3802	92-114:2061 152-175:1741
1425	6	13420	59-75:1823 112-127:3392 132-147:1707 180-193:2193 231-246:1810 331-346:2495
1428	1	1923	60-78:1923
1434	1	3041	111-129:3041
1436	2	4541	103-118:2057 295-309:2484
1444	1	1540	257-275:1540
1445	1	2610	199-219:2610
1449	3	6892	143-158:1938 181-198:2860 270-289:2094
1455	1	2481	241-256:2481
1459	5	10350	115-133:2128 183-195:2109 229-245:1520 288-307:2678 356-372:1915

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
1478	1	2281	56-71:2281
1484	1	2689	229-245:2689
1495	1	2478	146-162:2478
1496	2	5761	68-84:2749 144-163:3012
1500	3	6144	81-99:2768 118-132:1551 166-182:1825
1511	1	1528	76-91:1528
1515	1	1775	201-233:1775
1516	1	3335	71-93:3335
1523	3	5593	128-145:1794 348-365:1730 438-455:2069
1556	1	1521	147-166:1521
1559	1	2828	628-650:2828
1565	1	2718	306-332:2718
1567	1	2660	54-72:2660
1574	1	1922	504-519:1922
1575	1	2773	306-332:2773
1576	1	2661	218-239:2661
1583	1	2635	352-369:2635
1587	1	3196	518-538:3196
1589	1	2059	78-99:2059
1593	4	8614	164-178:2254 259-274:2312 325-340:2378 392-410:1670
1594	1	2673	339-357:2673
1616	1	2581	120-136:2581
1618	1	3544	324-344:3544
1619	1	1551	695-711:1551
1622	1	1516	765-780:1516
1635	1	3694	1258-1274:3694
1638	1	1606	105-121:1606
1640	1	4013	2045-2062:4013
1645	1	1722	80-96:1722
1655	1	2392	68-90:2392
1673	8	14475	61-80:1745 129-154:1690 235-251:1560 262-277:1971 350-368:2264 398-415:1642 521-537:1609 559-577:1994
1680	1	2286	145-162:2286
1684	3	6111	131-149:2670 162-176:1558 223-243:1883
1685	1	3127	709-725:3127
1686	4	8443	73-88:2001 114-132:2487

SEQ ID NO:	Number of Predicted Transmembrane Regions	Total Score	Domain Location:Score
			143-168:1531 288-311:2424
1687	1	2972	285-303:2972
1701	1	3206	88-113:3206

5

EXAMPLE 8

Prediction of Chromosomal Location of the Polynucleotides of the Invention

10

Chromosomal location of the polynucleotide sequences of the invention was determined by using the BLASTN algorithm (Altschul et al. Nucleic Acids Res. 25 pp. 3389-3402 herein incorporated by reference). SEQ ID NO: 1 through 852 were aligned to the sequence of the human genome (Version date November 3, 2002 from Genbank) using the BLASTN computer program.

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The chromosomal locations of the aligned human genome sequences were determined through the Genbank accession numbers of the aligned human genome sequences, which enabled retrieval of annotated chromosomal location from the Genbank database. The following table depicts the predicted chromosomal location of the polynucleotides of the invention (SEQ ID NO 1 through 852).

20

TABLE 7

SEQ ID NO:	Chromosomal location
1	11q
2	11q
3	10
4	3
6	16
7	15
8	6
10	5
12	1
13	15
14	7
18	5
19	1
20	14
21	11
22	Xp11.3-11.4
23	11
25	19
26	1

SEQ ID NO:	Chromosomal_location
28	11
29	19
32	9
34	17
35	19
36	3
37	17
38	4
40	4
41	6
43	2
44	19
45	11
46	X
47	1
49	20
50	1
51	5
52	1
53	19
55	19
56	4
57	4
59	11q
60	17
62	10
63	5
64	15
65	16
67	20
68	Xq22.1-23
70	10
71	8
72	21
73	2
75	8
76	3
77	9
78	7
79	19
80	16
81	3
82	5
83	13
84	1p36.11-36.31
85	1p32.1-33
86	1p36.11-36.31
87	8
88	3
89	15
90	6p24.1-25.3
91	1
94	3
95	20
96	17

SEQ ID NO:	Chromosomal_location
97	4
99	19
101	2
103	11q
104	2
105	X
106	19
108	4
109	13q12.11-12.3
110	17
111	12
112	2
113	X
114	3
117	10
118	5
119	16
120	19
121	X
122	1
123	5
124	12
125	1
126	16
127	11q
128	1
129	4
130	9q13-21.2
131	10
132	19
133	10
134	13
135	17
136	11q
137	8
138	2
140	5
141	6
142	1
143	19
144	5
146	3
147	5
148	11
149	7
151	19
152	14
154	16
155	3
156	16
157	9p23-24.3
160	20
162	10
163	1
164	20p11.1-11.23

SEQ ID NO:	Chromosomal_location
165	3
166	5
167	1
168	6
169	14
170	10
171	8
172	11
173	7
174	3
175	2
176	1p36.21-36.33
177	19
180	1q25.1-25.3
181	X
183	4
184	7
185	10
186	19
187	11q
188	10
189	Xp
191	16
192	8
193	2
195	3p
196	1
197	13
198	6q26-27
199	13
201	11
202	4
203	4
204	11
205	5
206	1
207	16
208	3
209	20
210	3
212	11
213	1
214	20
215	8
216	11q
217	11q
218	13
219	3
222	19
223	16
224	20
226	3
227	9q22.1-22.33
228	12
229	6p12.3-21.2

SEQ ID NO:	Chromosomal_location
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233	7
235	1
236	7
237	12
238	14
239	10
240	19
241	22q11.2
242	8
243	1q24
244	17
245	4
246	7
247	17
249	6
250	18
251	1
252	1
253	1
255	Xq23
256	12
258	1
259	22
260	X
261	1p31.2-32.3
263	6
264	3
265	17
266	16
268	10
270	2
271	2
272	9
273	5
274	1
275	9
276	1
277	18
278	21
281	12
282	1
284	5
285	3
286	5
287	12
289	6
290	3
291	10
292	16
293	3
294	1p31.2-32.3
295	4
296	11q
297	9

SEQ ID NO:	Chromosomal_location
298	10
299	19
300	7
302	2
303	1
304	17
305	14
306	6q22.22-23.3
307	11
308	16
310	5
312	19
313	1
314	6
315	19
316	16
317	12
320	6
321	12
322	1
324	15
325	10
326	4
327	11
328	1
329	1q24.1-25.2
330	9
332	6q14.2-16.1
333	19
334	7
335	19
336	5
338	22
339	22
340	1
341	3
342	16
343	9
344	19
345	5
346	20p11.21-11.23
347	Xp11.4-21.2
348	8
349	7
351	17
352	6
354	1
355	2
359	11
361	9
368	11
370	20
374	17
381	9
387	5

SEQ ID NO:	Chromosomal_location
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389	9
391	16
393	1
395	5
396	19
399	2
400	1
407	5
410	3
413	6
415	1
417	5
419	16
420	10
421	6
424	X
429	1
431	9
433	14
434	1
435	1
436	3
437	5
438	7
441	11
445	14
446	10
448	1
449	19
450	X
451	X
455	10
457	Xq25-Xq26
460	14
461	17
463	15
466	3
468	18
471	10
473	11
474	1
477	5
478	3
480	19
488	10
495	5
498	19
500	1
505	9
506	2
507	1
509	8
516	X
520	1

SEQ ID NO:	Chromosomal location
522	1p36.1-36.2
526	1p36.13-36.31
531	5
532	7
533	5
535	5
540	9
545	16
548	12
549	8
557	7
559	4
561	2
562	1p35.1-36.13
563	3
564	3
566	12
570	10
571	3
572	3
573	15
574	13
582	4
585	11
586	1
591	3
592	14
595	1
596	19
597	3
598	11
601	12
604	1
606	11
607	17
609	11
611	17
613	10
618	3
619	16
624	8
627	3p21.3
629	10
631	6
637	3
638	6q16-21
639	11q
641	2
646	11
648	7
651	4
654	4
655	9
656	14
660	X

SEQ ID NO:	Chromosomal_location
663	6
667	6
669	12
670	20p12.1-13
671	11
672	1
676	11
682	20
687	19
689	17
693	2
696	9
699	11
703	15
704	14
705	17
707	1
710	1
714	1
715	21q21.1-q21.2
717	5
718	22
720	9
721	11
725	12q
726	16
727	16
728	11
733	19
737	1
739	19
742	19
746	14
748	3
749	1
752	20
754	6
755	18
756	7
760	19
765	Xq22.1-22.3
766	17
768	1
770	3
771	11
772	10
775	19
776	19
777	14
778	3
782	17
783	1
787	Xq12-13.1
789	17
791	1

SEQ ID NO:	Chromosomal location
793	1
794	3
799	15
800	X
804	19
808	11
809	3
812	19
813	X
814	6
818	4
824	11q
826	15
829	17
830	5
831	11
833	8
834	11
835	22q12.2-13.1
836	18
839	21q22.2

EXAMPLE 9 **Purification of the Polypeptides of the Invention**

5 The polypeptides of the invention can be produced by first cloning the corresponding polynucleotides of the invention into a mammalian expression vector using established protocols that are familiar to those in skill of the art (for example, pCDNA3.1/His A, B, C Catalog Number V385-20 from Invitrogen, Carlsbad, California, herein incorporated by reference). Briefly, polynucleotides of the invention are amplified and isolated via agarose gel electrophoresis and gel excision. The polynucleotides are subsequently cloned into the pCDNA3.1/His A, B, C vectors to facilitate in-frame cloning with a polyhistidine metal-binding tag. The vectors with polynucleotides of the invention inserted can then be transfected into a mammalian cell line like COS-7 for high-level expression of the corresponding polypeptides of the invention.

15 The corresponding polypeptides of the invention that are produced by the transfected mammalian cell line can then be purified according to established protocols that are familiar to those of skill in the art (for example, the Ni-NTA Magnetic Agarose Beads protein purification protocol, Qiagen, Valencia, California, herein incorporated by reference). Briefly, assays utilizing Ni-NTA Magnetic Beads involve capture of the 6xHis-tagged protein — from a cell lysate or a purified-protein solution — followed by washing, binding of interaction partners, further washing, and finally elution of the interacting partner from the still immobilized 6xHis-tagged protein or elution of the

interacting-partner-6xHis-tagged- protein complex. Between each step, the beads are collected by attracting them to the side of the vessel, after placing near a magnet for 30–60 seconds. Purification procedures may even use crude cell extracts for binding of 6xHis-tagged protein.

The resulting purified polypeptides of the invention are then quantified, lyophilized and stored at 4 degrees Celcius or below, and used for standards in diagnostic kits for pre-eclampsia.

Example 10

Production of Specific Antibodies for the Polypeptides of the Invention

Cells expressing any of the polypeptides of the invention are identified using antibodies specific for SEQ ID NO: 853 through 1704. Polyclonal antibodies are produced by DNA vaccination or by injection of peptide antigens into rabbits or other hosts. An animal, such as a rabbit, is immunized with a peptide specific for one of SEQ ID NO: 853 through 1704 conjugated to a carrier protein, such as BSA (bovine serum albumin) or KLH (keyhole limpet hemocyanin). The rabbit is initially immunized with conjugated peptide in complete Freund's adjuvant, followed by a booster shot every two weeks with injections of conjugated peptide in incomplete Freund's adjuvant. Antibodies specific for a polypeptide of the invention are affinity purified from rabbit serum using peptides corresponding to the polypeptides of the invention coupled to Affi-Gel 10 (Bio-Rad), and stored in phosphate-buffered saline with 0.1% sodium azide. To determine that the polyclonal antibodies are specific for a polypeptide of the invention, an expression vector encoding a polypeptide of the invention is introduced into mammalian cells. Western blot analysis of protein extracts of non-transfected cells and the cells containing a polypeptide of the invention is performed using the polyclonal antibody sample as the primary antibody and a horseradish peroxidase-labeled anti-rabbit antibody as the secondary antibody. Detection of a band in the cells containing a polypeptide of the invention and lack thereof in the control cells indicates that the polyclonal antibodies are specific for the polypeptide of the invention in question.

Monoclonal antibodies are produced by injecting mice with a peptide derived from a polypeptide of the invention, with or without adjuvant. Subsequently, the mouse is boosted every 2 weeks until an appropriate immune response has been identified (typically 1-6 months), at which point the spleen is removed. The spleen is minced to release splenocytes, which are fused (in the presence of polyethylene glycol) with murine myeloma cells. The resulting cells (hybridomas) are grown in culture and selected for antibody production by clonal selection. The antibodies are secreted into the culture supernatant, facilitating the screening process, such as screening by an enzyme-linked immunosorbent assay (ELISA). Alternatively, humanized monoclonal antibodies are produced either by engineering a chimeric murine/human monoclonal antibody in which the murine-specific antibody regions are replaced by the human counterparts and produced in mammalian cells, or by using transgenic “knock out” mice in which the native antibody genes have been replaced by human antibody genes and immunizing the transgenic mice as described above.

EXAMPLE 11

Determination of mRNA Expression of the Polynucleotides of the Invention in Normal and Pre-eclampic Placental Tissues

Relative gene expression, at the mRNA level, across multiple placental tissues was measured using a real-time PCR system. This system consisted of a GeneAmp 5700 Sequence Detection System (Applied Biosystems) and GeneAmp 5700 SDS software (Applied Biosystems). The reaction mixture consists of SYBR Green PCR MasterMix (Applied Biosystems), oligos specific to one gene, and DEPC treated water. 20 ng mRNA equivalent cDNA (synthesized using MMLV RT enzyme from Invitrogen) is added to each reaction mixture. The samples are run on the GeneAmp 5700 Sequencing Detection System with a 30 second extension time and are analyzed at a fluorescence threshold of 0.5. Each cDNA is also run against an appropriate Housekeeping Gene Control that is used for normalization.

The real-time PCR protocol was performed on both SEQ ID NO: 357 and 551. After this analysis was performed, the relative expression ratios of the two polynucleotides of the invention were determined across a selection of placental tissues. The raw cycle count scores for each gene in the measured tissues were selected, with each score representing the number of doublings required to detect the message. Next, the inverse expression ratios were computed for each gene in each measured tissue using the following formula:

(2 raised to the power of the SEQ ID NO 347 raw cycle count score) divided by (2 raised to the power of the SEQ ID NO 551 raw cycle count score)

5 Finally, the computed ratios for each measured tissue were plotted on a log 10 scale as shown in Figure 1 of the drawings. The following table relates the X-axis labels of Figure 1 to the respective placental tissue source information.

10 TABLE 8

Label on X-axis for Figure 1	Detailed Tissue Source Information
10.1. PE BP	23 weeks of pregnancy, severe pre-eclampsia, basal-plate region
1.1 PE BP	23 weeks of pregnancy, severe pre-eclampsia, basal-plate region
7.1 PE BP	24 weeks of pregnancy, severe pre-eclampsia, basal-plate region
4.1 PE BP	29 weeks of pregnancy, severe pre-eclampsia, basal-plate region
5.1 PE BP	32 weeks of pregnancy, severe pre-eclampsia, basal-plate region
11.1 PE BP	38 weeks of pregnancy, pre-eclampsia, basal-plate region
ECL003 NP BP	34 weeks of pregnancy, non-pre-eclamptic placenta, basal-plate region
9.1 NP BP	39 weeks of pregnancy, non-pre-eclamptic placenta, basal-plate region
8.1 NP BP	40 weeks of pregnancy, non-pre-eclamptic placenta, basal-plate region
6.3 NP BP	41 weeks of pregnancy, non-pre-eclamptic placenta, basal-plate region
13.1 NP BP	39 weeks of pregnancy, elective Caesarian section, non-pre-eclamptic placenta, basal-plate region

15

EXAMPLE 12

Diagnostic Kit for Polypeptides of the Invention

A diagnostic kit can be made in order to determine the levels of selected polypeptides of the invention that are present in tissue samples obtained from a patient who is undergoing pregnancy. Such tissue samples may be from blood plasma, blood serum, amniotic fluid, or urine.

The components of the kit can be as follows: 1) one or more standards comprised of one or more polypeptides of the invention, prepared as described in example 9; 2) an antibody or a plurality of antibodies that are specific for the polypeptides of the invention that are being tested by the kit, prepared as described in example 10; 3) written instructions; 4) diluents for tissue samples and the standards; 5) a wash buffer; 6) color reagents; 7) stop solution; and 8) a microplate with bound antibody.

An example of such a kit is an ELISA (enzyme-linked immunosorbent assay) quantification that determines the concentration or concentrations of a polypeptide or polypeptides of the invention. The principle of the assay is to use the quantitative sandwich enzyme immunoassay technique where a Polyclonal antibody selective for binding a polypeptide of the invention is pre-coated onto a microplate into its wells. The standards and sample are then pipetted into the wells and any of the polypeptide of the invention that is present is bound to this immobilized Polyclonal antibody. Next, the wells are washed with washing buffer, and an enzyme-linked Polyclonal antibody that is specific for the polypeptide of the invention is added to the wells. Washing again is performed, then a substrate solution is added to the wells. Color subsequently develops in proportion to the amount of polypeptide of the invention that is bound in the first step. The color development is stopped using a stop solution, and the intensity of the color is measured by a microplate reader.

This results of this assay are used to determine one or more concentration levels of the polypeptides of the invention. The assay reaction is performed in the same tube or well, or may be in separate tubes or wells. The level or levels of polypeptides of the invention that are being determined by this assay can be used to diagnose those patients with pre-eclampsia.

EXAMPLE 13

Diagnostic Chip for Polypeptides of the Invention in Tissue Samples

The levels of polypeptides of the invention in biological tissue samples can be determined through the use of ProteinChip technology (Wright Jr., et al. Expert Review of Molecular Diagnostics 2002, Vol. 2 pp.549-63 hereby incorporated herein by reference). This process includes the addition of a few microliters of tissue sample onto the ProteinChip surface, which has both chemical (e.g., anionic, cationic, hydrophobic, hydrophilic, metal) and biochemical (antibody, receptor, DNA, enzyme probes attached to its surface. Subsequently, binding occurs between the polypeptides of the invention and their respective probes, and the chip is washed at least three times in order to elute unbound protein, lipids, salts, and other substances. Next, an energy-absorbent

molecule (EAM) such as sinapinic acid is added to the chip, and the chip is placed into a ProteinChip Reader which measures the molecular mass of the bound polypeptides. Peaks are subsequently produced from the ProteinChip Reader that are used to quantify the amount of polypeptides of the invention in the tissue sample